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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:19:14 : Search time 56.7539 Seconds
(without alignments)
2920.093 Million cell updates/sec

Title: US-09-925-576C-6

Perfect score: 2854
Sequence: 1 AAPFNGTMMQYFEWYLPDDG.....TRPWGTGEFVWTEPRLVAMP 515

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PCF_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
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- 14: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
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- 16: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2854	100.0	515	9	US-09-854-346-6
2	2854	100.0	515	9	US-09-918-543-6
3	2854	100.0	515	10	US-09-925-576C-6
4	2854	100.0	515	14	US-10-146-327-8
5	2854	100.0	515	16	US-10-477-725-6
6	2854	100.0	549	14	US-10-184-771-6
7	2847	99.8	514	12	US-10-644-187-6
8	2847	99.8	514	14	US-10-186-042-6
9	2836	99.4	549	14	US-10-081-872-104
10	2836	99.4	549	15	US-10-385-305-104
11	2832	99.2	549	14	US-10-081-872-92
12	2832	99.2	549	15	US-10-385-305-92
13	2787	97.7	515	9	US-09-795-211-4
14	2780	97.4	514	9	US-09-769-864-3
15	2780	97.4	514	9	US-09-902-188A-3

16	2780	97.4	514	12	US-10-665-667-3	Sequence 3, Appl1
17	2780	97.4	514	12	US-10-025-648-3	Sequence 3, Appl1
18	2780	97.4	514	12	US-10-327-837-3	Sequence 3, Appl1
19	2456	86.1	550	14	US-10-081-872-106	Sequence 106, App
20	2456	86.1	550	15	US-10-385-305-106	Sequence 106, App
21	2426	85.0	472	14	US-10-081-872-88	Sequence 88, Appl
22	2426	85.0	472	14	US-10-105-733-7	Sequence 7, Appl1
23	2426	85.0	472	14	US-10-081-739A-7	Sequence 7, Appl1
24	2426	85.0	472	15	US-10-385-305-88	Sequence 88, Appl
25	2414	84.6	546	15	US-10-081-872-134	Sequence 134, App
26	2414	84.6	546	15	US-10-385-305-134	Sequence 134, App
27	2410	84.4	615	14	US-10-081-872-128	Sequence 128, App
28	2410	84.4	615	15	US-10-385-305-128	Sequence 128, App
29	2410	84.4	644	14	US-10-081-872-136	Sequence 136, App
30	2410	84.4	644	15	US-10-385-305-136	Sequence 136, App
31	2402	84.2	564	14	US-10-081-872-120	Sequence 120, App
32	2402	84.2	564	15	US-10-385-305-120	Sequence 120, App
33	1910.5	66.9	516	9	US-09-986-676A-2	Sequence 2, Appl1
34	1910.5	66.9	516	16	US-10-399-161-8	Sequence 8, Appl1
35	1910.5	66.9	516	9	US-09-769-864-1	Sequence 1, Appl1
36	1909.5	66.9	485	9	US-09-769-864-7	Sequence 7, Appl1
37	1909.5	66.9	485	9	US-09-854-346-2	Sequence 2, Appl1
38	1909.5	66.9	485	9	US-09-902-188A-1	Sequence 1, Appl1
39	1909.5	66.9	485	9	US-09-918-543-2	Sequence 2, Appl1
40	1909.5	66.9	485	9	US-09-925-576C-2	Sequence 1, Appl1
41	1909.5	66.9	485	10	US-09-925-576C-2	Sequence 2, Appl1
42	1909.5	66.9	485	12	US-10-665-667-1	Sequence 1, Appl1
43	1909.5	66.9	485	12	US-10-665-667-7	Sequence 7, Appl1
44	1909.5	66.9	485	12	US-10-025-648-1	Sequence 1, Appl1
45	1909.5	66.9	485	12	US-10-025-648-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-854-346-6
Sequence 6, Application US/09854346
Patent No. US20020068352A1
GENERAL INFORMATION:
APPLICANT: No. US20020068352A1ozymes A/S
APPLICANT: Svendsen, Allan
APPLICANT: Jorgensen, Christel Thea
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OR INVENTION: Alpha-amylase variants with altered 1,6 activity
FILE REFERENCE: 6140-200-US
CURRENT APPLICATION NUMBER: US/09/854,346
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 515
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-09-854-346-6

Query Match 100.0%, Score 2854, DB 9, Length 515;
Best Local Similarity 100.0%, Pred. No. 1.8e-256;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAPFNGTMMQYFEWYLPDDGTLMTKVANEANNSSLSGTLALMPAYKGRSRVGGVY	60
DB	1	AAPFNGTMMQYFEWYLPDDGTLMTKVANEANNSSLSGTLALMPAYKGRSRVGGVY	60
QY	61	DLYDLGFNGKGTIVRTKYGTGAQYLOAIQAHAAGMWYADVVDHKGADGTEWDAVE	120
DB	61	DLYDLGFNGKGTIVRTKYGTGAQYLOAIQAHAAGMWYADVVDHKGADGTEWDAVE	120
QY	121	VNSDRNQELISGTQYLOAATKPPFGKNTYSSSKRWYHFDGVDMDRESRLSLITYFERG	180
DB	121	VNSDRNQELISGTQYLOAATKPPFGKNTYSSSKRWYHFDGVDMDRESRLSLITYFERG	180
QY	181	IGKAWDEVTENGNDYLYATADLMDHPVETELKNWGWYVNTNIDGFRDLAVGHK	240

Db 181 IKGAMDEVDTEANGVNDYLMYADLMDHBEVVTTELKNMGKMYVNTTNDGFRLLDAVKHIX 240
QY 241 FSEFPDMLSYVRSQSGKPLFTVGEYWSYDINGLAHYITKTDSGMSLFPAPLHNKFTYASK 300
Db 241 FSEFPDMLSYVRSQSGKPLFTVGEYWSYDINGLAHYITKTDSGMSLFPAPLHNKFTYASK 300
QY 301 SGGAPEMRLMTNMTLMKDOPTLAFTVFNHDEPQALQSWDPMFKPLAFAFILLTROEG 360
Db 301 SGGAPEMRLMTNMTLMKDOPTLAFTVFNHDEPQALQSWDPMFKPLAFAFILLTROEG 360
QY 361 YPCVFGDYGGIPOYNIPSLKSKIDPLLIARRDYAVGTQHDYLDHSDIIGWTRREGTEKP 420
Db 361 YPCVFGDYGGIPOYNIPSLKSKIDPLLIARRDYAVGTQHDYLDHSDIIGWTRREGTEKP 420
QY 421 GSGLAALITDGPGGSKMYVKGQAHGKVFYDLTGNRSDVTIINSDGWGEFKNVNGGSVSW 480
Db 421 GSGLAALITDGPGGSKMYVKGQAHGKVFYDLTGNRSDVTIINSDGWGEFKNVNGGSVSW 480
QY 481 VPRKTTVSTIARPIITTRPMTGFEFVWTEPRLVAMP 515
Db 481 VPRKTTVSTIARPIITTRPMTGFEFVWTEPRLVAMP 515

RESULT 2
US-09-918-543-6
; Sequence 6, Application US/09918543
; Patent No. US20020155574A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020155574A1ozymes N/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kjaerulff, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fuglsang, Claus Croone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062.200-US
; CURRENT APPLICATION NUMBER: US/09/918.543
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 515
; TYPE: PRF
; ORGANISM: Bacillus stearothermophilus
US-09-918-543-6

Query Match 100.0%; Score 2854; DB 9; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.8e-256;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEWYLPDDGTLMTKVANBANNNLSIGITLMLPRAVKGTSRSDVGYY 60
Db 1 AAFNGTMMQYFEWYLPDDGTLMTKVANBANNNLSIGITLMLPRAVKGTSRSDVGYY 60
QY 61 DLYDLGEFNQKGVTRKTKGTAKOYLQALQAAHAAQOVYADVDFDHKGADGETWDAVE 120
Db 61 DLYDLGEFNQKGVTRKTKGTAKOYLQALQAAHAAQOVYADVDFDHKGADGETWDAVE 120
QY 121 VNSPDNNGEISGYOIQAWTKDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
Db 121 VNSPDNNGEISGYOIQAWTKDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
QY 181 IKGAMDEVDTEANGVNDYLMYADLMDHBEVVTTELKNMGKMYVNTTNDGFRLLDAVKHIX 240
Db 181 IKGAMDEVDTEANGVNDYLMYADLMDHBEVVTTELKNMGKMYVNTTNDGFRLLDAVKHIX 240
QY 241 FSEFPDMLSYVRSQSGKPLFTVGEYWSYDINGLAHYITKTDSGMSLFPAPLHNKFTYASK 300
Db 241 FSEFPDMLSYVRSQSGKPLFTVGEYWSYDINGLAHYITKTDSGMSLFPAPLHNKFTYASK 300
QY 301 SGGAPEMRLMTNMTLMKDOPTLAFTVFNHDEPQALQSWDPMFKPLAFAFILLTROEG 360
Db 301 SGGAPEMRLMTNMTLMKDOPTLAFTVFNHDEPQALQSWDPMFKPLAFAFILLTROEG 360

QY 361 YPCVFGDYGGIPOYNIPSLKSKIDPLLIARRDYAVGTQHDYLDHSDIIGWTRREGTEKP 420
Db 361 YPCVFGDYGGIPOYNIPSLKSKIDPLLIARRDYAVGTQHDYLDHSDIIGWTRREGTEKP 420
QY 421 GSGLAALITDGPGGSKMYVKGQAHGKVFYDLTGNRSDVTIINSDGWGEFKNVNGGSVSW 480
Db 421 GSGLAALITDGPGGSKMYVKGQAHGKVFYDLTGNRSDVTIINSDGWGEFKNVNGGSVSW 480
QY 481 VPRKTTVSTIARPIITTRPMTGFEFVWTEPRLVAMP 515
Db 481 VPRKTTVSTIARPIITTRPMTGFEFVWTEPRLVAMP 515

RESULT 3
US-09-925-576C-6
; Sequence 6, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925.576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 515
; TYPE: PRF
; ORGANISM: Bacillus stearothermophilus
US-09-925-576C-6

Query Match 100.0%; Score 2854; DB 10; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.8e-256;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEWYLPDDGTLMTKVANBANNNLSIGITLMLPRAVKGTSRSDVGYY 60
Db 1 AAFNGTMMQYFEWYLPDDGTLMTKVANBANNNLSIGITLMLPRAVKGTSRSDVGYY 60
QY 61 DLYDLGEFNQKGVTRKTKGTAKOYLQALQAAHAAQOVYADVDFDHKGADGETWDAVE 120
Db 61 DLYDLGEFNQKGVTRKTKGTAKOYLQALQAAHAAQOVYADVDFDHKGADGETWDAVE 120
QY 121 VNSPDNNGEISGYOIQAWTKDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
Db 121 VNSPDNNGEISGYOIQAWTKDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
QY 181 IKGAMDEVDTEANGVNDYLMYADLMDHBEVVTTELKNMGKMYVNTTNDGFRLLDAVKHIX 240
Db 181 IKGAMDEVDTEANGVNDYLMYADLMDHBEVVTTELKNMGKMYVNTTNDGFRLLDAVKHIX 240
QY 241 FSEFPDMLSYVRSQSGKPLFTVGEYWSYDINGLAHYITKTDSGMSLFPAPLHNKFTYASK 300
Db 241 FSEFPDMLSYVRSQSGKPLFTVGEYWSYDINGLAHYITKTDSGMSLFPAPLHNKFTYASK 300
QY 301 SGGAPEMRLMTNMTLMKDOPTLAFTVFNHDEPQALQSWDPMFKPLAFAFILLTROEG 360
Db 301 SGGAPEMRLMTNMTLMKDOPTLAFTVFNHDEPQALQSWDPMFKPLAFAFILLTROEG 360
QY 361 YPCVFGDYGGIPOYNIPSLKSKIDPLLIARRDYAVGTQHDYLDHSDIIGWTRREGTEKP 420
Db 361 YPCVFGDYGGIPOYNIPSLKSKIDPLLIARRDYAVGTQHDYLDHSDIIGWTRREGTEKP 420
QY 421 GSGLAALITDGPGGSKMYVKGQAHGKVFYDLTGNRSDVTIINSDGWGEFKNVNGGSVSW 480
Db 421 GSGLAALITDGPGGSKMYVKGQAHGKVFYDLTGNRSDVTIINSDGWGEFKNVNGGSVSW 480
QY 481 VPRKTTVSTIARPIITTRPMTGFEFVWTEPRLVAMP 515
Db 481 VPRKTTVSTIARPIITTRPMTGFEFVWTEPRLVAMP 515

RESULT 4
US-10-146-327-8
; Sequence 8, Application US/10146327
; Publication No. US20030044954A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/10/146.327
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/537.168
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PA 1999 00437
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/127,427
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 515
; TYPE: PRF
; ORGANISM: Bacillus stearothermophilus
US-10-146-327-8

Query Match 100.0%; Score 2854; DB 14; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.8e-256;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAFNGTMOYFEMWLPDDGTLMTKVNANNNLSIGITLMLPPAYKTSRSDVGYV 60
Db 1 AAFNGTMOYFEMWLPDDGTLMTKVNANNNLSIGITLMLPPAYKTSRSDVGYV 60
Qy 61 DLYDLGFNKGTVRTYKGTQAQYLOAIQAHAAGMAYADVDFDHGAGDTEWVAVE 120
Db 61 DLYDLGFNKGTVRTYKGTQAQYLOAIQAHAAGMAYADVDFDHGAGDTEWVAVE 120
Qy 121 VNSDRNOEISGTQIOAWTKFDPGNGNTYSSFKMWHFDDGMDKSLSTIYFRG 180
Db 121 VNSDRNOEISGTQIOAWTKFDPGNGNTYSSFKMWHFDDGMDKSLSTIYFRG 180
Qy 181 IGAAMDVEVTENGNDYLYADLMDHPEVTELKMGKMYVNTNIDGFRIDAVAHIK 240
Db 181 IGAAMDVEVTENGNDYLYADLMDHPEVTELKMGKMYVNTNIDGFRIDAVAHIK 240
Qy 241 FSPFPDWLSYRSQTKPLFTVGEYMSYDINKLHNYITKTGTMSLFDAPLHNFYASK 300
Db 241 FSPFPDWLSYRSQTKPLFTVGEYMSYDINKLHNYITKTGTMSLFDAPLHNFYASK 300
Qy 301 SGCAFMDRTMTNTLMDQPTLAVTFVDNHDTEBGOALQSWVDWPFPLAFAFLTRQEG 360
Db 301 SGCAFMDRTMTNTLMDQPTLAVTFVDNHDTEBGOALQSWVDWPFPLAFAFLTRQEG 360
Qy 361 YPCVFYGDYIGIPOYNIPLSKSKIDPLIARRDYAGTQHDYLDHSDIIGTREGTEKP 420
Db 361 YPCVFYGDYIGIPOYNIPLSKSKIDPLIARRDYAGTQHDYLDHSDIIGTREGTEKP 420
Qy 421 GSGIAALITDGPSSKMYVKGQAHAKVFDLTGNRSDVTYINSDGGEFKNVGSYSVW 480
Db 421 GSGIAALITDGPSSKMYVKGQAHAKVFDLTGNRSDVTYINSDGGEFKNVGSYSVW 480
Qy 481 VPKRTVSTIARPTTTPMTGEFRTWTEPRVLVAMP 515
Db 481 VPKRTVSTIARPTTTPMTGEFRTWTEPRVLVAMP 515

RESULT 5
US-10-477-725-6

; Sequence 6, Application US/10477725
; Publication No. US20040096952A1
; GENERAL INFORMATION:
; APPLICANT: NOVOTYMS A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Thisted, Thomas
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: Alpha-amylase variant with altered properties
; FILE REFERENCE: 10162.204-US
; CURRENT APPLICATION NUMBER: US/10/477.725
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 515
; TYPE: PRF
; ORGANISM: Bacillus stearothermophilus
US-10-477-725-6

Query Match 100.0%; Score 2854; DB 16; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.8e-256;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAFNGTMOYFEMWLPDDGTLMTKVNANNNLSIGITLMLPPAYKTSRSDVGYV 60
Db 1 AAFNGTMOYFEMWLPDDGTLMTKVNANNNLSIGITLMLPPAYKTSRSDVGYV 60
Qy 61 DLYDLGFNKGTVRTYKGTQAQYLOAIQAHAAGMAYADVDFDHGAGDTEWVAVE 120
Db 61 DLYDLGFNKGTVRTYKGTQAQYLOAIQAHAAGMAYADVDFDHGAGDTEWVAVE 120
Qy 121 VNSDRNOEISGTQIOAWTKFDPGNGNTYSSFKMWHFDDGMDKSLSTIYFRG 180
Db 121 VNSDRNOEISGTQIOAWTKFDPGNGNTYSSFKMWHFDDGMDKSLSTIYFRG 180
Qy 181 IGAAMDVEVTENGNDYLYADLMDHPEVTELKMGKMYVNTNIDGFRIDAVAHIK 240
Db 181 IGAAMDVEVTENGNDYLYADLMDHPEVTELKMGKMYVNTNIDGFRIDAVAHIK 240
Qy 241 FSPFPDWLSYRSQTKPLFTVGEYMSYDINKLHNYITKTGTMSLFDAPLHNFYASK 300
Db 241 FSPFPDWLSYRSQTKPLFTVGEYMSYDINKLHNYITKTGTMSLFDAPLHNFYASK 300
Qy 301 SGCAFMDRTMTNTLMDQPTLAVTFVDNHDTEBGOALQSWVDWPFPLAFAFLTRQEG 360
Db 301 SGCAFMDRTMTNTLMDQPTLAVTFVDNHDTEBGOALQSWVDWPFPLAFAFLTRQEG 360
Qy 361 YPCVFYGDYIGIPOYNIPLSKSKIDPLIARRDYAGTQHDYLDHSDIIGTREGTEKP 420
Db 361 YPCVFYGDYIGIPOYNIPLSKSKIDPLIARRDYAGTQHDYLDHSDIIGTREGTEKP 420
Qy 421 GSGIAALITDGPSSKMYVKGQAHAKVFDLTGNRSDVTYINSDGGEFKNVGSYSVW 480
Db 421 GSGIAALITDGPSSKMYVKGQAHAKVFDLTGNRSDVTYINSDGGEFKNVGSYSVW 480
Qy 481 VPKRTVSTIARPTTTPMTGEFRTWTEPRVLVAMP 515
Db 481 VPKRTVSTIARPTTTPMTGEFRTWTEPRVLVAMP 515

RESULT 6
US-10-184-771-6
; Sequence 6, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184.771
; CURRENT FILING DATE: 2002-06-28

;; PRIOR APPLICATION NUMBER: US/09/636,252
;; PRIOR FILING DATE: 2000-08-10
;; PRIOR APPLICATION NUMBER: 08/683,838
;; PRIOR FILING DATE: 1996-07-18
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 6
;; LENGTH: 549
;; TYPE: PRF
;; ORGANISM: B. stearothermophilus
US-10-184-771-6

Query Match 100.0%; Score 2854; DB 14; Length 549;
Best Local Similarity 100.0%; Pred. No. 2e-256;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFPGTMMQYFEWYLPDDGTLMTKVAANEANNSLSLGTALMLPPAYKTSRSDVGYGVY 60
DB 35 AAFPGTMMQYFEWYLPDDGTLMTKVAANEANNSLSLGTALMLPPAYKTSRSDVGYGVY 94
QY 61 DLYDLGFNOKGTVRTKTKQAQYLOAIQAHAAGMAYADVDFDHKGADGTEWDAVE 120
DB 95 DLYDLGFNOKGTVRTKTKQAQYLOAIQAHAAGMAYADVDFDHKGADGTEWDAVE 154
QY 121 VNPSDRNOEISGTYYQIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTYYQIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 214
QY 181 IGRAMDVEVDTENGYDLYMAYADLMDHPEVYTELKNMGKMYVNTNIDGRDLDAVHKIK 240
DB 215 IGRAMDVEVDTENGYDLYMAYADLMDHPEVYTELKNMGKMYVNTNIDGRDLDAVHKIK 274
QY 241 FSPFPDMLSYRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLHNFYTAASK 300
DB 275 FSPFPDMLSYRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLHNFYTAASK 334
QY 301 SGGAFDMRTLMTNLTMLKQDPTLAFTVDNHDTEPGALQSWVDPWFKPLAVALILTRQEG 360
DB 335 SGGAFDMRTLMTNLTMLKQDPTLAFTVDNHDTEPGALQSWVDPWFKPLAVALILTRQEG 394
QY 361 YPCVFGDYGYGIPOYNIPLSKSIDPILLARRDYAGTGHYLDHSDIIGWTRREGTEKRP 420
DB 395 YPCVFGDYGYGIPOYNIPLSKSIDPILLARRDYAGTGHYLDHSDIIGWTRREGTEKRP 454
QY 421 GSGLAALITDPPGSGKMYYVKGQAHAKVFDLTGNRSDVTYIINSDMGGEFKVNGGSVSW 480
DB 455 GSGLAALITDPPGSGKMYYVKGQAHAKVFDLTGNRSDVTYIINSDMGGEFKVNGGSVSW 514
QY 481 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAMP 515
DB 515 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAMP 549

RESULT 7
US-10-644-187-6

;; Sequence 6, Application US/10644187
;; Publication No. US20040048351A1
;; GENERAL INFORMATION:
;; APPLICANT: Svendsen, Allan
;; APPLICANT: Borchert, Torben
;; APPLICANT: Bisgaard-Frantzen, Henrik
;; TITLE OF INVENTION: Alpha-Amylase Mutants
;; FILE REFERENCE: 4796.204-US
;; CURRENT APPLICATION NUMBER: US/10/644,187
;; CURRENT FILING DATE: 2003-08-20
;; PRIOR APPLICATION NUMBER: 09/182,859
;; PRIOR FILING DATE: 1998-10-29
;; PRIOR APPLICATION NUMBER: 0515/96
;; PRIOR FILING DATE: 1996-04-30
;; PRIOR APPLICATION NUMBER: 0712/96
;; PRIOR FILING DATE: 1996-06-28
;; PRIOR APPLICATION NUMBER: 0775/96
;; PRIOR FILING DATE: 1996-07-11

;; PRIOR APPLICATION NUMBER: 1263/96
;; PRIOR FILING DATE: 1996-11-08
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 6
;; LENGTH: 514
;; TYPE: PRF
;; ORGANISM: Bacillus stearothermophilus
US-10-644-187-6

Query Match 99.8%; Score 2847; DB 12; Length 514;
Best Local Similarity 100.0%; Pred. No. 8.1e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFPGTMMQYFEWYLPDDGTLMTKVAANEANNSLSLGTALMLPPAYKTSRSDVGYGVY 60
DB 1 AAFPGTMMQYFEWYLPDDGTLMTKVAANEANNSLSLGTALMLPPAYKTSRSDVGYGVY 60
QY 61 DLYDLGFNOKGTVRTKTKQAQYLOAIQAHAAGMAYADVDFDHKGADGTEWDAVE 120
DB 61 DLYDLGFNOKGTVRTKTKQAQYLOAIQAHAAGMAYADVDFDHKGADGTEWDAVE 120
QY 121 VNPSDRNOEISGTYYQIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
DB 121 VNPSDRNOEISGTYYQIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
QY 181 IGRAMDVEVDTENGYDLYMAYADLMDHPEVYTELKNMGKMYVNTNIDGRDLDAVHKIK 240
DB 181 IGRAMDVEVDTENGYDLYMAYADLMDHPEVYTELKNMGKMYVNTNIDGRDLDAVHKIK 240
QY 241 FSPFPDMLSYRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLHNFYTAASK 300
DB 241 FSPFPDMLSYRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLHNFYTAASK 300
QY 301 SGGAFDMRTLMTNLTMLKQDPTLAFTVDNHDTEPGALQSWVDPWFKPLAVALILTRQEG 360
DB 301 SGGAFDMRTLMTNLTMLKQDPTLAFTVDNHDTEPGALQSWVDPWFKPLAVALILTRQEG 360
QY 361 YPCVFGDYGYGIPOYNIPLSKSIDPILLARRDYAGTGHYLDHSDIIGWTRREGTEKRP 420
DB 361 YPCVFGDYGYGIPOYNIPLSKSIDPILLARRDYAGTGHYLDHSDIIGWTRREGTEKRP 420
QY 421 GSGLAALITDPPGSGKMYYVKGQAHAKVFDLTGNRSDVTYIINSDMGGEFKVNGGSVSW 480
DB 421 GSGLAALITDPPGSGKMYYVKGQAHAKVFDLTGNRSDVTYIINSDMGGEFKVNGGSVSW 480
QY 481 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAMP 514
DB 481 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAMP 514

RESULT 8
US-10-186-042-6

;; Sequence 6, Application US/10186042
;; Publication No. US20030171236A1
;; GENERAL INFORMATION:
;; APPLICANT: Svendsen, Allan
;; APPLICANT: Borchert, Torben
;; APPLICANT: Bisgaard-Frantzen, Henrik
;; TITLE OF INVENTION: Alpha-Amylase Mutants
;; FILE REFERENCE: 4796.204-US
;; CURRENT APPLICATION NUMBER: US/10/186,042
;; CURRENT FILING DATE: 2002-06-28
;; PRIOR APPLICATION NUMBER: 09/672,459
;; PRIOR FILING DATE: 2000-09-28
;; PRIOR APPLICATION NUMBER: 09/182,859
;; PRIOR FILING DATE: 1998-10-29
;; PRIOR APPLICATION NUMBER: 0515/96
;; PRIOR FILING DATE: 1996-04-30
;; PRIOR APPLICATION NUMBER: 0712/96
;; PRIOR FILING DATE: 1996-06-28
;; PRIOR APPLICATION NUMBER: 0775/96
;; PRIOR FILING DATE: 1996-07-11

;; PRIOR APPLICATION NUMBER: 1263/96
;; PRIOR FILING DATE: 1996-11-08
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 6
;; LENGTH: 514
;; TYPE: PRS
;; ORGANISM: Bacillus stearothermophilus
US-10-186-042-6

Query Match 99.8%; Score 2847; DB 14; Length 514;
Best Local Similarity 100.0%; Pred. No. 8.1e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AAPPNGMOMYFEMYLPPDGLTMTKVNANNNISLIGITLMLPPAYKGRSRSDVGVY 60
DB 1 AAPPNGMOMYFEMYLPPDGLTMTKVNANNNISLIGITLMLPPAYKGRSRSDVGVY 60
QY 61 DLYDLSEFNKGIVRTKYGKAYLQAIQAHAAGMADVAVFPHKGADGTEWDAVE 120
DB 61 DLYDLSEFNKGIVRTKYGKAYLQAIQAHAAGMADVAVFPHKGADGTEWDAVE 120
QY 121 VNPSDRNOBISGTYQIQAWTKFDPGSGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
DB 121 VNPSDRNOBISGTYQIQAWTKFDPGSGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
QY 181 IGRAMDMEVTEENGNDYLYADLMDHPEVTELEKMGKMYNTTNIIDGFRDVAVGHK 240
DB 181 IGRAMDMEVTEENGNDYLYADLMDHPEVTELEKMGKMYNTTNIIDGFRDVAVGHK 240
QY 241 FSPFPDMLSYRSQTKPLFTVGEWYSYDINKLHNTTKTDGTMSLPDAPLHNFYASK 300
DB 241 FSPFPDMLSYRSQTKPLFTVGEWYSYDINKLHNTTKTDGTMSLPDAPLHNFYASK 300
QY 301 SGGA FDMRTIMTNTLMKQPTLAVTFVNDHTEPGALQSWDPWFKPLAVALITRQEG 360
DB 301 SGGA FDMRTIMTNTLMKQPTLAVTFVNDHTEPGALQSWDPWFKPLAVALITRQEG 360
QY 361 YPCVFGDYDGIGIQYNIPSLKSKIDPLLIARROYAYGTQHDYLDHSIIGMTREGGTEKP 420
DB 361 YPCVFGDYDGIGIQYNIPSLKSKIDPLLIARROYAYGTQHDYLDHSIIGMTREGGTEKP 420
QY 421 GSGLAALITDGPSSKMYVKGQAGKVFYDLTGNRSDDYTTNSDNGEFGKNGSSVW 480
DB 421 GSGLAALITDGPSSKMYVKGQAGKVFYDLTGNRSDDYTTNSDNGEFGKNGSSVW 480
QY 481 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAM 514
DB 481 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAM 514
```

RESULT 9
US-10-081-872-104
;; Sequence 104, Application US/10081872
;; Publication No. US20030125534A1
;; GENERAL INFORMATION:
;; APPLICANT: Callen, Walter
;; APPLICANT: Richardson, Toby
;; APPLICANT: Frey, Gerhard
;; APPLICANT: Short, Jay M.
;; APPLICANT: Mathur, Eric J.
;; APPLICANT: Gray, Kevin A.
;; APPLICANT: Kerovo, Janne S.
;; APPLICANT: Slupka, Malgorzata
;; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
;; FILE REFERENCE: 09010-108001
;; CURRENT APPLICATION NUMBER: US/10/081,872
;; CURRENT FILING DATE: 2002-02-21
;; PRIOR APPLICATION NUMBER: US 60/270,495
;; PRIOR FILING DATE: 2001-02-21
;; PRIOR APPLICATION NUMBER: US 60/270,496
;; PRIOR FILING DATE: 2001-02-21

;; PRIOR APPLICATION NUMBER: US 60/291,122
;; PRIOR FILING DATE: 2001-05-14
;; NUMBER OF SEQ ID NOS: 321
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 104
;; LENGTH: 549
;; TYPE: PRS
;; ORGANISM: Environmental
US-10-081-872-104

Query Match 99.4%; Score 2836; DB 14; Length 549;
Best Local Similarity 99.4%; Pred. No. 9.4e-255;
Matches 512; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 AAPPNGMOMYFEMYLPPDGLTMTKVNANNNISLIGITLMLPPAYKGRSRSDVGVY 60
DB 35 AAPPNGMOMYFEMYLPPDGLTMTKVNANNNISLIGITLMLPPAYKGRSRSDVGVY 94
QY 61 DLYDLSEFNKGIVRTKYGKAYLQAIQAHAAGMADVAVFPHKGADGTEWDAVE 120
DB 95 DLYDLSEFNKGIVRTKYGKAYLQAIQAHAAGMADVAVFPHKGADGTEWDAVE 154
QY 121 VNPSDRNOBISGTYQIQAWTKFDPGSGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
DB 155 VNPSDRNOBISGTYQIQAWTKFDPGSGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 214
QY 181 IGRAMDMEVTEENGNDYLYADLMDHPEVTELEKMGKMYNTTNIIDGFRDVAVGHK 240
DB 215 IGRAMDMEVTEENGNDYLYADLMDHPEVTELEKMGKMYNTTNIIDGFRDVAVGHK 274
QY 241 FSPFPDMLSYRSQTKPLFTVGEWYSYDINKLHNTTKTDGTMSLPDAPLHNFYASK 300
DB 275 FSPFPDMLSYRSQTKPLFTVGEWYSYDINKLHNTTKTDGTMSLPDAPLHNFYASK 334
QY 301 SGGA FDMRTIMTNTLMKQPTLAVTFVNDHTEPGALQSWDPWFKPLAVALITRQEG 360
DB 335 SGGA FDMRTIMTNTLMKQPTLAVTFVNDHTEPGALQSWDPWFKPLAVALITRQEG 394
QY 361 YPCVFGDYDGIGIQYNIPSLKSKIDPLLIARROYAYGTQHDYLDHSIIGMTREGGTEKP 420
DB 395 YPCVFGDYDGIGIQYNIPSLKSKIDPLLIARROYAYGTQHDYLDHSIIGMTREGGTEKP 454
QY 421 GSGLAALITDGPSSKMYVKGQAGKVFYDLTGNRSDDYTTNSDNGEFGKNGSSVW 480
DB 455 GSGLAALITDGPSSKMYVKGQAGKVFYDLTGNRSDDYTTNSDNGEFGKNGSSVW 514
QY 481 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAM 515
DB 515 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAM 549
```

RESULT 10
US-10-385-305-104
;; Sequence 104, Application US/10385305
;; Publication No. US20040018607A1
;; GENERAL INFORMATION:
;; APPLICANT: Callen, Walter
;; APPLICANT: Richardson, Toby
;; APPLICANT: Frey, Gerhard
;; APPLICANT: Short, Jay M.
;; APPLICANT: Mathur, Eric J.
;; APPLICANT: Gray, Kevin A.
;; APPLICANT: Kerovo, Janne S.
;; APPLICANT: Slupka, Malgorzata
;; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
;; FILE REFERENCE: 09010-108001
;; CURRENT APPLICATION NUMBER: US/10/385,305
;; CURRENT FILING DATE: 2003-03-06
;; PRIOR APPLICATION NUMBER: US/10/081,872
;; PRIOR FILING DATE: 2002-02-21
;; PRIOR APPLICATION NUMBER: US 60/270,495
;; PRIOR FILING DATE: 2001-02-21

;; PRIOR APPLICATION NUMBER: US 60/270,496
;; PRIOR FILING DATE: 2001-02-21
;; PRIOR APPLICATION NUMBER: US 60/291,122
;; PRIOR FILING DATE: 2001-05-14
;; NUMBER OF SEQ ID NOS: 321
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 104
;; LENGTH: 549
;; TYPE: PRF
;; ORGANISM: Environmental
US-10-385-305-104

Query Match 99.4%; Score 2836; DB 15; Length 549;
Best Local Similarity 99.4%; Pred. No. 9.4e-255;
Matches 512; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 AAFNGTMMQYFEMYLPPDGLTMTKVAANEANLSSIGITLMLPPAYKGTSRSDVGCVY 60
DB 35 AAFNGTMMQYFEMYLPPDGLTMTKVAANEANLSSIGITLMLPPAYKGTSRSDVGCVY 94
QY 61 DLYDLGEFNOKGIVRTKTKGKAOYLQALQAAHAAQMOTYADVFDHKGADGTEWDAYE 120
DB 95 DLYDLGEFNOKGIVRTKTKGKAOYLQALQAAHAAQMOTYADVFDHKGADGTEWDAYE 154
QY 121 VNPSDRNOEISGTYYQIQAMTKFDPGRGNTYSSFKRWYHFDGVDMDESRKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTYYQIQAMTKFDPGRGNTYSSFKRWYHFDGVDMDESRKLSRIYKFRG 214
QY 181 IGRAMDVEVTENGENYDYLMTADLMDHPEVYTELKMGKMYVNTNIDGFRDLDAVGHK 240
DB 215 IGRAMDVEVTENGENYDYLMTADLMDHPEVYTELKMGKMYVNTNIDGFRDLDAVGHK 274
QY 241 FSFPFDMLSYRSQTKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLNHKFTYASK 300
DB 275 FSFPFDMLSYRSQTKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLNHKFTYASK 334
QY 301 SGGAFDMRTMTNTLTKMDQPTLAVTFVDNHDPGQALQSWDPMFKPLAAYAFILTRQEG 360
DB 335 SGGAFDMRTMTNTLTKMDQPTLAVTFVDNHDPGQALQSWDPMFKPLAAYAFILTRQEG 394
QY 361 YPCVFYGDYGIPOYNIPLSKSKIDPLIARBYAGTQHDYLDHSDIIGWTRREGTEKRP 420
DB 395 YPCVFYGDYGIPOYNIPLSKSKIDPLIARBYAGTQHDYLDHSDIIGWTRREGTEKRP 454
QY 421 GSGLAALITDGPGGSKMYVYKQAHGKVFYDLGNRSDTVITNSDGMGEFKNVNGSVSW 480
DB 455 GSGLAALITDGPGGSKMYVYKQAHGKVFYDLGNRSDTVITNSDGMGEFKNVNGSVSW 514
QY 481 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515
DB 515 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAMP 549
```

RESULT 11
US-10-081-872-92
;; Sequence 92, Application US/10081872
;; Publication No. US20030125534A1
;; GENERAL INFORMATION:
;; APPLICANT: Callen, Walter
;; APPLICANT: Richardson, Toby
;; APPLICANT: Frey, Gerhard
;; APPLICANT: Short, Jay M.
;; APPLICANT: Mathur, Eric J.
;; APPLICANT: Gray, Kevin A.
;; APPLICANT: Kervuo, Janne S.
;; APPLICANT: Slupeka, Malgorzata
;; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
;; FILE REFERENCE: 09010-108001
;; CURRENT APPLICATION NUMBER: US/10/081,872
;; PRIOR FILING DATE: 2002-02-21
;; PRIOR APPLICATION NUMBER: US 60/270,495
;; PRIOR FILING DATE: 2001-02-21

;; PRIOR APPLICATION NUMBER: US 60/270,496
;; PRIOR FILING DATE: 2001-02-21
;; PRIOR APPLICATION NUMBER: US 60/291,122
;; PRIOR FILING DATE: 2001-05-14
;; NUMBER OF SEQ ID NOS: 321
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 92
;; LENGTH: 549
;; TYPE: PRF
;; ORGANISM: Bacterial
US-10-081-872-92

Query Match 99.2%; Score 2832; DB 14; Length 549;
Best Local Similarity 99.4%; Pred. No. 2.2e-254;
Matches 512; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 AAFNGTMMQYFEMYLPPDGLTMTKVAANEANLSSIGITLMLPPAYKGTSRSDVGCVY 60
DB 35 AAFNGTMMQYFEMYLPPDGLTMTKVAANEANLSSIGITLMLPPAYKGTSRSDVGCVY 94
QY 61 DLYDLGEFNOKGIVRTKTKGKAOYLQALQAAHAAQMOTYADVFDHKGADGTEWDAYE 120
DB 95 DLYDLGEFNOKGIVRTKTKGKAOYLQALQAAHAAQMOTYADVFDHKGADGTEWDAYE 154
QY 121 VNPSDRNOEISGTYYQIQAMTKFDPGRGNTYSSFKRWYHFDGVDMDESRKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTYYQIQAMTKFDPGRGNTYSSFKRWYHFDGVDMDESRKLSRIYKFRG 214
QY 181 IGRAMDVEVTENGENYDYLMTADLMDHPEVYTELKMGKMYVNTNIDGFRDLDAVGHK 240
DB 215 IGRAMDVEVTENGENYDYLMTADLMDHPEVYTELKMGKMYVNTNIDGFRDLDAVGHK 274
QY 241 FSFPFDMLSYRSQTKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLNHKFTYASK 300
DB 275 FSFPFDMLSYRSQTKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLNHKFTYASK 334
QY 301 SGGAFDMRTMTNTLTKMDQPTLAVTFVDNHDPGQALQSWDPMFKPLAAYAFILTRQEG 360
DB 335 SGGAFDMRTMTNTLTKMDQPTLAVTFVDNHDPGQALQSWDPMFKPLAAYAFILTRQEG 394
QY 361 YPCVFYGDYGIPOYNIPLSKSKIDPLIARBYAGTQHDYLDHSDIIGWTRREGTEKRP 420
DB 395 YPCVFYGDYGIPOYNIPLSKSKIDPLIARBYAGTQHDYLDHSDIIGWTRREGTEKRP 454
QY 421 GSGLAALITDGPGGSKMYVYKQAHGKVFYDLGNRSDTVITNSDGMGEFKNVNGSVSW 480
DB 455 GSGLAALITDGPGGSKMYVYKQAHGKVFYDLGNRSDTVITNSDGMGEFKNVNGSVSW 514
QY 481 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515
DB 515 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAMP 549
```

RESULT 12
US-10-385-305-92
;; Sequence 92, Application US/10385305
;; Publication No. US20040018607A1
;; GENERAL INFORMATION:
;; APPLICANT: Callen, Walter
;; APPLICANT: Richardson, Toby
;; APPLICANT: Frey, Gerhard
;; APPLICANT: Short, Jay M.
;; APPLICANT: Mathur, Eric J.
;; APPLICANT: Gray, Kevin A.
;; APPLICANT: Kervuo, Janne S.
;; APPLICANT: Slupeka, Malgorzata
;; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
;; FILE REFERENCE: 09010-108001
;; CURRENT APPLICATION NUMBER: US/10/385,305
;; PRIOR FILING DATE: 2003-03-06
;; PRIOR APPLICATION NUMBER: US/10/081,872
;; PRIOR FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: US 60/270,495
 ; PRIOR FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: US 60/270,496
 ; PRIOR FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: US 60/291,122
 ; PRIOR FILING DATE: 2001-05-14
 ; NUMBER OF SEQ ID NOS: 321
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 92
 ; LENGTH: 549
 ; TYPE: PR1
 ; ORGANISM: Bacterial
 ; US-10-385-305-92

Query Match 99.2%; Score 2832; DB 15; Length 549;
 Best Local Similarity 99.4%; Pred. No. 2,2e-254;
 Matches 512; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAFNGTMQYFEMWLPDDGTLMTKVNANNNLSLIGITLMLPAPYKGTSRSDVGYGY 60
 DB 35 AAFNGTMQYFEMWLPDDGTLMTKVNANNNLSLIGITLMLPAPYKGTSRSDVGYGY 94
 QY 61 DLYDLGFNKGAVRTKYGKAYLOAIQAHAAGMADVADVDFDHKGADGTEWDAVE 120
 DB 95 DLYDLGFNKGAVRTKYGKAYLOAIQAHAAGMADVADVDFDHKGADGTEWDAVE 154
 QY 121 VNPSDRNOEISGTQIOAWTKFDPGKGNYSFKRMWYHFDGVDMSRKLSTIYKFRG 180
 DB 155 VNPSDRNOEISGTQIOAWTKFDPGKGNYSFKRMWYHFDGVDMSRKLSTIYKFRG 214
 QY 181 IGRAMPDEVDTENGNDYLYADLMDHPEVTELEKMGKMYVNTNIDGFRLDVAGHIK 240
 DB 215 IGRAMPDEVDTENGNDYLYADLMDHPEVTELEKMGKMYVNTNIDGFRLDVAGHIK 274
 QY 241 FSEFPDWLSYRSQTKPFLTVGEYSYDINKLHNYITKTDGWSLFDAPLANKFYTASK 300
 DB 275 FSEFPDWLSYRSQTKPFLTVGEYSYDINKLHNYITKTDGWSLFDAPLANKFYTASK 334
 QY 301 SGGA FDMRTMTNTLMKDQPLAVTFVNDHTEPGQALQSWDPWFEPFLVAFILITROEG 360
 DB 335 SGGA FDMRTMTNTLMKDQPLAVTFVNDHTEPGQALQSWDPWFEPFLVAFILITROEG 394
 QY 361 YPCVFYGDYIGIPOYNIPLSKSIDPILARRDAYTOHDYLDHSDIIGTREGTEKXP 420
 DB 395 YPCVFYGDYIGIPOYNIPLSKSIDPILARRDAYTOHDYLDHSDIIGTREGTEKXP 454
 QY 421 GSGIAALITDGPSSKMYVKGQAHGKVFYDLTGNRS DVTYINS DGMGEFVNGGSVSW 480
 DB 455 GSGIAALITDGPSSKMYVKGQAHGKVFYDLTGNRS DVTYINS DGMGEFVNGGSVSW 514
 QY 481 VPKRTVSTIARPIITRPWTGEPFRWTEPRLVAMP 515
 DB 515 VPKRTVSTIARPIITRPWTGEPFRWTEPRLVAMP 549

RESULT 13
 US-09-795-211-4
 ; Sequence 4, Application US/09795211
 ; Publication No. US20020183226A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Procter & Gamble Company
 ; APPLICANT: Kaesturi, Chandrika
 ; APPLICANT: Wandersat, Mark E.
 ; APPLICANT: Song, Brian X.
 ; TITLE OF INVENTION: LIQUID DETERGENT COMPOSITION EXHIBITING ENHANCED a-AMYLASE ENZY
 ; FILE REFERENCE: Detergent Composition
 ; CURRENT APPLICATION NUMBER: US/09/795,211
 ; CURRENT FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 515

; TYPE: PR1
 ; ORGANISM: alkaliphilicbaciillus
 ; US-09-795-211-4

Query Match 97.7%; Score 2787; DB 9; Length 515;
 Best Local Similarity 98.1%; Pred. No. 3.1e-250;
 Matches 505; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAFNGTMQYFEMWLPDDGTLMTKVNANNNLSLIGITLMLPAPYKGTSRSDVGYGY 60
 DB 1 AAFNGTMQYFEMWLPDDGTLMTKVNANNNLSLIGITLMLPAPYKGTSRSDVGYGY 60
 QY 61 DLYDLGFNKGAVRTKYGKAYLOAIQAHAAGMADVADVDFDHKGADGTEWDAVE 120
 DB 61 DLYDLGFNKGAVRTKYGKAYLOAIQAHAAGMADVADVDFDHKGADGTEWDAVE 120
 QY 121 VNPSDRNOEISGTQIOAWTKFDPGKGNYSFKRMWYHFDGVDMSRKLSTIYKFRG 180
 DB 121 VNPSDRNOEISGTQIOAWTKFDPGKGNYSFKRMWYHFDGVDMSRKLSTIYKFRG 180
 QY 181 IGRAMPDEVDTENGNDYLYADLMDHPEVTELEKMGKMYVNTNIDGFRLDVAGHIK 240
 DB 181 IGRAMPDEVDTENGNDYLYADLMDHPEVTELEKMGKMYVNTNIDGFRLDVAGHIK 240
 QY 241 FSEFPDWLSYRSQTKPFLTVGEYSYDINKLHNYITKTDGWSLFDAPLANKFYTASK 300
 DB 241 FSEFPDWLSYRSQTKPFLTVGEYSYDINKLHNYITKTDGWSLFDAPLANKFYTASK 300
 QY 301 SGGA FDMRTMTNTLMKDQPLAVTFVNDHTEPGQALQSWDPWFEPFLVAFILITROEG 360
 DB 301 SGGA FDMRTMTNTLMKDQPLAVTFVNDHTEPGQALQSWDPWFEPFLVAFILITROEG 360
 QY 361 YPCVFYGDYIGIPOYNIPLSKSIDPILARRDAYTOHDYLDHSDIIGTREGTEKXP 420
 DB 361 YPCVFYGDYIGIPOYNIPLSKSIDPILARRDAYTOHDYLDHSDIIGTREGTEKXP 420
 QY 421 GSGIAALITDGPSSKMYVKGQAHGKVFYDLTGNRS DVTYINS DGMGEFVNGGSVSW 480
 DB 421 GSGIAALITDGPSSKMYVKGQAHGKVFYDLTGNRS DVTYINS DGMGEFVNGGSVSW 480
 QY 481 VPKRTVSTIARPIITRPWTGEPFRWTEPRLVAMP 515
 DB 481 VPKRTVSTIARPIITRPWTGEPFRWTEPRLVAMP 515

RESULT 14
 US-09-769-864-3
 ; Sequence 3, Application US/09769864
 ; Patent No. US20010039253A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Borchert, Torben V.
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Nielsen, Bjarne
 ; APPLICANT: Nissen, Torben L.
 ; APPLICANT: Kjaerulf, Soren
 ; TITLE OF INVENTION: Alpha-Amylase Mutants
 ; FILE REFERENCE: 5368.200-US
 ; CURRENT APPLICATION NUMBER: US/09/769,864
 ; CURRENT FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 09/183,412
 ; PRIOR FILING DATE: 1998-10-30
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 514
 ; TYPE: PR1
 ; ORGANISM: Bacillus stearothermophilus
 ; US-09-769-864-3
 Query Match 97.4%; Score 2780; DB 9; Length 514;
 Best Local Similarity 98.1%; Pred. No. 1.4e-249;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITALMLPPAYKTSRSDVGYY 60
 DB 1 AAFNGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITALMLPPAYKTSRSDVGYY 60
 QY 61 DLYDLGFENQKGYRTKTKYKAQYLOAIQAHAAGQYADVFDHKGADGTEWDAVE 120
 DB 61 DLYDLGFENQKGYRTKTKYKAQYLOAIQAHAAGQYADVFDHKGADGTEWDAVE 120
 QY 121 VNPSDRNOEISGTQYIOAMTKFDPGKNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
 DB 121 VNPSDRNOEISGTQYIOAMTKFDPGKNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
 QY 181 IGRAMDMEVDTEGNGYDIYADLMDHPEVYTELKNGKMYVNTNIDGFRDLDAVHKIK 240
 DB 181 IGRAMDMEVDTEGNGYDIYADLMDHPEVYTELKNGKMYVNTNIDGFRDLDAVHKIK 240
 QY 241 FSPFPDMLSVRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGTMSLPDAPLHNFYTASK 300
 DB 241 FSPFPDMLSVRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGTMSLPDAPLHNFYTASK 300
 QY 301 SGGAFFDMKTLMTNTLMKOPTLAATFVNDHTEPGQALQSWDVPWFKPLAFAFILTROEG 360
 DB 301 SGGAFFDMKTLMTNTLMKOPTLAATFVNDHTEPGQALQSWDVPWFKPLAFAFILTROEG 360
 QY 361 YPCVFYGDYGIPOYNIPSLKSIDPLLIARRDYAGTQHDYLDHSDIIGWTRREGTEKP 420
 DB 361 YPCVFYGDYGIPOYNIPSLKSIDPLLIARRDYAGTQHDYLDHSDIIGWTRREGTEKP 420
 QY 421 GSGLAALITDGPGSKMYVVKQAKGVFDLTGNRSPTVTINSDGWGEFKNVNGSVSW 480
 DB 421 GSGLAALITDGPGSKMYVVKQAKGVFDLTGNRSPTVTINSDGWGEFKNVNGSVSW 480
 QY 481 VPRKTVSTIARPIITRRPWTGEFVRWTEPRLVAM 514
 DB 481 VPRKTVSTIARPIITRRPWTGEFVRWTEPRLVAM 514

RESULT 15

US-09-902-188A-3
 Sequence 3, Application US/09902188A
 Patent No. US2002009896A1
 GENERAL INFORMATION:
 APPLICANT: Bisgaard-Frantzen, Henrik
 Svendsen, Allan
 TITLE OF INVENTION: Amylase Variants
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. US2002009896A1o No. US2002009896A1disk of No. US2002009896A1
 STREET: 405 Lexington Avenue, Suite 6400
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/902,188A
 FILING DATE: 10-Jul-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/354,191
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4318, 204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 867 0123

TELEFAX: 212 867 0298
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 514 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-902-188A-3

Query Match 97.4%; Score 2780; DB 9; Length 514;
 Best Local Similarity 98.1%; Pred. No. 1,4e-249;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITALMLPPAYKTSRSDVGYY 60
 DB 1 AAFNGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITALMLPPAYKTSRSDVGYY 60
 QY 61 DLYDLGFENQKGYRTKTKYKAQYLOAIQAHAAGQYADVFDHKGADGTEWDAVE 120
 DB 61 DLYDLGFENQKGYRTKTKYKAQYLOAIQAHAAGQYADVFDHKGADGTEWDAVE 120
 QY 121 VNPSDRNOEISGTQYIOAMTKFDPGKNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
 DB 121 VNPSDRNOEISGTQYIOAMTKFDPGKNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
 QY 181 IGRAMDMEVDTEGNGYDIYADLMDHPEVYTELKNGKMYVNTNIDGFRDLDAVHKIK 240
 DB 181 IGRAMDMEVDTEGNGYDIYADLMDHPEVYTELKNGKMYVNTNIDGFRDLDAVHKIK 240
 QY 241 FSPFPDMLSVRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGTMSLPDAPLHNFYTASK 300
 DB 241 FSPFPDMLSVRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGTMSLPDAPLHNFYTASK 300
 QY 301 SGGAFFDMKTLMTNTLMKOPTLAATFVNDHTEPGQALQSWDVPWFKPLAFAFILTROEG 360
 DB 301 SGGAFFDMKTLMTNTLMKOPTLAATFVNDHTEPGQALQSWDVPWFKPLAFAFILTROEG 360
 QY 361 YPCVFYGDYGIPOYNIPSLKSIDPLLIARRDYAGTQHDYLDHSDIIGWTRREGTEKP 420
 DB 361 YPCVFYGDYGIPOYNIPSLKSIDPLLIARRDYAGTQHDYLDHSDIIGWTRREGTEKP 420
 QY 421 GSGLAALITDGPGSKMYVVKQAKGVFDLTGNRSPTVTINSDGWGEFKNVNGSVSW 480
 DB 421 GSGLAALITDGPGSKMYVVKQAKGVFDLTGNRSPTVTINSDGWGEFKNVNGSVSW 480
 QY 481 VPRKTVSTIARPIITRRPWTGEFVRWTEPRLVAM 514
 DB 481 VPRKTVSTIARPIITRRPWTGEFVRWTEPRLVAM 514

Search completed: October 7, 2004, 00:57:27
 Job time: 57.7539 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 58.3101 Seconds
(without alignments)
2340.424 Million cell updates/sec

Title: US-09-925-576C-8
Perfect score: 2666
Sequence: 1 ANINGTLMOQFEWYMPNDQ.....SEGWGEFVNGSIVYQR 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2666	100.0	483	2	AAR72447
2	2666	100.0	483	2	AAR78267
3	2666	100.0	483	2	AAW31404
4	2666	100.0	483	2	AAV15418
5	2666	100.0	483	2	AAV29852
6	2666	100.0	483	2	AAV07384
7	2666	100.0	483	2	AAV99605
8	2666	100.0	483	3	AAV97545
9	2666	100.0	483	5	ABB06936
10	2666	100.0	483	5	AAU12152
11	2666	100.0	483	5	AAE26534
12	2666	100.0	483	5	AAU47853
13	2666	100.0	483	5	ABB76589
14	2666	100.0	531	2	AAR98007
15	2666	100.0	630	2	AAW22523
16	2666	100.0	630	2	AAW23603
17	2663	99.9	483	2	AAV57985
18	2663	99.9	483	2	AAV88438
19	2663	99.9	483	2	AAV81475
20	2663	99.9	483	2	AAV14498
21	2663	99.9	483	2	AAV39742
22	2663	99.9	483	4	AAV65876
23	2663	99.9	487	2	AAV57987
24	2663	99.9	487	2	AAW80189
25	2663	99.9	487	4	AAV65881

26	2663	99.9	512	1	AAV70753	AAV70753
27	2663	99.9	512	2	AAV73509	AAV73509
28	2663	99.9	512	2	AAV00769	AAV00769
29	2663	99.9	512	4	AAV07097	AAV07097
30	2663	99.9	512	4	AAV65875	AAV65875
31	2663	99.9	512	4	AAV65877	AAV65877
32	2661	99.8	483	5	AAU12165	AAU12165
33	2661	99.8	483	5	AAU12161	AAU12161
34	2660	99.8	483	2	AAV58000	AAV58000
35	2660	99.8	483	2	AAV58002	AAV58002
36	2660	99.8	483	2	AAV57992	AAV57992
37	2660	99.8	483	2	AAV80192	AAV80192
38	2660	99.8	483	5	AAU12162	AAU12162
39	2660	99.8	483	5	AAU12163	AAU12163
40	2660	99.8	483	2	AAV80215	AAV80215
41	2660	99.8	487	2	AAV80191	AAV80191
42	2660	99.8	487	2	AAV57437	AAV57437
43	2660	99.7	483	2	AAV10576	AAV10576
44	2659	99.7	483	2	AAV58007	AAV58007
45	2659	99.7	483	2	AAV58007	AAV58007

ALIGNMENTS

RESULT 1	AAV72447	standard; protein; 483 AA.
ID	AAV72447	
XX	AAV72447	
AC	AAV72447	
XX	25-MAR-2003 (revised)	
DT	01-DEC-1995 (first entry)	
DT	01-DEC-1995	
XX	Bacillus licheniformis alpha amylase (mature protein).	
DE	Bacillus licheniformis alpha amylase (mature protein).	
XX	Alpha amylase; variant; enzyme; detergent; additive; dishwashing;	
KW	washing; Bacillus licheniformis; Bacillus amyloliquefaciens;	
KW	Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;	
KW	thermostable.	
XX	Bacillus licheniformis.	
OS	Bacillus licheniformis.	
XX	WO9510603-A1.	
PN	WO9510603-A1.	
XX	20-APR-1995.	
PD	20-APR-1995.	
XX	05-OCT-1994; 94MO-DK000370.	
PF	05-OCT-1994; 94MO-DK000370.	
XX	08-OCT-1993; 93DK-00001133.	
PR	02-FEB-1994; 94DK-00000140.	
XX	(NOVO) NOVO-NORDISK AS.	
PA	(NOVO) NOVO-NORDISK AS.	
XX	Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;	
PI	Van Der Zee P;	
XX	WPI; 1995-161790/21.	
DR	N-PSDB; AA088066.	
XX	New Bacillus derived alpha-amylase variants - having amino acid	
PT	modifications to improve washing and/or dishwashing performance.	
XX	Claim 6; Page 72; 105pp; English.	
PS	Variant alpha amylase enzymes which have improved washing and/or as	
XX	detergent additives. The enzymes have one or more amino acid residues	
CC	added, deleted or substituted. The variants can also be used for textile	
CC	desizing prior to scouring, bleaching and dyeing. The variants have	
CC	improved thermostability, acid/alkaline stability; low temperature	
CC	optimum; pH optimum; higher hydrolysis velocity and improved tolerance	
CC	to other composition constituents, e.g. oxidation agents. (Updated on 25-MAR	
CC	-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)	

XX Sequence 483 AA;
SQ
Query Match 100.0%; Score 2666; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 1,7e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASAYLAHGITAVWIPPAVKGTSQADVGYAYD 60
DB 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASAYLAHGITAVWIPPAVKGTSQADVGYAYD 60
QY 61 LYDGEFHQKGTVRTKTKYGTGELQSAIKSLHSRDINVGDVVNNHKGADATEDVAVEV 120
DB 61 LYDGEFHQKGTVRTKTKYGTGELQSAIKSLHSRDINVGDVVNNHKGADATEDVAVEV 120
QY 121 DPADRNRVISGEHLIKAMTHFHPGSGTSDPKMWHYFDGTDWDESRKLNRIYKFOGK 180
DB 121 DPADRNRVISGEHLIKAMTHFHPGSGTSDPKMWHYFDGTDWDESRKLNRIYKFOGK 180
QY 181 AMDWEVSENGNVDYLMADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVKHKFSF 240
DB 181 AMDWEVSENGNVDYLMADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVKHKFSF 240
QY 241 LRDVNNHVRKTKGEMFTVAEYQNDLGALENTYLNKTNFNHSVFDVPLHYQFHAASDQGG 300
DB 241 LRDVNNHVRKTKGEMFTVAEYQNDLGALENTYLNKTNFNHSVFDVPLHYQFHAASDQGG 300
QY 301 GYDMRKILNGTVVSKPLKSVTFVDNHDTPQGSLSTVQWPKPLAVAFILTRBSGYPO 360
DB 301 GYDMRKILNGTVVSKPLKSVTFVDNHDTPQGSLSTVQWPKPLAVAFILTRBSGYPO 360
QY 361 VFYGDWYGTGDSQREIPALKHKIEPIILKARKQYAGAOHDYFDHHDIVGWTREGDSSVA 420
DB 361 VFYGDWYGTGDSQREIPALKHKIEPIILKARKQYAGAOHDYFDHHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSSEGGEFHVNGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSSEGGEFHVNGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483
RESULT 2
ID AAR78267 standard; protein; 483 AA.
XX AAR78267;
XX 17-JAN-1996 (first entry)
DT
XX Bacillus licheniformis alpha amylase (mature protein).
DE
XX
XX Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch;
KM thermostable; methionine; Bacillus licheniformis;
KM Bacillus amyloliquefaciens; Bacillus stearothermophilus.
XX
OS Bacillus licheniformis.
XX
XX WO9521247-A1.
XX
XX PD 10-AUG-1995.
XX
XX PF 05-OCT-1994; 94WO-DK000371.
XX
XX PR 02-FEB-1994; 94DK-00000141.
XX
XX PA (NOVO) NOVO-NORDISK AS.
XX
XX PI Toft AH, Marcher D, Pedersen HH, Nilsson TE;
XX WPI; 1995-283767/37.
DR

DR N-PSDB; AAQ95031.
XX
XX Use of an oxidation stable alpha amylase - for simultaneous desizing and
PT bleaching or scouring of fabrics contg. starch or starch derivs.
XX
XX Claim 6; Page 22; 37pp; English.
XX
XX Oxidation stable alpha amylases can be used for the simultaneous desizing
CC and bleaching or scouring of a fabric comprising starch or starch
CC derivatives. They exhibit a better heat stability, especially in the
CC presence of oxidising agents. They are obtained from a parent alpha
CC amylase by replacing one or more methionine residues with any amino acid
CC different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or
CC Asp. The parent alpha amylase is derived from a Bacillus species. This is
CC the wild type (unmodified) alpha amylase
XX
XX Sequence 483 AA;
SQ
Query Match 100.0%; Score 2666; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 1,7e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASAYLAHGITAVWIPPAVKGTSQADVGYAYD 60
DB 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASAYLAHGITAVWIPPAVKGTSQADVGYAYD 60
QY 61 LYDGEFHQKGTVRTKTKYGTGELQSAIKSLHSRDINVGDVVNNHKGADATEDVAVEV 120
DB 61 LYDGEFHQKGTVRTKTKYGTGELQSAIKSLHSRDINVGDVVNNHKGADATEDVAVEV 120
QY 121 DPADRNRVISGEHLIKAMTHFHPGSGTSDPKMWHYFDGTDWDESRKLNRIYKFOGK 180
DB 121 DPADRNRVISGEHLIKAMTHFHPGSGTSDPKMWHYFDGTDWDESRKLNRIYKFOGK 180
QY 181 AMDWEVSENGNVDYLMADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVKHKFSF 240
DB 181 AMDWEVSENGNVDYLMADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVKHKFSF 240
QY 241 LRDVNNHVRKTKGEMFTVAEYQNDLGALENTYLNKTNFNHSVFDVPLHYQFHAASDQGG 300
DB 241 LRDVNNHVRKTKGEMFTVAEYQNDLGALENTYLNKTNFNHSVFDVPLHYQFHAASDQGG 300
QY 301 GYDMRKILNGTVVSKPLKSVTFVDNHDTPQGSLSTVQWPKPLAVAFILTRBSGYPO 360
DB 301 GYDMRKILNGTVVSKPLKSVTFVDNHDTPQGSLSTVQWPKPLAVAFILTRBSGYPO 360
QY 361 VFYGDWYGTGDSQREIPALKHKIEPIILKARKQYAGAOHDYFDHHDIVGWTREGDSSVA 420
DB 361 VFYGDWYGTGDSQREIPALKHKIEPIILKARKQYAGAOHDYFDHHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSSEGGEFHVNGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSSEGGEFHVNGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483
RESULT 3
ID AAW31404 standard; protein; 483 AA.
XX AAW31404;
XX
XX 17-OCT-2003 (revised)
DT
XX 11-MAY-1996 (first entry)
DT
XX
XX Bacillus licheniformis Termamyl alpha-amylase.
XX
XX Termamyl; alpha-amylase; enzyme engineering; protein engineering; starch;
KM liquefaction; saccharification; sweetener; textile desizing;
KM detergent additive.
DR

XX OS *Bacillus licheniformis*; strain ATCC 27811.
 XX PN MO9741213-A1.
 XX PD 06-NOV-1997.
 XX PF 30-APR-1997; 97WO-DK000197.
 XX PR 30-APR-1996; 96DK-00000515.
 XX PR 28-JUN-1996; 96DK-00000712.
 XX PR 11-JUL-1996; 96DK-00000775.
 XX PR 08-NOV-1996; 96DK-00001263.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Svendsen A, Borchert TV, Bisgaard-Frantzen H;
 XX DR WPI; 1997-549718/50.
 XX DR N-PSDB; AAV02471.
 XX PT Termamyl-like alpha-amylase variants with improved properties - e.g.
 XX PT increased stability at low pH and low calcium, useful as detergent
 XX PT additives and in industrial starch processing e.g. liquefaction.
 XX PS Claim 1; Page 82; 101pp; English.
 CC This protein comprises Termamyl alpha-amylase (see AAW31404) of *Bacillus*
 CC *licheniformis* ATCC 27811. The invention relates to novel variants
 CC (mutants) of Termamyl-like alpha-amylases that have alpha-amylase
 CC activity and exhibit an alteration in at least one property selected
 CC from: substrate specificity; binding or cleavage pattern; thermal
 CC stability; pH/activity or pH/stability profile; stability towards
 CC oxidation; Ca²⁺ dependency and specific activity. The variant has one or
 CC more mutations selected from: (a) the mutations A181E, D, Q, N, V; I201
 CC (bulkier amino acid) including I201W, F, L; Y203Q, Q9K, L, E, F11R, K, E;
 CC E12Q; D100N, L; V101H, R, K, D, E, F, V102A, T; I103H, K; N104R, K, D;
 CC H105R, K, D, E, W, F; L196R, K, D, E, F, Y; I212R, K, D, E; L230H, K, I;
 CC A232G, H, F, S, V; V233D, K234L, E; I236R, K, N, H, D, E; L241R, K, D, E,
 CC F; A260S; W263H; Q264R, D, K, E; N265K, R, D; A269R, K, D, E; L270R, K, D,
 CC H, D, E; V283H, D; F284H; D285N, L; V286R, K, H, D, E; Y290R, E, K;
 CC V122R, K, D, E; F323H; D325N; N326K, H, D, L; H327Q, N, E, D, F; Q220L, E
 CC G332D; Q333R, K, H, E, L; S334A, V, T, L, I, D; L335G, A, S, T, N,
 CC E336R + R375E; T337D, K; T338D, E; T338D; Q360K, R, E; D365N; G371D, R;
 CC (b) substitutions at positions H68, H91, H247, R305, K306, H382, K389,
 CC H405, H406, H450 or R483; (c) the mutations H440Y, H142Y, H159Y, H140D +
 CC H142R, H140K + H142D; or H142Y + H156Y; (d) deletion of 3 amino acids
 CC within the partial sequence from T369 to I377, including K370-D372 or
 CC D372-Q374; (e) replacement of T369-I377 by IPHNSV, IPTHGV or IQQNT; (f)
 CC substitutions at positions R169 or R173, including R169Y, L, F, T or
 CC R173I, L, F, T; (g) the mutations H156D, I201F, I212F, A209L or T, or
 CC V208I; (h) substitutions at positions N172, A181, N188, N190, H207,
 CC A209, A210, E211, Q264 or N265, including N172R, H, K, A181T, N188P, D207,
 CC N190L, F; H205C; D207Y; A209L, T, V; A210S, E211Q, Q264A, E, L, K, S, T;
 CC N265A, S, T, Y, or (Q264S + N265Y); and (i) the mutations H156Y + A181T +
 CC A209V; H156Y + A181T + N190F + A209V + Q264S; A1* + N2* + L3V + M1ST +
 CC R23K + S29A + A30E + Y31H + A33S + E34D + H35I + H156Y + A209V
 CC (where * indicates deletion of the amino acid residue); A1* + N2* + L3V +
 CC M1ST + R23K + S29A + A30E + Y31H + A33S + E34D + H35I + H156Y + A181T +
 CC N90F + A209V; or A1* + N2* + L3V + M1ST + R23K + S29A + A30E + Y31H +
 CC A33S + E34D + H35I + H156Y + A181T + N190F + A209V + Q264S. Also claimed
 CC are constructs comprising DNA (see AAV02471) encoding such a variant, and
 CC recombinant expression vectors and transformed cells containing the DNA.
 CC The alpha-amylase variant is useful as a detergent additive and can also
 CC be used in industrial starch processing e.g. liquefaction (claimed) or
 CC saccharification to produce sweeteners, e.g. in textile desizing (claimed) or
 CC (claimed). (Updated on 17-OCT-2003 to standardise OS field)
 XX SQ Sequence 483 AA;
 Query Match 100.0%; Score 2666; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1, 7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFENYMPNDQGMRLONDSAYLAHEGTTAVMIPPAYKGTSGADVGAYD 60
 DB 1 ANINGTLMQYFENYMPNDQGMRLONDSAYLAHEGTTAVMIPPAYKGTSGADVGAYD 60
 QY 61 LYLDFEHOQKGTGRTKGTGELQSAIKLSHSDINVGQVNVNHHKGAATEVTAVEV 120
 DB 61 LYLDFEHOQKGTGRTKGTGELQSAIKLSHSDINVGQVNVNHHKGAATEVTAVEV 120
 QY 121 DPADRRNVISGEHLIKAMTHFFPGKSTSDPEKMHVHFGDTWDESRKLNRYKFGK 180
 DB 121 DPADRRNVISGEHLIKAMTHFFPGKSTSDPEKMHVHFGDTWDESRKLNRYKFGK 180
 QY 181 AMDMEVSNENGDYLMYADIDYDHPDVAEIKRMGTVANELODGFRLDAVHKIKSF 240
 DB 181 AMDMEVSNENGDYLMYADIDYDHPDVAEIKRMGTVANELODGFRLDAVHKIKSF 240
 QY 241 LRDVNHVREKTKEMFTVAEYQNDIGALENYLKNTPHNSVDPVLAHQFHAASIQG 300
 DB 241 LRDVNHVREKTKEMFTVAEYQNDIGALENYLKNTPHNSVDPVLAHQFHAASIQG 300
 QY 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHDTQGSLESTVQTPWPLAVALITRESGVPQ 360
 DB 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHDTQGSLESTVQTPWPLAVALITRESGVPQ 360
 QY 361 VFYGDWYGTGDSOREIPALKKHLEPILKARKQYAYGAOHDPDHDIVGWTREGDSVA 420
 DB 361 VFYGDWYGTGDSOREIPALKKHLEPILKARKQYAYGAOHDPDHDIVGWTREGDSVA 420
 QY 421 NSGLAALITDGGKAKMYVGRONAGETWHDITGNRSEPVVINSNGEFPVNGSVSIY 480
 DB 421 NSGLAALITDGGKAKMYVGRONAGETWHDITGNRSEPVVINSNGEFPVNGSVSIY 480
 QY 481 VOR 483
 DB 481 VOR 483
 RESULT 4
 AAV15418
 ID AAV15418 standard; protein; 483 AA.
 XX AAV15418;
 AC AAV15418;
 XX 22-JUL-1999 (first entry)
 DT 22-JUL-1999 (first entry)
 XX *Bacillus licheniformis* alpha-amylase protein.
 DB *Bacillus licheniformis* alpha-amylase protein.
 XX Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
 KW sweetener; ethanol; starch; textile desizing; starch liquefaction;
 KM saccharification process.
 OS *Bacillus licheniformis*.
 XX MO9923211-A1.
 XX 14-MAY-1999.
 XX 30-OCT-1998; 98WO-DK000471.
 XX 30-OCT-1997; 97DK-00001240.
 XX 14-JUL-1998; 98DK-00000936.
 XX (NOVO) NOVO-NORDISK AS.
 XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nielsen TL;
 PI Kjærulff S;
 XX WPI; 1999-326987/27.
 XX New Termamyl-like alpha-amylase variants.
 PT Claim 38; Page 82-84; 115pp; English.
 XX PS

XX The specification describes termamyl-like alpha-amylase variants that
 CC have altered amino acid sequences to improve properties. The variants are
 CC produced by creating one or more of the following mutations in amino acid
 CC sequence of the parent termamyl-like alpha-amylase: T144, K142, F143,
 CC D144, F145, P146, G147, R148, Q174, R181, G182, D183, G184, K185,
 CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
 CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
 CC K311, B346, K385, G456, K458, P459, G460, T461, V462, T463. The
 CC variants can be used for washing and/or dishwashing. They can also be
 CC used in the production of sweeteners and ethanol from starch, and/or for
 CC textile desizing, and in starch liquefaction and/or saccharification
 CC processes. The present amylase can function as the parent sequence in the
 CC production of the variants of the invention

XX Sequence 483 AA:

Query Match 100.0%; Score 2666; DB 2; Length 483;

Best Local Similarity 100.0%; Pred. No. 1.7e-224;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQFEYMWPMNDGQHMRLONDSATLAHGHTAWIPPAKYGTSQADVGYGAYD 60
 DB 1 ANLNGTLMQFEYMWPMNDGQHMRLONDSATLAHGHTAWIPPAKYGTSQADVGYGAYD 60
 QY 61 LYDGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
 DB 61 LYDGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
 QY 121 DPADRRNVISGEHLIKAMTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRIYKFGK 180
 DB 121 DPADRRNVISGEHLIKAMTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRIYKFGK 180
 QY 121 DPADRRNVISGEHLIKAMTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRIYKFGK 180
 DB 121 DPADRRNVISGEHLIKAMTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRIYKFGK 180
 QY 181 AMDWEVSENGNNDYLMYADIDYDHPDVAEIKRWGTYANELQDGFRLDAVKHIFSF 240
 DB 181 AMDWEVSENGNNDYLMYADIDYDHPDVAEIKRWGTYANELQDGFRLDAVKHIFSF 240
 QY 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNSVFDVPLHYQFHAASTOGG 300
 DB 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNSVFDVPLHYQFHAASTOGG 300
 QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTWFKPLAFAFLITRESGYPQ 360
 DB 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTWFKPLAFAFLITRESGYPQ 360
 QY 361 VFYGDWYGTGDSQREIPALKKHIEPIILKARKQYAGAODYFDHDIIVGWTREGSSVA 420
 DB 361 VFYGDWYGTGDSQREIPALKKHIEPIILKARKQYAGAODYFDHDIIVGWTREGSSVA 420
 QY 421 NSGLAALITDGPAGAKRMVYGRONAGEFTWHDITGNRSEPVVINSBGGEFHVNGSVSIT 480
 DB 421 NSGLAALITDGPAGAKRMVYGRONAGEFTWHDITGNRSEPVVINSBGGEFHVNGSVSIT 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 5
 ID AAY29852
 AAAY29852 standard; protein; 483 AA.

XX AAY29852;

XX 18-NOV-1999 (first entry)

XX Bacillus licheniformis Termamyl-like alpha-amylase Val54.

XX Alpha-amylase; Termamyl-like alpha-amylase; glucose syrup; starch.

XX Bacillus licheniformis.

XX MO9946399-A1.

XX 16-SEP-1999.
 PD 08-MAR-1999; 99NO-DK000114.
 PF 09-MAR-1998; 98DX-00000321.
 PR (NOVO) NOVO-NORDISK AS.
 PA Norman BE, Hendriksen HV;
 PI WPI; 1999-551422/46.
 DR N-PSDB; AAZ21078.
 XX Preparation of a glucose syrup, using a Termamyl-like alpha-amylase.

XX Claim 8, Page 26-28; 36pp; English.

XX A method has been developed for the preparation of a glucose syrup using
 CC a Termamyl-like alpha-amylase containing a substitution at Val(54). The
 CC glucose syrup obtained by the process is useful as an ingredient in food
 CC products. The Termamyl-like alpha-amylase facilitates the preparation of
 CC glucose syrups suitable for the food industry, previously only possible
 CC using acid hydrolysis. The present sequence represents Bacillus
 CC licheniformis Termamyl-like alpha-amylase

XX Sequence 483 AA:

Query Match 100.0%; Score 2666; DB 2; Length 483;

Best Local Similarity 100.0%; Pred. No. 1.7e-224;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQFEYMWPMNDGQHMRLONDSATLAHGHTAWIPPAKYGTSQADVGYGAYD 60
 DB 1 ANLNGTLMQFEYMWPMNDGQHMRLONDSATLAHGHTAWIPPAKYGTSQADVGYGAYD 60
 QY 61 LYDGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
 DB 61 LYDGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
 QY 121 DPADRRNVISGEHLIKAMTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRIYKFGK 180
 DB 121 DPADRRNVISGEHLIKAMTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRIYKFGK 180
 QY 121 DPADRRNVISGEHLIKAMTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRIYKFGK 180
 DB 121 DPADRRNVISGEHLIKAMTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRIYKFGK 180
 QY 181 AMDWEVSENGNNDYLMYADIDYDHPDVAEIKRWGTYANELQDGFRLDAVKHIFSF 240
 DB 181 AMDWEVSENGNNDYLMYADIDYDHPDVAEIKRWGTYANELQDGFRLDAVKHIFSF 240
 QY 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNSVFDVPLHYQFHAASTOGG 300
 DB 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNSVFDVPLHYQFHAASTOGG 300
 QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTWFKPLAFAFLITRESGYPQ 360
 DB 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTWFKPLAFAFLITRESGYPQ 360
 QY 361 VFYGDWYGTGDSQREIPALKKHIEPIILKARKQYAGAODYFDHDIIVGWTREGSSVA 420
 DB 361 VFYGDWYGTGDSQREIPALKKHIEPIILKARKQYAGAODYFDHDIIVGWTREGSSVA 420
 QY 421 NSGLAALITDGPAGAKRMVYGRONAGEFTWHDITGNRSEPVVINSBGGEFHVNGSVSIT 480
 DB 421 NSGLAALITDGPAGAKRMVYGRONAGEFTWHDITGNRSEPVVINSBGGEFHVNGSVSIT 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 6
 ID AAY07384
 AAAY07384 standard; protein; 483 AA.

AAV07384;
16-JUL-1999 (first entry)
Wild type Termamyl (RTM)-like alpha-amylase protein #4.
Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
ethanol.
Bacillus sp.
Key Location/Qualifiers
Misc-difference 190 /note= "optionally altered to any amino acid except an
Asn residue"
Misc-difference 201 /note= "optionally altered to any amino acid except an
Ile residue"
Misc-difference 211 /note= "optionally altered to any amino acid except an
Asp residue"
Misc-difference 214 /note= "optionally altered to any amino acid except a Glu
residue"
Misc-difference 264 /note= "optionally altered to any amino acid except a Glu
residue"
W09919467-A1.
22-APR-1999.
13-OCT-1998; 98WO-DK000444.
13-OCT-1997; 97DK-00001172.
(NOVO) NOVO-NORDISK AS.
Svendsen A, Borchert TV, Bisgard-Frantzen H;
WPI; 1999-277632/23.
Variant alpha-amylases - useful as detergents or for textile desizing or
starch liquefaction.
Claim 1; Page 67-68; 93pp; English.
This sequence represents the parent sequence for new variants of a parent
Termamyl-like alpha-amylase with alpha-amylase activity. The variants
comprise mutations in 2-6 regions/positions relative to an alpha-amylase
from either of two Bacillus species in W09526397, B. stercoriorumophilus,
B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
amylase variants are detergent additives for use in detergents for
dishwashing, manual or automatic laundry. The variants can also be used
for textile desizing or starch liquefaction (e.g. for production of
sweeteners or ethanol)
Sequence 483 AA;
Query Match 100.0%; Score 2666; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.7e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

121 DPADNRNVIISGEHLIKAWTHFFHPGRGSTYSDFKMWHFPGTDWDSRKLNRIFYKQK 180
181 AMDMEVSNENGANDYLMYADIDYDHPVAAEIKRMGTWYANEIQDGFRLDAVGHIFSF 240
181 AMDMEVSNENGANDYLMYADIDYDHPVAAEIKRMGTWYANEIQDGFRLDAVGHIFSF 240
241 LRDVNVHREKTKGEMETVAEYQNDIGALENYLAKTNFHSVPDPLHYQFHAATQGG 300
241 LRDVNVHREKTKGEMETVAEYQNDIGALENYLAKTNFHSVPDPLHYQFHAATQGG 300
301 GYDMRKILNCTVSVSKPLKSVTVVDNHDTPQGSLESTVQTFKPLAAYATILRESGYPQ 360
301 GYDMRKILNCTVSVSKPLKSVTVVDNHDTPQGSLESTVQTFKPLAAYATILRESGYPQ 360
361 VFYGDWYGTGDSOREIPALKHKEPIILKARKOYAGAOHDYFDHDIYQMTREGDSVA 420
361 VFYGDWYGTGDSOREIPALKHKEPIILKARKOYAGAOHDYFDHDIYQMTREGDSVA 420
421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSSEGMGEFHVNGGSYSIY 480
421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSSEGMGEFHVNGGSYSIY 480
481 VQR 483
481 VQR 483
481 VQR 483

RESULT 7
AA99605
ID AA99605 standard; protein; 483 AA.
AA99605;
04-SEP-2000 (first entry)
Bacillus licheniformis Termamyl alpha-amylase.
Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
Baccharification; muten; mutanc; enzyme stability; hybrid.
Bacillus licheniformis.
W0200029560-A1.
25-MAY-2000.
16-NOV-1999; 99WO-DK000628.
16-NOV-1998; 98DK-00001495.
(NOVO) NOVO-NORDISK AS.
Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;
WPI; 2000-38777/33.
N-PSDB; AAA46483.
Variant of parent termamyl-like alpha amylase useful for washing, textile
desizing and starch liquefaction, comprising alterations in one or more
solvent exposed amino acid residues.
Claim 8; Page 58-59; 80pp; English.
The present sequence is a parent alpha-amylase from which mutants with
increased stability at acidic pH, low calcium concentration and high
temperatures have been derived. The enzyme is commercially available as
Termamyl. A variant may contain mutations in one or more solvent exposed
amino acid residues to increase the overall hydrophobicity of the enzyme
or the overall number of methyl groups in the side chains of exposed
residues may be increased. The mutations can be incorporated by site-
directed mutagenesis or by random mutagenesis. As a result of their
increased stability, the variants are suitable for the industrial

processing of starch, i.e. starch liquefaction and saccharification. They may also be useful for washing, dishwashing and textile desizing. Hybrid alpha-amylases comprising partial amino acid sequences derived from two or more alpha-amylases have also been created in order to increase enzyme stability

Sequence 483 AA;

Query Match 100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.7e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEWYMPNDGQHRRLQNDSAVLAHGIITAVWIIPPAKYKTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFEWYMPNDGQHRRLQNDSAVLAHGIITAVWIIPPAKYKTSQADVGYGAYD 60
QY 61 LYDGEFHQKGTVRTKYGKGELOSATKSLHSRDINVGDVVYINHGKADATEDVTAVEV 120
DB 61 LYDGEFHQKGTVRTKYGKGELOSATKSLHSRDINVGDVVYINHGKADATEDVTAVEV 120
QY 121 DPADRRNVIISGEHLIKAWTHFHFPGRGSTYSDFKWMYHFDGTWDSRKLNRITYKQK 180
DB 121 DPADRRNVIISGEHLIKAWTHFHFPGRGSTYSDFKWMYHFDGTWDSRKLNRITYKQK 180
QY 181 AMDWEVSNGNVDYLMYADIDYHPDVAAEIKKGTWYANELQDGFRLDAVGHKFSF 240
DB 181 AMDWEVSNGNVDYLMYADIDYHPDVAAEIKKGTWYANELQDGFRLDAVGHKFSF 240
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENVYLNKTNFNSVDFVPLHYQFHAASQGG 300
DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENVYLNKTNFNSVDFVPLHYQFHAASQGG 300
QY 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHTQPGQSLESTVQWFKPLAYAFILTRSGYRQ 360
DB 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHTQPGQSLESTVQWFKPLAYAFILTRSGYRQ 360
QY 361 VFYGDWYGTGKDSQREIPALKKIEPIILKARKQYAGAHQYFPHHDIVGWTREGDSVA 420
DB 361 VFYGDWYGTGKDSQREIPALKKIEPIILKARKQYAGAHQYFPHHDIVGWTREGDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGFHVNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 8

AAV97545 standard; protein; 483 AA.

AAV97545;

12-FEB-2001 (first entry)

B. licheniformis termamyl-like alpha amylase.

Termamyl-like alpha-amylase; variant; starch liquefaction; fuel; detergent composition; laundry cleaning composition; ethanol production; dish washing cleaning composition; hard surface cleaning composition; industrial ethanol production; textile desizing.

Bacillus licheniformis.

MO200060059-A2.

12-OCT-2000.

28-MAR-2000; 2000WO-DK000148.

30-MAR-1999; 99DK-00000437.

XX (NOVO) NOVO NORDISK AS.
PA Andersen C, Jorgensen CT, Bisgard-Frantzen H, Svendsen A;
PI Kjaerliff S;
PI Kjaerliff S;
XX WPI: 2001-015656/02.
DR N-PSDB; AAA37849.
XX
XX
PT New variants of parent Termamyl-like alpha-amylase, useful in starch
PT liquefaction, in detergent compositions and in ethanol production,
PT exhibit altered cleavage pattern relative to the parent.
PS Claim 1; Page 60-62; 78pp; English.

CC This sequence represents a termamyl-like alpha amylase. The invention
CC relates to a variant (I) of parent Termamyl-like alpha-amylase comprising
CC alteration at one or more of the positions W13, G48, T49, S50, O51, A52,
CC D53, V54, G57, G107, G108, A111, S168 and M197. The alterations in (I)
CC are independently an insertion of an amino acid downstream of the amino
CC acid which occupies the position of deletion or substitution of the amino
CC acid which occupies the position with a different amino acid. The variant
CC has alpha-amylase activity. (I) or compositions containing it are useful
CC in starch liquefaction, in detergent compositions such as laundry, dish
CC washing and hard surface cleaning compositions, ethanol production such
CC as fuel, drinking and industrial ethanol production, desizing of
CC textiles, fabrics or garments. (I) exhibits a reduced capability of
CC cleaving a substrate close to the branching point, and further exhibits
CC improved substrate specificity and/or improved specific activity relative
CC to the parent alpha-amylase

Sequence 483 AA;

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.7e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEWYMPNDGQHRRLQNDSAVLAHGIITAVWIIPPAKYKTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFEWYMPNDGQHRRLQNDSAVLAHGIITAVWIIPPAKYKTSQADVGYGAYD 60
QY 61 LYDGEFHQKGTVRTKYGKGELOSATKSLHSRDINVGDVVYINHGKADATEDVTAVEV 120
DB 61 LYDGEFHQKGTVRTKYGKGELOSATKSLHSRDINVGDVVYINHGKADATEDVTAVEV 120
QY 121 DPADRRNVIISGEHLIKAWTHFHFPGRGSTYSDFKWMYHFDGTWDSRKLNRITYKQK 180
DB 121 DPADRRNVIISGEHLIKAWTHFHFPGRGSTYSDFKWMYHFDGTWDSRKLNRITYKQK 180
QY 181 AMDWEVSNGNVDYLMYADIDYHPDVAAEIKKGTWYANELQDGFRLDAVGHKFSF 240
DB 181 AMDWEVSNGNVDYLMYADIDYHPDVAAEIKKGTWYANELQDGFRLDAVGHKFSF 240
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENVYLNKTNFNSVDFVPLHYQFHAASQGG 300
DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENVYLNKTNFNSVDFVPLHYQFHAASQGG 300
QY 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHTQPGQSLESTVQWFKPLAYAFILTRSGYRQ 360
DB 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHTQPGQSLESTVQWFKPLAYAFILTRSGYRQ 360
QY 361 VFYGDWYGTGKDSQREIPALKKIEPIILKARKQYAGAHQYFPHHDIVGWTREGDSVA 420
DB 361 VFYGDWYGTGKDSQREIPALKKIEPIILKARKQYAGAHQYFPHHDIVGWTREGDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGFHVNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 9
 ABB06936
 ID ABB06936 standard; protein; 483 AA.
 XX
 AC ABB06936;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE B. licheniformis termamyl-like alpha-amylase protein SEQ ID NO:8.
 XX
 KW Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 KW washing; sweetener; ethanol; starch.
 XX
 OS Bacillus licheniformis.
 XX
 PN WO20016712-A2.
 XX
 PD 13-SEP-2001.
 XX
 PE 07-MAR-2001; 2001WO-DK000144.
 XX
 PR 08-MAR-2000; 2000DK-00000376.
 PR 15-MAR-2000; 2000US-0189857P.
 PR 23-FEB-2001; 2001DK-00000303.
 PR 26-FEB-2001; 2001US-0271382P.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Andersen C, Borchert TV, Nielsen BR;
 XX
 DR WPI; 2002-239612/29.
 DR N-PSDB; ABL50567.
 XX
 PT Novel variant of parent termamyl-like alpha-amylase useful as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 8; Page 142-143; 153pp; English.
 XX
 CC The present invention describes a variant of a parent termamyl-like alpha
 CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 CC positions of a group of 31 possible amino acid positions. The alteration
 CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
 CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
 CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
 CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
 CC washing and/or dishwashing, textile desizing, and starch liquefaction.
 CC (I) is useful as a component in hard surface cleaning detergent
 CC composition, and for producing sweeteners and ethanol from starch. (I)
 CC has altered solubility, preferably increased solubility, in particular
 CC under washing, dish washing or hard surface cleaning conditions. The
 CC present sequence represents a Bacillus licheniformis termamyl-like alpha-
 CC amylase which is used in the exemplification of the present invention
 XX
 SQ Sequence 483 AA;
 XX
 Query Match 100.0%; Score 2666; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 ANLNGTLMQYFEMWYNDQGMRLQNDSDAVIAEHGITAIVWIPYKGTSGADVGYAYD 60
 DB 1 ANLNGTLMQYFEMWYNDQGMRLQNDSDAVIAEHGITAIVWIPYKGTSGADVGYAYD 60
 QY 61 LYDLSEPHOKGTGVRKYGTGKGLQSAIKSLHSRDLNVYGVVINKGADATEDTAVAEV 120
 DB 61 LYDLSEPHOKGTGVRKYGTGKGLQSAIKSLHSRDLNVYGVVINKGADATEDTAVAEV 120
 QY 121 DPADNRNVIAGEHLIKAWTHFHPGPGSTYSDPKMWHYFDGTDWDESKLNRIFYKFOOK 180
 DB 121 DPADNRNVIAGEHLIKAWTHFHPGPGSTYSDPKMWHYFDGTDWDESKLNRIFYKFOOK 180

181 AMDWEVSNGNNDYLMYADIDYDHPVAAEIKKMGWYANELOLDGFRDVAVKIKRSF 240
 181 AMDWEVSNGNNDYLMYADIDYDHPVAAEIKKMGWYANELOLDGFRDVAVKIKRSF 240
 QY 241 LRDVNNHVRKTKGEMTVAEYQNDIGALENINAKTNFNHNSVDVPLHYFPHAASTOGG 300
 DB 241 LRDVNNHVRKTKGEMTVAEYQNDIGALENINAKTNFNHNSVDVPLHYFPHAASTOGG 300
 QY 301 GYDMRKLLNGTVSKHPLKSTFTPDNHDTPGQSLSTVQWFPFLAFAFLITRESGPQ 360
 DB 301 GYDMRKLLNGTVSKHPLKSTFTPDNHDTPGQSLSTVQWFPFLAFAFLITRESGPQ 360
 QY 361 VFYGDMTGKGDSDREIPALKHKIEPIIKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA 420
 DB 361 VFYGDMTGKGDSDREIPALKHKIEPIIKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA 420
 QY 421 NSGLAALITDGPQGAKKMYVGRONAGETWHDITGNRSEPVYINSEGWGEFHVNGSVSIV 480
 DB 421 NSGLAALITDGPQGAKKMYVGRONAGETWHDITGNRSEPVYINSEGWGEFHVNGSVSIV 480
 QY 481 VQR 483
 DB 481 VQR 483
 RESULT 10
 AAU12152
 ID AAU12152 standard; protein; 483 AA.
 XX
 AC AAU12152;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Bacillus TERMAMYL alpha-amylase.
 XX
 KW TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;
 KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
 KW amylpectin; limit dextrin; NOVAMYL.
 XX
 OS Bacillus licheniformis.
 XX
 PN WO200188107-A2.
 XX
 PD 22-NOV-2001.
 XX
 PE 10-MAY-2001; 2001WO-DK000323.
 XX
 PR 12-MAY-2000; 2000DK-00000779.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Svendsen A, Jorgensen CT, Nielsen BR;
 XX
 DR WPI; 2002-106123/14.
 DR N-PSDB; AAS20025.
 XX
 PT New variant of parent Termamyl-like alpha-amylase for use as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 5; Fig 1; 84pp; English.
 XX
 CC The invention relates to a variant of parent TERMAMYL-like alpha-amylase
 CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
 CC or at position 234, where the variant has alpha-amylase activity and each
 CC position corresponds to a position of a parent Termamyl-like alpha-
 CC amylase sequence having a Bacillus licheniformis alpha-amylase sequence
 CC of 483 amino acids, given in specification. The variant alpha-amylase, a
 CC detergent additive comprising the variant or a detergent composition
 CC comprising the variant, is useful for washing and/or dishwashing or
 CC textile desizing. The alpha-amylase is useful for starch liquefaction or
 CC ethanol production and as a component in a hard surface cleaning

CC detergent composition, and for producing sweeteners from starch. The
CC variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage
CC activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
CC branch linkage cleavage activity of amylopectin or a limit dextrin
CC prepared by THERMAMYL (RPM) or NOVAMYL (RPM). The present sequence is the
CC THERMAMYL alpha-amyase upon which the variants of the invention are based
XX
SQ Sequence 483 AA;

Query Match 100.0%; Score 2666; DB 5; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.7e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFWMYPNDGQHMRLQNDASAYLAHEGITAAMIIPRAYKGTSGADVGAYD 60
Db 1 ANLNGTLMQYFWMYPNDGQHMRLQNDASAYLAHEGITAAMIIPRAYKGTSGADVGAYD 60
QY 61 LYDGEFHQKGTVRTKTYGTGKSELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
Db 61 LYDGEFHQKGTVRTKTYGTGKSELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
QY 121 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDPKMWHYFPGTMDSESKLNRIYKFGK 180
Db 121 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDPKMWHYFPGTMDSESKLNRIYKFGK 180
QY 181 AMDWEVSNENGNVDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKHKFSF 240
Db 181 AMDWEVSNENGNVDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKHKFSF 240
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNTKTNFNSVFDVPLHYQFHAASFOGG 300
Db 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNTKTNFNSVFDVPLHYQFHAASFOGG 300
QY 301 GYDMRKLLNGTVVSKPLKSVTFVDNHDTPGQSLSTVQWPKPLAFAFLITRESGPQ 360
Db 301 GYDMRKLLNGTVVSKPLKSVTFVDNHDTPGQSLSTVQWPKPLAFAFLITRESGPQ 360
QY 361 VFYGDWYGTGDSQREIPALKHKIEPIILKARKQYAYGAQHDYFDHDI VGTWREGDSVA 420
Db 361 VFYGDWYGTGDSQREIPALKHKIEPIILKARKQYAYGAQHDYFDHDI VGTWREGDSVA 420
QY 421 NSGLAALITDGPQAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
Db 421 NSGLAALITDGPQAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY 481 VQR 483
Db 481 VQR 483

RESULT 11
AAE26534
ID AAE26534 standard; protein; 483 AA.
XX
AC AAE26534;
XX
DT 13-DEC-2002 (first entry)
XX
DE Bacillus licheniformis alpha-amyase protein.
XX
KW Alpha amyase; alpha-1,4-glucan-4-glucanohydrolase; EC 3.2.1.1;
KM dishwashing; textile desizing; detergent; paper; starch liquefaction;
KM laundry; alcohol production; ethanol production; pulp; beer; brewing;
KM sweetener; enzyme.
XX
OS Bacillus licheniformis.
XX
PN WO200231124-A2.
XX
PD 18-Apr-2002.
XX
PF 12-OCT-2001; 2001WO-DK00668.
XX

PR 13-OCT-2000; 2000DK-00001533.
PR 23-OCT-2000; 2000US-0242692P.
PR 02-OCT-2001; 2001DK-00001442.
PR 03-OCT-2001; 2001US-0326752P.
XX
PA (NOVO) NOVOZYMES AS.
XX
PI Andersen C;
XX
DR WPI: 2002-463264/49.
DR N-PSDB; AAD44363.
XX
PT KSM-K36 or KSM-K38 variant from Bacillus for cleaning dishes, textile
PT desizing, starch liquefaction and ethanol production has alpha-amyase
PT activity.
XX
PS Disclosure; Page 60-62; 69pp; English.
XX
CC The present invention relates to KSM-K36 or KSM-K38 variant of parent
CC alpha-amyases (alpha-1,4-glucan-4-glucanohydrolases, EC 3.2.1.1) from
CC Bacillus. The variants have alpha-amyase activity and exhibit an amino
CC acid alteration such as an insertion, deletion or substitution of the
CC parent alpha-amyase. The variants are useful for washing and/or dish-
CC washing, textile desizing, starch liquefaction and alcohol production,
CC particularly ethanol production. They are also useful as components in
CC detergent compositions for e.g. laundry, dishwashing and hard surface cleaning
CC in beer making and in production of sweeteners. The present sequence is Bacillus
CC licheniformis alpha-amyase protein
XX
SQ Sequence 483 AA;

Query Match 100.0%; Score 2666; DB 5; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.7e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFWMYPNDGQHMRLQNDASAYLAHEGITAAMIIPRAYKGTSGADVGAYD 60
Db 1 ANLNGTLMQYFWMYPNDGQHMRLQNDASAYLAHEGITAAMIIPRAYKGTSGADVGAYD 60
QY 61 LYDGEFHQKGTVRTKTYGTGKSELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
Db 61 LYDGEFHQKGTVRTKTYGTGKSELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
QY 121 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDPKMWHYFPGTMDSESKLNRIYKFGK 180
Db 121 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDPKMWHYFPGTMDSESKLNRIYKFGK 180
QY 181 AMDWEVSNENGNVDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKHKFSF 240
Db 181 AMDWEVSNENGNVDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKHKFSF 240
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNTKTNFNSVFDVPLHYQFHAASFOGG 300
Db 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNTKTNFNSVFDVPLHYQFHAASFOGG 300
QY 301 GYDMRKLLNGTVVSKPLKSVTFVDNHDTPGQSLSTVQWPKPLAFAFLITRESGPQ 360
Db 301 GYDMRKLLNGTVVSKPLKSVTFVDNHDTPGQSLSTVQWPKPLAFAFLITRESGPQ 360
QY 361 VFYGDWYGTGDSQREIPALKHKIEPIILKARKQYAYGAQHDYFDHDI VGTWREGDSVA 420
Db 361 VFYGDWYGTGDSQREIPALKHKIEPIILKARKQYAYGAQHDYFDHDI VGTWREGDSVA 420
QY 421 NSGLAALITDGPQAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
Db 421 NSGLAALITDGPQAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY 481 VQR 483
Db 481 VQR 483

RESULT 12
 AAB47853
 ID AAB47853 standard; protein; 483 AA.
 XX
 AC AAB47853;
 XX
 DT 02-APR-2002 (first entry)
 XX
 DE Bacillus termamyl alpha amylase.
 XX
 KM Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;
 KM starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
 KM bakery; cereal bar; ice cream; coffee whitener; salad dressing;
 KM cured meat; fermented meat; spice.
 XX
 OS Bacillus licheniformis.
 XX
 PN WO200196537-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 13-JUN-2001; 2001WO-DK000404.
 XX
 PR 14-JUN-2000; 2000DK-00000917.
 PR 20-JUN-2000; 2000US-0212852P.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Nielsen BR, Weibye M;
 XX
 DR WPI; 2002-098064/13.
 DR N-PSDB; AAI72214.
 XX
 PT New modified alpha-amylase derived from the genus Bacillus and/or is a
 PT Termamyl-like alpha-amylase, which has been pre-oxidized for producing
 PT maltodextrin or glucose syrup.
 XX
 PS Claim 5; Page 36-37; 47pp; English.
 XX
 CC The sequences given in AAB47850-56 show modified alpha-amylases derived
 CC from the genus Bacillus. These alpha amylases are Termamyl-like alpha-
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30
 CC kDa has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours
 XX
 SQ Sequence 483 AA;
 Query Match 100.0%; Score 2666; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1,7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 AMDWEVSNGNDYIMYADIDYDHPVAAEIKRWGTWYANEQLDGFRLDAVHKIKSF 240
 DB 181 AMDWEVSNGNDYIMYADIDYDHPVAAEIKRWGTWYANEQLDGFRLDAVHKIKSF 240
 QY 241 LRDVNVHVRREKTKGEMTVAEYWNNDGALFNLYNTKTNPNHNSVDFVPLHYGFHAASVTOGG 300
 DB 241 LRDVNVHVRREKTKGEMTVAEYWNNDGALFNLYNTKTNPNHNSVDFVPLHYGFHAASVTOGG 300
 QY 301 GYDWRKLLNGTVVSKHPLKSTFTVDNHDTPGQSLBSTVQTFWFLVAFILITRESGYPQ 360
 DB 301 GYDWRKLLNGTVVSKHPLKSTFTVDNHDTPGQSLBSTVQTFWFLVAFILITRESGYPQ 360
 QY 361 VFYGDWYGTGDSQREIPALKHKIEPLTKARKQYAGAHQDPDHDIVGWTREGDSVA 420
 DB 361 VFYGDWYGTGDSQREIPALKHKIEPLTKARKQYAGAHQDPDHDIVGWTREGDSVA 420
 QY 421 NSGIAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSRGGEFFVNGSVISY 480
 DB 421 NSGIAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSRGGEFFVNGSVISY 480
 QY 481 VQR 483
 DB 481 VQR 483
 RESULT 13
 ABB76589
 ID ABB76589 standard; protein; 483 AA.
 XX
 AC ABB76589;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Termamyl-like-alpha-amylase #4.
 DE Termamyl-like-alpha-amylase #4.
 XX
 KM Termamyl; alpha amylase; starch liquefaction; ethanol production;
 KM textile desizing; detergent; enzyme.
 XX
 OS Bacillus licheniformis.
 XX
 PN WO200210355-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 12-JUL-2001; 2001WO-DK000488.
 XX
 PR 01-AUG-2000; 2000DK-00001160.
 PR 12-SEP-2000; 2000DK-00001354.
 PR 10-NOV-2000; 2000DK-00001687.
 PR 26-APR-2001; 2001DK-00000655.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;
 XX
 DR WPI; 2002-280633/32.
 DR N-PSDB; ABL96210.
 XX
 PT Variant of parent Termamyl-like alpha amylase, useful in detergent
 PT compositions, for starch liquefaction, ethanol production, washing and/or
 PT dish washing, and textile desizing.
 XX
 PS Claim 1; Fig 4; 90pp; English.
 XX
 CC This invention relates to variants of a parent Termamyl-like alpha-
 CC amylase. These are used for starch liquefaction, ethanol production,
 CC detergent, and textile desizing. The amylases have altered stability,
 CC particularly at high temperatures from 70-120pH and low pH in the
 CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
 CC amylase
 XX
 SQ Sequence 483 AA;

[illegible]

PR 24-NOV-1994; 94DK-00001343.
PA (NOVO) NOVO-NORDISK AS.
PI Bjornvad ME, Prento A;
XX
XX WPI; 1996-268613/27.
DR N-PSDB; AATJ3228.
XX
XX PT Prodn. of self-oligomerising peptide(s) with reduced allergenicity - used
in household and personal cleaning prods., and in food and feeds etc.
PS Disclosure; Page 61-63; 85pp; English.

CC A polypeptide (AAR98007) is composed of Terym[alpha-amylase, a linker
derived from the IgG3 hinge domain and a leucine zipper from the GCM4
yeast transcription factor. It was produced by PCR amplification of the
Terym[gene and ligation of synthetic oligonucleotides (see also
AA333229-32) encoding the leucine zipper and linker. Upon expression in
E.coli, using a vector including the pelB signal sequence, the Terym[
product self-oligomerised into a dimer that was secreted into the
periplasm. The method constitutes an industrially applicable process for
producing a biologically active polypeptide that self-oligomerises owing
to the presence of leucine zippers, the enlarged size of the resulting
polypeptide leading to a reduction in its allergenicity. (Updated on 27-
AUG-2003 to correct OS field.)

Sequence 531 AA;

Query Match	100.0%	Score 2666	DB 2	Length 531
Best Local Similarity	100.0%	Pred. No. 1	9e-224	
Matches 483	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ANINGTLMQYFEWYMPNDGCHRRRLONDSAYLAHGGITAAVMPDAYKGISQADVGYA	60	
Db	1	ANINGTLMQYFEWYMPNDGCHRRRLONDSAYLAHGGITAAVMPDAYKGISQADVGYA	60	
QY	61	LYDLGFHFKGVTRFKYGTGKELQSATKSLSRSDINYYGDPVYNHKGADATEDVTA	120	
Db	61	LYDLGFHFKGVTRFKYGTGKELQSATKSLSRSDINYYGDPVYNHKGADATEDVTA	120	
QY	121	DPADRRNVISGHHLIKAWTHFHPFGSGTYSDFPKMHVHFDGTMDBSRLNRIYKFG	180	
Db	121	DPADRRNVISGHHLIKAWTHFHPFGSGTYSDFPKMHVHFDGTMDBSRLNRIYKFG	180	
QY	181	AAMDWEVSNENGYDYLMYADIDYDHPVYAAEIKRMGWYVYANELQDGFSLDVAKH	240	
Db	181	AAMDWEVSNENGYDYLMYADIDYDHPVYAAEIKRMGWYVYANELQDGFSLDVAKH	240	
QY	241	LDVWVNHVREKTKGEMPTVAEYWNQDGALENTLNKTNFNHSHVDDVPLHYGF	300	
Db	241	LDVWVNHVREKTKGEMPTVAEYWNQDGALENTLNKTNFNHSHVDDVPLHYGF	300	
QY	301	GYDMRKLLNGTVVNSKHPLKSVTPVDNHDHPGQSLSTVQTWPKPLA	360	
Db	301	GYDMRKLLNGTVVNSKHPLKSVTPVDNHDHPGQSLSTVQTWPKPLA	360	
QY	361	VFYGMYGTGKDSOREIPALKHKLEPILKARKOYAGAQHDYFDHHDIGVMTRE	420	
Db	361	VFYGMYGTGKDSOREIPALKHKLEPILKARKOYAGAQHDYFDHHDIGVMTRE	420	
QY	421	NSGLAALLTDPBGAKKMYVGRONAGATGMDIGNNSEPVVINSBGMGEFHN	480	
Db	421	NSGLAALLTDPBGAKKMYVGRONAGATGMDIGNNSEPVVINSBGMGEFHN	480	
QY	481	VQR 483		
Db	481	VQR 483		
RESULT 15				
AAW22523				
AAW22523				
standard; protein; 630 AA				


```

XX AAM2523;
XX
AC 17-OCT-2003 (revised)
XX 08-FEB-1998 (first entry)
DT
XX Alpha-amylase-Cena cellulose binding domain hybrid enzyme.
XX
XX Desizing; cellulose; fabric; enzyme hybrid; Termamyl; alpha-amylase;
XX cellulose binding domain; Cena; Bacillus licheniformis;
XX Cellulomonas fiml; protein secretion.
XX
XX Bacillus licheniformis.
XX Cellulomonas fiml; strain ATCC 484.
OS
OS Chimeric.
XX
XX Key location/Qualifiers
XX Peptide 1..29
XX /label= Sig_peptide
XX /note= "Termamyl signal peptide"
XX Protein 20..630
XX /label= Mat_protein
XX /note= "CBD (aa29-147)-Termamyl (aa148-630) hybrid"
XX
XX MO9728256-A1.
XX
XX 07-AUG-1997.
XX
XX 29-JAN-1997; 97WO-DK000041.
XX
XX 29-JAN-1996; 96DK-00000093.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Von Der Osten C, Bjornvad M, Vind J, Raemussen MD;
XX WPI; 1997-402610/37.
XX N-PSDB; AAT77063.
XX
XX Desizing cellulose-containing fabric or textile using an enzyme hybrid -
XX which comprises a catalytically active amino acid sequence of a non-
XX cellulolytic enzyme linked to an amino acid sequence comprising a
XX cellulose binding domain.
XX
XX Example 3; Page 60; 72pp; English.
XX
XX This protein sequence comprises a hybrid enzyme in which Bacillus
XX licheniformis alpha-amylase (Termamyl) signal peptide is linked to the
XX cellulose binding domain (CBD) of Cellulomonas fiml Cena, which is
XX further linked to mature Termamyl polypeptide. The CBD-Termamyl fusion
XX has been expressed and secreted as an approx. 85 kDa protein in Bacillus
XX subtilis PL2306 transformants. A claimed process for desizing cellulose-
XX containing fabric or textile comprises treating the fabric or textile
XX with a modified enzyme (enzyme hybrid) comprising a non-cellulolytic
XX enzyme linked to a CBD. The process gives improved enzyme performance by
XX modifying the enzyme so as to increase its affinity for celluloseic
XX fabric. A desizing composition suitable for use in the process comprises
XX the enzyme hybrid and a wetting agent. (Updated on 17-OCT-2003 to
XX standardise OS field)
XX
XX Sequence 630 AA;
SQ

```

Query Match 100.0%; Score 2666; DB 2; Length 630;
 Best Local Similarity 100.0%; Pred. No. 2.5e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ANLNGTLNQYFEWYMPNQGHRRLONDSAYLAHGTAWMPPAYKGTSGADVGXGAYD 60
DB 148 ANLNGTLNQYFEWYMPNQGHRRLONDSAYLAHGTAWMPPAYKGTSGADVGXGAYD 207
QY 61 LYDLGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGVDVINHKGGADATEDVTAAVEV 120
DB 208 LYDLGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGVDVINHKGGADATEDVTAAVEV 267

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QY 121 DPADRRNVLISGEHLIKAMTHFHPGRGSTYSDFKMHWHFPGTDWDSRKLNRLYKFGOK 180
DB 268 DPADRRNVLISGEHLIKAMTHFHPGRGSTYSDFKMHWHFPGTDWDSRKLNRLYKFGOK 327
QY 181 AMDWEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVHIKFSF 240
DB 328 AMDWEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVHIKFSF 387
QY 241 LRDMVNHVRREKTKEMFTVAEYQNDGALENYLNKTNNHNSVYPDPLHYQFHAASTQGG 300
DB 388 LRDMVNHVRREKTKEMFTVAEYQNDGALENYLNKTNNHNSVYPDPLHYQFHAASTQGG 447
QY 301 GYDMRKILNGTVVSKHPLKSVTFVDNHDTPGQSLBESTVQOTWPKPLAAYATILTRSGYPO 360
DB 448 GYDMRKILNGTVVSKHPLKSVTFVDNHDTPGQSLBESTVQOTWPKPLAAYATILTRSGYPO 507
QY 361 VFYGDWYGTGDSOREIPALKHKIEPILKARKOYAGAODYPDHDIVGWTREGDSSVA 420
DB 508 VFYGDWYGTGDSOREIPALKHKIEPILKARKOYAGAODYPDHDIVGWTREGDSSVA 567
QY 421 NSGLAALITDGPQGAQKMYVGRQNAGETWHDITGNRSEPVVINSSEGVGFHVNGGSVSIY 480
DB 568 NSGLAALITDGPQGAQKMYVGRQNAGETWHDITGNRSEPVVINSSEGVGFHVNGGSVSIY 627
QY 481 VQR 483
DB 628 VQR 630

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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 / Search time 14.8246 Seconds
(without alignments)
3134.012 Million cell updates/sec

Title: US-09-925-576C-8
Perfect score: 2666
Sequence: 1 ANLNGTLMOQFEMWYMPMDQ.....SEGGMFHVNGSVSYVQR 483

Scoring table: BLOSUM62
Gapop 10.0, Gapept 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.78.*
2: p1r1.*
3: p1r2.*
4: p1r3.*
5: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2654	99.5	512	1	ALBSL
2	2184	81.9	514	1	ALBSN
3	1879	70.5	518	1	A27705
4	1786.5	67.0	549	1	A54541
5	1780.5	66.8	549	1	A24549
6	1776.5	66.6	549	1	A24436
7	1715	64.3	548	1	ALBSF
8	1262	47.3	493	2	S15713
9	1244	46.7	492	2	AH2079
10	1233	46.2	484	2	G95160
11	1228	46.1	484	2	P98026
12	1108	41.6	491	2	C68781
13	1091.5	40.9	506	2	G98247
14	1090	40.9	495	2	AD3038
15	1060	39.8	494	1	B45738
16	1053	39.5	494	1	AD0751
17	1047	39.3	495	1	A45738
18	1047	39.3	495	2	B50962
19	1028	38.6	495	2	B85810
20	1024	19.7	217	2	A19506
21	340	12.8	1196	2	A29130
22	321	12.0	826	2	B96720
23	311.5	11.7	421	2	S10514
24	310	11.6	421	2	A55861
25	304	11.4	440	2	S14958
26	302.5	11.3	482	2	S31478
27	300	11.3	437	2	S14956
28	298	11.2	713	2	S09196
29	294	11.0	713	1	ALBSG1

30	292.5	11.0	413	1	ALMT3	alpha-amylase (EC
31	292	11.0	718	1	ALBSGC	cyclomaltoextrin
32	291.5	10.9	718	1	ALBSG6	cyclomaltoextrin
33	290.5	10.9	437	2	JC7138	alpha-amylase (EC
34	290	10.9	437	2	JT0946	alpha-amylase 3B -
35	289	10.8	438	2	S14957	alpha-amylase (EC
36	288	10.8	712	1	ALBSG3	cyclomaltoextrin
37	286	10.7	713	2	A58800	cyclomaltoextrin
38	284.5	10.7	423	2	T09942	alpha-amylase (EC
39	281	10.5	435	2	S12625	alpha-amylase (EC
40	280	10.5	435	1	JC7137	alpha-amylase (EC
41	279	10.5	713	2	ALBSG7	cyclomaltoextrin
42	277.5	10.4	710	2	S63598	cyclomaltoextrin
43	276.5	10.4	718	1	ALBSMX	cyclomaltoextrin
44	275.5	10.3	439	2	T02956	alpha-amylase (EC
45	271.5	10.2	528	1	ALBSK	alpha-amylase (EC

ALIGNMENTS

RESULT 1

ALBSL

alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis

N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C:Species: Bacillus licheniformis

C>Date: 30-Jun-1987 #sequence revision 24-Apr-1998 #ext change 15-Sep-2000

C:Accession: A91997; B24549; A91796; A21663; I39774; I39772; A26151; S53788; A00844

J:Yukki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Teukagoshi, N.; Uda, S.

J: Biochem. 98, 1147-1156, 1985

A:Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylase deduced from the DNA sequences.

A:Reference number: A91997; MUID:86111694; PMID:2418011

A:Accession: A91997

A:Molecule type: DNA

A:Residues: 1-162; 'R', 164-512 <YDU>

A:Cross-references: GB:X03236; NID:g39551; PIDN:CAA26981.1; PID:g39552

A:Experimental source: NCIB 8061

R:Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.

J: Bacteriol. 158, 369-372, 1984

A:Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase

A:Reference number: A91817; MUID:86195857; PMID:3009417

A:Accession: B24549

A:Molecule type: DNA

A:Residues: 1-338; 'G', 340-348; 'S', 350-512 <GRA>

A:Cross-references: GB:M13256; NID:g142510; PIDN:AAA2240.1; PID:g142511

A:Experimental source: NCIB 8061

R:Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.

J: Bacteriol. 158, 369-372, 1984

A:Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase

A:Reference number: A91796; MUID:84185455; PMID:6609154

A:Accession: A91796

A:Molecule type: DNA

A:Residues: 1-104 <STE>

A:Cross-references: GB:K01984; NID:g142432; PIDN:AAA22193.1; PID:g142433

R:Shabkov, M.; Palva, I.

Eur. J. Biochem. 145, 567-572, 1984

A:Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amylase

A:Reference number: A21663; MUID:85076654; PMID:6334606

A:Accession: A21663

A:Molecule type: DNA

A:Residues: 1-3; 'H', 5-12; 'P', 14-47; 'R', 49-61; 'V', 63; 'D', 65-67; 'VA', 70-71; 'S', 73-80; 'D', 82

A:Experimental source: Chromosomal DNA of ATCC 14580

A>Note: the authors translated the codon GGT for residue 48 as Gly and GAC for residue 64

R:laoid, B.M.; Chambliss, G.H.; McConnell, D.J.

J: Bacteriol. 171, 2435-2442, 1989

A:Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent

A:Reference number: I39773; MUID:89213924; PMID:2540150

A:Accession: I39774

A:Molecule type: DNA

A:Status: translated from GB/EMBL/DBD

A:Residues: 1-29 <LAO>

A:Cross-references: GB:M26412; NID:g341477; PIDN:AAA22237.1; PID:g516590

A:Experimental source: Chromosomal DNA of ATCC 14580

A>Note: the authors translated the codon GGT for residue 48 as Gly and GAC for residue 64

R:laoid, B.M.; Chambliss, G.H.; McConnell, D.J.

J: Bacteriol. 171, 2435-2442, 1989

A:Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent

A:Reference number: I39773; MUID:89213924; PMID:2540150

A:Accession: I39774

A:Molecule type: DNA

A:Status: translated from GB/EMBL/DBD

A:Residues: 1-29 <LAO>

A:Cross-references: GB:M26412; NID:g341477; PIDN:AAA22237.1; PID:g516590

R.;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
 Gene 96, 37-41, 1990
 A>Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
 A/Reference number: 139772; MUID:91092499; PMID:2265757
 A/Accession: 139772
 A>Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-32, 'I' <JOR>
 A/Cross-references: GB:M62637; NID:g142498; PIDN:AAA2232.1; PID:g142499
 R;Kum, H.; Fietzek, P.P.; Lampen, J.O.
 J. Bacteriol. 149, 372-373, 1982
 A>Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: compar
 A/Reference number: A26151; MUID:82098050; PMID:6172418
 A/Accession: A26151
 A/Molecule type: protein
 A/Residues: 30-37, 'E', 39-41, 'X', 43-47 <KUH>
 R;Machius, M.; Wiegand, G.; Huber, R.
 J. Mol. Biol. 246, 545-559, 1995
 A>Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2
 A/Reference number: S53788; MUID:95182462; PMID:7877175
 A/Accession: S53788
 A/Molecule type: protein
 A/Residues: 1'D, 220-227 <MAC>
 A/Note: sequence represents amino end of an internal fragment created by a single enzyme
 R;Machius, M.; Wiegand, G.; Huber, R.
 submitted to the Brookhaven Protein Data Bank, July 1995
 A/Reference number: A65206; PDB:1BPL
 A/Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210;222-511
 A/Note: Chese structural studies suggest 163 is leu rather than Arg
 R;Song, H.K.; Hwang, K.Y.; Chang, C.; Suh, S.W.
 submitted to the Brookhaven Protein Data Bank, October 1996
 A/Reference number: A66860; PDB:1VTS
 A/Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210;222-511
 A/Accession: A66860
 A/Note: amyL
 C/Function:
 A>Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Pathway: glycogen/starch degradation
 C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
 C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacc
 F;1-29/Domin: signal sequence #status predicted <SIG>
 F;30-512/Product: alpha-amylase #status predicted <MAT>
 F;227-360/Domin: alpha-amylase core homology <AMY>
 F;133,229,264/Binding site: calcium (Asn, Asp, His) #status experimental
 F;260,290,357/Active site: Asp, Glu, Asp #status experimental

Query Match 99.5%; Score 2654; DB 1; Length 512;
 Best Local Similarity 99.4%; Pred. No. 9.8e-181;
 Matches 480; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANINGTMOYFEWMPNDGQWRLQNDASVLAHGHTAWIPPAVYGTSGADVGYGAYD 60
 DB 30 ANINGTMOYFEWMPNDGQWRLQNDASVLAHGHTAWIPPAVYGTSGADVGYGAYD 89
 QY 61 LYLDGEFHQGTAVTKTKTGELQSAIKSLHSRDINYGAVINHKGADATEDVAVEV 120
 DB 90 LYLDGEFHQGTAVTKTKTGELQSAIKSLHSRDINYGAVINHKGADATEDVAVEV 149
 QY 121 DPADRNVIIGSEHLIKAMTHFHPGRGTYSDFKMWHYHFDGTDWDSRKLNIYKQOK 180
 DB 150 DPADRNVIIGSEHLIKAMTHFHPGRGTYSDFKMWHYHFDGTDWDSRKLNIYKQOK 209
 QY 181 AMWENVENGNVDYMYADIDYHPRVAEIKRWGWYANEOLODFRLDAVKHKFSF 240
 DB 210 AMWENVENGNVDYMYADIDYHPRVAEIKRWGWYANEOLODFRLDAVKHKFSF 269
 QY 241 LRDMVNVREKGTKEMTVAEYQNDGALENYLNKTFNHSFEDVYLHOFPAASTOGG 300
 DB 270 LRDMVNVREKGTKEMTVAEYQNDGALENYLNKTFNHSFEDVYLHOFPAASTOGG 329
 QY 301 GYDMRKILNSTVVSKEPLKAVTFVDNHDTPGQSLSESTVQTWKPLAVALTLRESGYPO 360
 DB 330 GYDMRKILNSTVVSKEPLKAVTFVDNHDTPGQSLSESTVQTWKPLAVALTLRESGYPO 389

QY 361 VFGVDMYGTGDSQRETPALXKITEPLTKARKOYAGACHDYDPDHDIVGWTREGDSSVA 420
 DB 390 VFGVDMYGTGDSQRETPALXKITEPLTKARKOYAGACHDYDPDHDIVGWTREGDSSVA 449
 QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNSESPVINSSEGGEFHVAGGSVSIY 480
 DB 450 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNSESPVINSSEGGEFHVAGGSVSIY 509
 QY 481 VQR 483
 DB 510 VQR 512

RESULT 2
 ALBSN
 N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C/Species: Bacillus amyloliquefaciens
 C/Date: 30-Nov-1980 #sequence revision 30-Jun-1987 #text_change 18-Jun-1999
 C/Accession: A92389; A90307; I39756; I39763; A00843
 R;Takkinen, K.; Fellersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L.
 J. Biol. Chem. 258, 1007-1013, 1983
 A>Title: Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced fr
 A/Reference number: A92389; MUID:83108808; PMID:6185474
 A/Contents: PUB110
 A/Accession: A92389
 A/Molecule type: DNA
 A/Residues: 1-514 <TK>
 A/Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA221;
 R;Chung, J. 185, 387-395, 1980
 Biochem. J. 185, 387-395, 1980
 A>Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amylase.
 A/Reference number: A90307; MUID:80241725; PMID:6156571
 A/Accession: A90307
 A/Molecule type: protein
 A/Residues: 32-53, 'I', 55-63, 'I', 65-78, 'D', 80-83, 'S', 85-222 <CH>
 R;Palva, I.; Fellersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;
 Gene 15, 43-51, 1981
 A>Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t
 A/Reference number: I39756; MUID:82051296; PMID:6170539
 A/Accession: I39756
 A>Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-96 <RES>
 A/Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298
 R;Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karenen, S.
 Gene 59, 161-170, 1987
 A>Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amylase cells by its own
 A/Reference number: I39763; MUID:88137952; PMID:2830166
 A/Accession: I39763
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-39 <RE2>
 A/Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431
 C/Function:
 A>Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Pathway: glycogen/starch degradation
 C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
 C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
 F;1-31/Domin: signal sequence #status predicted <SIG>
 F;32-514/Product: alpha-amylase #status predicted <MT>
 F;229-362/Domin: alpha-amylase core homology <AMY>
 F;133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
 F;262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match 81.9%; Score 2184; DB 1; Length 514;
 Best Local Similarity 80.3%; Pred. No. 2.3e-147;
 Matches 388; Conservative 44; Mismatches 49; Indels 2; Gaps 1;

QY 3 LNTGLMOYFEWMPNDGQWRLQNDASVLAHGHTAWIPPAVYGTSGADVGYGAYDLY 62
 DB 32 LNTGLMOYFEWMPNDGQWRLQNDASVLAHGHTAWIPPAVYGTSGADVGYGAYDLY 91

```

Qy 63 DLGEFHQKGVTRTKYGTGKELQSAIKSLHSRDINVGDVVINKHGADATEDVTAVEVDP 122
Db 92 DLGEFHQKGVTRTKYGTGKSELQSAIKSLHSRNVDVVLNKHAGADATEDVTAVEVNP 151
Qy 123 ADNRNVIAGEHLIKAMTHFHPGRGSTYSPFKMWHYFDGTDWDESKLARIYKF--QK 180
Db 152 ANRQVTESEYQIYKAMVDFPRGRGNTYSPFKMWHYFDGADWDESKRISIFKFRGEK 211
Qy 181 AMDVEVSENGNVDYLYMADIDVHDHPVAEIKRWGTYANELQDGFRLDAYKHIFSF 240
Db 212 AMDVEVSENGNVDYLYMADVDYDHPVAETKMGIMYANESLDFRIDAAGHIFSF 271
Qy 241 LRDVNVHREKTKEMFTVAEYQNDLGALENYLNTKTNFNSVDPVPLHYQFHAASQGG 300
Db 272 LRDVNVHREKTKEMFTVAEYQNDLGALENYLNTKTNFNSVDPVPLHYQFHAASQGG 331
Qy 301 GYDMRKLINGTVSKHPLKSVTFVNDHDTOPGSLSTVQTFWPKPLAYAFILTRREGSPQ 360
Db 332 GYDMRKLINGTVSKHPLKSVTFVNDHDTOPGSLSTVQTFWPKPLAYAFILTRREGSPQ 391
Qy 361 VFYGDWYGTGKDSOREIPALKHKIEPIIKARKQYVGAQHDYFDHDIIVGWTREGSSVA 420
Db 392 VFYGDWYGTGKDSOREIPALKHKIEPIIKARKQYVGAQHDYFDHDIIVGWTREGSSVA 451
Qy 421 NSGIALITDGPQAKRMVYGRONAGETWHDITGNRSEPVYINSEGMGEFHVNGGSVSY 480
Db 452 KSGIALITDGPQAKRMVYGRONAGETWHDITGNRSDTVKISDGMGEFHVNGGSVSY 511
Qy 481 VQR 483
Db 512 VQR 514

```

RESULT 3

```

alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C:Species: Bacillus sp.
C:Date: 31-Mar-1999 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
A:Accession: A27705
R:Tokamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yaman, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A:Title: Nucleotide sequence of the maltotetraose-producing amylase gene from an alkalophilic
A:Reference number: A27705; MUID:88162814; PMID:3258152
A:Accession: A27705
A:Molecule type: DNA
A:Residues: 1-518 <TSU>
A:Cross-references: GB:M18862; NID:G142496; PID:AAA22231.1; PID:G142497
A:Experimental source: chromosomal DNA of strain 707
A:Note: amino end of mature protein also determined
C:Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F/1-33/Domain: signal sequence #status predicted <SIG>
F/34-518/Product: alpha-amylase #status experimental <MAT>
F/236-369/Domain: alpha-amylase core homology <AMY>
F/139,228,273/Binding site: calcium (Asn, Asp, His) #status predicted
F/269,299,366/Active site: Asp, Glu, Asp #status predicted

```

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Query Match 70.5%; Score 1879; DB 1; Length 518;
Best Local Similarity 67.8%; Pred. No. 1e-125;
Matches 329; Conservative 67; Mismatches 79; Indels 10; Gaps 4;

```

```

Qy 4 NGTLMQYFEMTENDGQWRRLQNDASVLAHGTAVWIPPAKYGTSGADVGYAYD 63
Db 39 NGTLMQYFEMTLPNDGNMNRNLNSDASNLKSGITAVWIPPAWKASQNDVGAYAYD 98
Qy 64 LGEFHQKGVTRTKYGTGKELQSAIKSLHSRDINVGDVVINKHGADATEDVTAVEV 123

```

```

Db 99 LGEFHQKGVTRTKYGTGKELQSAIKSLHSRDINVGDVVINKHGADATEDVTAVEVNP 158
Qy 124 DNRNVIAGEHLIKAMTHFHPGRGSTYSPFKMWHYFDGTDWDESKLARIYKFQ--GK 180
Db 159 NRQVTESEYQIYKAMVDFPRGRGNTYSPFKMWHYFDGTDWDESKLARIYKFQ--GK 218
Qy 181 AMDVEVSENGNVDYLYMADIDVHDHPVAEIKRWGTYANELQDGFRLDAYKHIFSF 240
Db 219 AMDVEVSENGNVDYLYMADIDVHDHPVAEIKRWGTYANELQDGFRLDAYKHIFSF 278
Qy 241 LRDVNVHREKTKEMFTVAEYQNDLGALENYLNTKTNFNSVDPVPLHYQFHAASQGG 300
Db 279 LRDVNVHREKTKEMFTVAEYQNDLGALENYLNTKTNFNSVDPVPLHYQFHAASQGG 338
Qy 301 GYDMRKLINGTVSKHPLKSVTFVNDHDTOPGSLSTVQTFWPKPLAYAFILTRREGSPQ 360
Db 339 NYDMRKLINGTVSKHPLKSVTFVNDHDTOPGSLSTVQTFWPKPLAYAFILTRREGSPQ 398
Qy 361 VFYGDWYGTGKDSOREIPALKHKIEPIIKARKQYVGAQHDYFDHDIIVGWTREGSSVA 428
Db 399 VFYGDWYGTGKDSOREIPALKHKIEPIIKARKQYVGAQHDYFDHDIIVGWTREGSSVA 453
Qy 419 VANSGLALITDGPQAKRMVYGRONAGETWHDITGNRSEPVYINSEGMGEFHVNGGSVSY 478
Db 454 HPMNSGLALITDGPQAKRMVYGRONAGETWHDITGNRSEPVYINSEGMGEFHVNGGSVSY 513
Qy 479 IYVQR 483
Db 514 IYVQR 518

```

RESULT 4

```

alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DNI792)
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus stearothermophilus
C:Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
A:Accession: A54541
R:Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEBS Microbiol. Lett. 77, 271-276, 1991
A:Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A:Reference number: A54541
A:Accession: A54541
A:Molecule type: DNA
A:Residues: 1-549 <JOR>
A:Cross-references: GB:X59476
A:Experimental source: chromosomal DNA of strain DNI792
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetic:
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacchi
F/1-34/Domain: signal sequence #status predicted <SIG>
F/35-549/Product: alpha-amylase #status predicted <MAT>
F/235-368/Domain: alpha-amylase core homology <AMY>
F/139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F/266,298,365/Active site: Asp, Glu, Asp #status predicted

```

```

Query Match 67.0%; Score 1786.5; DB 1; Length 549;
Best Local Similarity 64.7%; Pred. No. 4e-119;
Matches 314; Conservative 68; Mismatches 98; Indels 5; Gaps 2;

```

```

Qy 1 ANLNGTLMQYFEMTENDGQWRRLQNDASVLAHGTAVWIPPAKYGTSGADVGYAYD 60
Db 36 APNGTLMQYFEMTLPNDGNMNRNLNSDASNLKSGITAVWIPPAWKASQNDVGAYAYD 95
Qy 61 LGEFHQKGVTRTKYGTGKELQSAIKSLHSRDINVGDVVINKHGADATEDVTAVEV 120
Db 96 LGEFHQKGVTRTKYGTGKELQSAIKSLHSRDINVGDVVINKHGADATEDVTAVEV 155

```


C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F/1-34/Domain: signal sequence #status predicted <SIG>
F/35-549/Product: alpha-amylase #status experimental <MAT>
F/235-368/Domain: alpha-amylase core homology <AMY>
F/139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F/268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 66.6%; Score 1776.5; DB 1; Length 549;
Best Local Similarity 64.7%; Pred. No. 2.1e-118;
Matches 314; Conservative 66; Mismatches 100; Indels 5; Gaps 2;

```
QY 1 ANLNGTLMQYFEWMPNDGQWRLQNDASVLAHGTAWIPRAYKTSQADVGYAYD 60
DB 36 APFGTMMQYFEWLPDGLMTWVANEANLSSIGITALMLPPAYKTSQADVGYAYD 95
QY 61 LYDGEFHQKGTVTKTKGTGELQSAIKSLHSRDINYGDVVNHKGGADATEDVTAVEV 120
DB 96 LYDGEFNQKGAVTTKTKGTQAYIQALQAAHAGQYADVVPDHKGGADTEWDAVEV 155
QY 121 DPADRNVISGEHLIKAMTFHFPGRGSTYSDFKMHYHFDGTDWDSRKLRIYKFO-- 178
DB 156 NPSDRNGEISGTQIQAWTKDFPGRGNTYSSFKRWYHFDGVDMDSRKLRIYKRG 215
QY 179 GKAMDVEVSNENGYDYLMTADIDYHPDVAAEIKRGTYANELQDGRDLAVKIKF 238
DB 216 GKAMDVEVDENGYDYLMADIDMDHPEVTELSKMGKVVNTNIDGRDLAVKIKF 275
QY 239 SFLADWNVHREKTKGKMFVAEYQNDLGALENYLKNFNSHVPVPLHYOFHAATQ 298
DB 276 SFPEDMLSTVRSQTKPLFTVGEYWSYDINKLHNYIMKNTGMSLFPALPNKKYTKS 335
QY 299 GGGYDMKRLNGTVVSKHPLKSVTFVNDHDTOPQSLSTVQTWFKPLAAYAFILTR 358
DB 336 GGTDTMTMTNTLMKQPTLAVTFVNDHDTOPQALQSWDPFKPLAAYAFILTR 395
QY 359 PÖVFYGMGTGKDSQREIPALKEIPILKARKQYAGAHDFDHHDIVGTRBDDSS 418
DB 396 PCVFYGGDYGI---PÖYNIPLSKIDPLIARDYVAGTÖHDYLDSDIIGWTR 452
QY 419 VANSGLAALLTDGPGKRWYVGRONAGETMHDITGRSEVNVNSHGEFHNNGSVS 478
DB 453 KPQSGLAALLTDGPGSKRMVYGRQAGKVFYDLTGKRSPTVTIINSOGWGEFKN 512
QY 479 IYVOR 483
DB 513 VWVPR 517
```

RESULT 7
ALBSF

alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DY-5) plasmid
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus stearothermophilus
C/Date: 30-Jun-1997 #sequence_revision 30-Jun-1987 #text_change 16-Feb-1997
C/Accession: A91999; B91804; A00845
R/Ihara, H.; Sasaki, T.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uda, S.
J. Biochem. 98, 95-103, 1985
A/Title: Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology bet
A/Reference number: A91999; MUID:86008166; PMID:3876333
A/Accession: A91999
A/Molecule type: DNA
A/Residues: 1-548 <IH1>
A/Cross-references: GB:X02769
A/Experimental source: plasmid pHI300 from strain DY-5
A/Accession: B91999
A/Molecule type: protein
A/Residues: 35-48 <IH2>
A/Experimental source: strain DY-5
R/Tsukagoshi, N.; Iritani, S.; Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata,

J. Bacteriol. 164, 1182-1187, 1985
A/Title: Efficient synthesis and secretion of a thermophilic alpha-amylase by protein-pr
A/Reference number: A91804; MUID:86059211; PMID:2999073
A/Contents: B9A01
A/Accession: A91804
A/Molecule type: DNA
A/Residues: 1-29, 'Q', '31-75', 'W', '77-122' <TSU>
A/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C/Genetics:
A/Genome: plasmid
A/Scat. codon: GTG
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F/1-34/Domain: signal sequence #status predicted <SIG>
F/35-548/Product: alpha-amylase #status experimental <MAT>
F/235-368/Domain: alpha-amylase core homology <AMY>
F/139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F/268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 64.3%; Score 1715; DB 1; Length 548;
Best Local Similarity 63.1%; Pred. No. 4.8e-114;
Matches 306; Conservative 67; Mismatches 106; Indels 6; Gaps 3;

```
QY 1 ANLNGTLMQYFEWMPNDGQWRLQNDASVLAHGTAWIPRAYKTSQADVGYAYD 60
DB 36 APFGTMMQYFEWLPDGLMTWVANEANLSSIGITALSLPPAYKTSQADVGYAYD 95
QY 61 LYDGEFHQKGTVTKTKGTGELQSAIKSLHSRDINYGDVVNHKGGADATEDVTAVEV 120
DB 96 LYDGEFNQKGAVTTKTKGTQAYIQALQAAHAGQYADVVPDHKGGADTEWDAVEV 155
QY 121 DPADRNVISGEHLIKAMTFHFPGRGSTYSDFKMHYHFDGTDWDSRKLRIYKFO-- 178
DB 156 NPSDRNGEISGTQIQAWTKDFPGRGNTYSSFKRWYHFDGVDMDSRKLRIYKRG 215
QY 179 GKAMDVEVSNENGYDYLMTADIDYHPDVAAEIKRGTYANELQDGRDLAVKIKF 238
DB 216 GKAMDVEVDENGYDYLMADIDMDHPEVTELSKMGKVVNTNIDGRDLAVKIKF 275
QY 239 SFLADWNVHREKTKGKMFVAEYQNDLGALENYLKNFNSHVPVPLHYOFHAATQ 298
DB 276 SFPEDMLSTVRSQTKPLFTVGEYWSYDINKLHNYITKNTGMSLFPALPNKKYTKS 335
QY 299 GGGYDMKRLNGTVVSKHPLKSVTFVNDHDTOPQSLSTVQTWFKPLAAYAFILTR 358
DB 336 GGFADMTMTNTLMKQPTLAVTFVNDHDTNPAKRC-SHGRPFKPLAAYAFILTR 394
QY 359 PÖVFYGMGTGKDSQREIPALKEIPILKARKQYAGAHDFDHHDIVGTRBDDSS 418
DB 396 PCVFYGGDYGI---PÖYNIPLSKIDPLIARDYVAGTÖHDYLDSDIIGWTR 451
QY 419 VANSGLAALLTDGPGKRWYVGRONAGETMHDITGRSEVNVNSHGEFHNNGSVS 478
DB 452 KPQSGLAALLTDGPGSKRMVYGRQAGKVFYDLTGKRSPTVTIINSOGWGEFKN 511
QY 479 IYVOR 483
DB 512 VWVPR 516
```

RESULT 8

alpha-amylase (EC 3.2.1.1) - Bacillus circulans
C/Species: Bacillus circulans
C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C/Accession: S15713
R/Marcel, T.
submitted to the EMBL Data Library, May 1991
A/Reference number: S15713
A/Accession: S15713


```
QY 64 LGEEHOKGVATKXGKELQSAIKSLHSRDINVGAVINHGKADATEDVTAVEVPA 123
D 63 LGEEHOKGVATKXGKEDYVQALQALKAQGIQPMADVLNHNKAADHREAFVYIEVDV 122
QY 124 DRNREVIAGEHLIKAWTHFHPGRSGTYSDFKMHYHFDGTDWDSRKLNRITYKQG--KA 181
D 123 DRVTELGEPFTINQMTSFTFDGRDVTYNGFHMWHYHFGTDYDAKRKSGIYLLIQGNKG 182
QY 182 WDE--VSNENGVNLYMADIDYDHPVAEIKRWGTWYANELQDGFRLDAVKHKFS 239
D 183 WANEELVDNENGVNLYMADIDYDHPVAEIKRWGTWYANELQDGFRLDAVKHKFS 242
QY 240 FLRDVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFNSHVFDPYLFHQAASQ 299
D 243 FMRNFIDMEKRYGDDYVGEFPMNPKDKEANLDLEKTEEHFHDVDRLOHNLFEASQ 302
QY 300 GGYDMRLKLVGSKPLKSVTFVNDHTOPQGSLESTVQWTKPLAFAVILTRREGYP 359
D 303 ANYDLRGIFFTSLVELKPKDAVTFVNDHTOPQGSLESTVQWTKPLAFAVILTRREGYP 362
QY 360 QVEFGDMYGTGKSQREIPALKHKEPILKARKQAYGAOHYEDHNDIVGWTREGDSSV 419
D 363 CVFYGDYVYGSQYAO--DFKEILDRLLAIKDLAYGEQNDYFDHANCIGWVSGAEN- 419
QY 420 ANSGALALITDPGAGARMYVGRONAGETWHDITGNSEPVINSSEGMEPHVNGSVSI 479
D 420 -QSPVAVLISNDQNSKSMFVGQEMTQTFVLDLGNHOGVTTIDEGYGFPPVARSYSV 478
QY 480 Y 480
D 479 W 479
```

RESULT 11

```
alpha-amylase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)
P98026
C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C/Accession: P98026
R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
a, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Balaz, R.H.; Jaskunas, S.R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:2143245; PMID:11544234
A/Accession: P98026
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-484 <KIR>
A/Cross-references: GB:AE007317; PIDN:AL00043.1; PID:915458876; GSPDB:GN00174
A/Genetics:
A/Gene: amy
C/Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C/Keywords: glycosidase; hydrolase
```

```
Query Match 46.1%; Score 1228; DB 2; Length 484;
Best Local Similarity 48.2%; Pred. No. 1.5e-79;
Matches 232; Conservative 75; Mismatches 166; Indels 8; Gaps 4;

QY 4 NGTLMQFEWMPNDGQHWRRLQNDASVLAHEGITA VWPAYKGTSGQADYGYADLYD 63
D 3 NGTLMQFEWMPNDGQHWRRLQNDASVLAHEGITA VWPAYKGTSGQADYGYADLYD 62
QY 64 LGEEHOKGVATKXGKELQSAIKSLHSRDINVGAVINHGKADATEDVTAVEVPA 123
D 63 LGEEHOKGVATKXGKEDYVQALQALKAQGIQPMADVLNHNKAADHREAFVYIEVDV 122
QY 124 DRNREVIAGEHLIKAWTHFHPGRSGTYSDFKMHYHFDGTDWDSRKLNRITYKQG--KA 181
D 123 DRVTELGEPFTINQMTSFTFDGRDVTYNGFHMWHYHFGTDYDAKRKSGIYLLIQGNKG 182
```

```
QY 182 WDE--VSNENGVNLYMADIDYDHPVAEIKRWGTWYANELQDGFRLDAVKHKFS 239
D 183 WANEELVDNENGVNLYMADIDYDHPVAEIKRWGTWYANELQDGFRLDAVKHKFS 242
QY 240 FLRDVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFNSHVFDPYLFHQAASQ 299
D 243 FMRNFIDMEKRYGDDYVGEFPMNPKDKEANLDLEKTEEHFHDVDRLOHNLFEASQ 302
QY 300 GGYDMRLKLVGSKPLKSVTFVNDHTOPQGSLESTVQWTKPLAFAVILTRREGYP 359
D 303 ANYDLRGIFFTSLVELKPKDAVTFVNDHTOPQGSLESTVQWTKPLAFAVILTRREGYP 362
QY 360 QVEFGDMYGTGKSQREIPALKHKEPILKARKQAYGAOHYEDHNDIVGWTREGDSSV 419
D 363 CVFYGDYVYGSQYAO--DFKEILDRLLAIKDLAYGEQNDYFDHANCIGWVSGAEN- 419
QY 420 ANSGALALITDPGAGARMYVGRONAGETWHDITGNSEPVINSSEGMEPHVNGSVSI 479
D 420 -QSPVAVLISNDQNSKSMFVGQEMTQTFVLDLGNHOGVTTIDEGYGFPPVARSYSV 478
QY 480 Y 480
D 479 W 479
```

RESULT 12

```
alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C68781
C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C/Accession: C68781
R/Bolotin, A.; Mincer, P.; Manger, S.; Jallou, O.; Malame, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A/Reference number: A86625; MUID:21235186; PMID:11337471
A/Accession: C68781
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-491 <SNO>
A/Cross-references: GB:AE005176; PID:912724224; PIDN:AAK05349.1; GSPDB:GN00146
A/Experimental source: strain IL1403
A/Genetics:
A/Gene: amyL
C/Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
```

```
Query Match 41.6%; Score 1108; DB 2; Length 491;
Best Local Similarity 41.7%; Pred. No. 5e-71;
Matches 204; Conservative 93; Mismatches 168; Indels 24; Gaps 7;

QY 6 TLMQFEWMPNDGQHWRRLQNDASVLAHEGITA VWPAYKGTSGQADYGYADLYD 64
D 3 TLMQFEWMPNDGQHWRRLQNDASVLAHEGITA VWPAYKGTSGQADYGYADLYD 62
QY 65 GEEHOKGVATKXGKELQSAIKSLHSRDINVGAVINHGKADATEDVTAVEVPA 123
D 63 GEEHOKGVATKXGKEDYVQALQALKAQGIQPMADVLNHNKAADHREAFVYIEVDV 122
QY 124 DRNREVIAGEHLIKAWTHFHPGRSGTYSDFKMHYHFDGTDWDSRKLNRITYKQG--KA 181
D 123 DRVTELGEPFTINQMTSFTFDGRDVTYNGFHMWHYHFGTDYDAKRKSGIYLLIQGNKG 182
QY 182 WDE--VSNENGVNLYMADIDYDHPVAEIKRWGTWYANELQDGFRLDAVKHKFS 239
D 183 WANEELVDNENGVNLYMADIDYDHPVAEIKRWGTWYANELQDGFRLDAVKHKFS 242
QY 240 FLRDVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFNSHVFDPYLFHQAASQ 299
D 243 FMRNFIDMEKRYGDDYVGEFPMNPKDKEANLDLEKTEEHFHDVDRLOHNLFEASQ 302
QY 300 GGYDMRLKLVGSKPLKSVTFVNDHTOPQGSLESTVQWTKPLAFAVILTRREGYP 359
D 303 ANYDLRGIFFTSLVELKPKDAVTFVNDHTOPQGSLESTVQWTKPLAFAVILTRREGYP 362
QY 360 QVEFGDMYGTGKSQREIPALKHKEPILKARKQAYGAOHYEDHNDIVGWTREGDSSV 419
D 363 CVFYGDYVYGSQYAO--DFKEILDRLLAIKDLAYGEQNDYFDHANCIGWVSGAEN- 419
QY 420 ANSGALALITDPGAGARMYVGRONAGETWHDITGNSEPVINSSEGMEPHVNGSVSI 479
D 420 -QSPVAVLISNDQNSKSMFVGQEMTQTFVLDLGNHOGVTTIDEGYGFPPVARSYSV 478
QY 480 Y 480
D 479 W 479
```

QY 362 FYGMMYKKSGSQRIPALKKHIEPI-----LKARQVAYGQCHYPFDHDIWGVTRE 414
 |||::|||
 Db 360 FMSGLYG-----IES--HNVPVEGNLRTMLAKRDSFLKENYIFDHPDILIGWTNI 409
 QY 415 GDSSVANSGLAALLTTDFGGAKRMRYVRQNRAGETMHMDITGKRSEPVYINSQGWEEFYNG 474
 |||::|||::|||::|||::|||::|||::|||
 Db 410 LKIDNKEYSGLCILLTNKNGSSKYMILDKAVAGKVIYIDLFGHEHLPITLDNGAGAEFYND 469
 QY 475 GSVSIIYQR 483
 |||::|||
 Db 470 GSVSIVWDK 478

RESULT 13

cytoplasmic alpha-amylase (1,4-alpha-d-glucan glucanohydrolase) [imported] - Agrobacterium
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C:Accession: G98247
R:Goodner, B.; Hinkley, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, B.;
A.: Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G98247
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1556 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:ig15159379; GSFDB:GN00170
C:Genetics:
A:Gene: AGR_L_1863
A:Map position: linear chromosome
A:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match	40.9%	Score 1031.5;	DB 2;	Length 506;
Best Local Similarity	44.3%	Pred. No. 7.7e-70;		
Matches 219; Conservative	80;	Mismatches 178;	Indels 17;	Gaps 6;

```

Qy 2 NING-TIMQVEBWMIPNDQGMRLQNDSAVLAHEGITAWEIPRAYKGTSGA-DVYGAY 59
Db 11 NMAGRITLQFHMWYIPDQGLKMSBEAEKASLACKGILTDWLPAYKGAAMGYSVGDITY 70
Qy 60 DLYDLGEFHQGIYRKTYKGBELQSAIKSLHSDINVYGDVYNHKGADATEDVTAVE 119
Db 71 DLFPLGEPDQGGVATKXGDBRAALEHAGKTLKONGIRIVHDVVLNHMGADEKEKAVRR 130
Qy 120 VDPADRRRVISGEHLIKMTHTFHPRGSGTYSDBKMTMYHEDGDMDESKLTANITYFGG 179
Db 131 VNPDRDITDDEDPPALAYTRFTFPPGRNGKSKFTWDLKCSGVADHLEPTDEIDFRLVN 190
Qy 180 K----AMDWEVSNNNGVNDYLMVADIDYDHDHVAALIKRMGTWANELOLDFGLDVAVK 235
Db 191 EYDGEWNNBEVDQNGNPNFDYLMGADVEPRNAAVVEELKYMGRWLSQGVQVDFRLDAKH 250
Qy 236 IKESFLADWNVHVAEKGKEMFTVAEYQONDGLALENTAKTNHNSVFRVPLHYOHA 295
Db 251 IPANFFPDWGHMBEYVDPDLFEVAEYWHPDLEAKSLBELVDKQMLFDVALHSHSDA 310
Qy 296 STQGGGVDMRLKLTNGTVASKPLKSVTFVNDHNDPOQGSLESTVQTWFKPLAYAFITRE 355
Db 311 SKQGGDDPMRSILPQGLSVSAVPRDHAVTLLVDNHDPQLQSLSEAPVPEPMFKPLAYAILLRE 370
Qy 356 SGYQVRYGDMYGTK-----GDSQRELPALKNKTEPILKAKQVAYGAQNDYPRHND 407
Db 371 EGVACVFPDPLFGNISYTDYTDGNDGNEYKIDIPALICLPKLLEARSFRANGQOTDIFPDAS 429
Qy 408 IVGTTRGSDSVANSGLAALITDGPGAKRMYVRQUNAGETWMDITGNRSEPVYNSEGW 467
Db 430 CIAIRIRIGTADA--PGCVVWMSNGBPEBKQADLPEBAGSVWRDPLGHRHEHITLDESCK 487
Qy 468 GEPHVNGGSVSIVY 481
Db 488 GTFPTNGGSVSVMV 501

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RESULT 14
AD3038

RESULT 14

alpha-amylase amya [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: ADJ038
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, J.; Gillet, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClelland,
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.

A;Title:

A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD3038
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1495 <KUR>
A:Cross-reference: GB:AB008689; PTDN:PALM44722.1; PID:gl1742354; GSPDB:GN00187
A:Experimental source: Strain C58 (Dupont)
C:Genetics:
C:Gene: amyA
A:Map position: linear chromosome
A:Superfamily: alpha-amyase, amyloidiquefaciens type; alpha-amyase core homology

Query Match 40.9%; Score 1090; DB 2; Length 495;

Matches 217; Conservative 79; Mismatches 177; Indels 16; Gaps 5;

6 TIMOYFEWMPNDGOHWRRLONDSAYLAEHGITAVWIPPAYKGTSA-DVGYGAYDLYDL

5 T L O E F H W Y P D G C K T W S E V A R K A E S T A K M G T I N V M T P R A Y K G A A G Y S V G Y D T Y D I E D I

[illegible][illegible][illegible]

123 KIDIDBDFALMAY IN IFFONUNGNIBNE I NDNCEB DV CHIEER A EDOITAEVNUOZO ZO

181 AWDWEVSNGNYDLYMAYDIDYDHPDVAEELKRWGIMIANELQJDDGFRDDAVAHINFSF 240

Db 185 EWNEEVDQENGNF DYLNGADVEFRNRAYEELKTYGRWLSEQVQVDGFRLDAAKHLPAWF 24

241 LRDMVNHVREKTGKEMFTVAEYWÖNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTÖGG 300

Db 245 FRDWVGHMETVDPDLFVVAEYWHPDLEALKSYLELVDKQLMLFDVALHHSFHDASKQGG 304

301 GYDMRKLNGTVSKHPLKSVTFVDNHDTPGQSLBSTVQTFEKLAYAFILTRSGYPQ 360

305 DEFMSTFDGSLVAVPDHATLVNDHDTOPLOSLFAPVEPWFKPLAYATILLREEGVPC 364

361 YEVGDMYTK-----GDSQRETPAI.KHKTEPTI.KARKOYAYGAOHVYEDHHDIVGWT 412

367 YUWNU TCGUYMTGNCUNWVUTDATE CI DVI TEAPREANCPDNTFNDACTAET 433

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

[illegible]

Table 1

Variable	Mean	SD	Range
Age	60.7	8.9	45-78
Gender			
Male	10		
Female	10		
Marital status			
Married	10		
Single	10		
Widowed	10		
Divorced	10		
Educational level			
High school or less	10		
Bachelor's degree	10		
Master's degree	10		
PhD	10		
Occupation			
Retired	10		
Professional	10		
Managerial	10		
Technical	10		
Clerical	10		
Unemployed	10		
Health status			
Excellent	10		
Good	10		
Fair	10		
Poor	10		
Very poor	10		
Functional status			
Independent	10		
Dependent	10		
Mental health			
Stable	10		
Unstable	10		
Social support			
High	10		
Low	10		
Life satisfaction			
High	10		
Low	10		

[illegible]

DB 482 NGGSVSVWV 490

RESULT 15

B45738
alpha-amylase (EC 3.2.1.1), cytosolic - *Salmonella typhimurium*
N,Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: *Salmonella typhimurium*

C>Date: 07-Apr-1994 #sequence revision 18-Aug-1995 #text change 18-Jun-1999
C/Accession: B45738
R/Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 174, 6644-6652, 1992
A/Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.
A/Reference number: A45738; MUID:93015717; PMID:1400215
A/Accession: B45738
A/Molecule type: DNA
A/Residues: 1-494 <RAH>
A/Cross-references: GB:L01643; NID:g154043; PIDN:AAA27110.1; PID:g154045
C/Genetics:
A/Gene: amyA
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C/Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
F/202-335/Domain: alpha-amylase core homology <AMY>
F/239,265,332/Active site: His, Glu, Asp #status predicted

Query March 39.8%; Score 1060; DB 1; Length 494;
Best Local Similarity 42.4%; Pred. No. 1,38-67;
Matches 208; Conservative 88; Mismatches 179; Indels 16; Gaps 6;

```
QY 4 NGTLMQYFEWYMPNDQGMRLQNSAYLAHGIITAVWIPYKGTSA-DVGYGAYDLY 62
Db 3 NPTLLQYFHWYYPDGKLMSELARADGLNDIGINMWLPACKGASGVSGYDTYDLF 62
QY 63 DLGEFHOKGVTRYKGTGELQSAIKSLHSDINVGDVVINHGKADATEDVTAYEVD 122
Db 63 DLGEFDQKGTATKYGDKRQLTATDALKKNNIAVLDDVVVNHKMGADKKERIRVQRVNO 122
QY 123 ADNRKRVSGEHLIAKMTHEHPPGSGTYSDEKMTWHFPGTMDKSRKLRITYK---FQ 178
Db 123 DDKTQIDNITIECGWTRTYTPARAGQSNFTWYHCGSGIDHIEPDEDEGFIKIVNDYT 182
QY 179 GKAWDMEVSNENGNVYDLYADIDYDHPVNAEIKRWGTWYANELQDGFRLDAVKIKF 238
Db 183 GDSKNDQVDDMGNFIDLMGNIIDFRNHAYTEIKYARWMEQTHCDGFRLLDAVKIIPA 242
QY 239 SFLADWVNHVREKTKGEMFTVAEYWNQDLGALENYLNKTNFNHSPFVPLHYQFHAATQ 298
Db 243 WFYKEMTIEHQAVAPKPLFIYAAYSHVEDLQTYIDQVQDKTMLPDAPLQMKFHEASRQ 302
QY 299 GCGYDMKRLANGTVSKHPLKSVTFVNDHDPQGSLESTVQTEKPLAVAFILTRSGY 358
Db 303 GAEDYMRHIFGTIVLEADPFHATVTVANHDTPQLALBAPVEPWPFKPLAYALILRENGV 362
QY 359 POFVYGMVGT-----KGSOR-ETPALGKIEPIIKAKOYAYGAQHDFPDHDI 410
Db 363 PSVFYPLDYKASYDSGSENGETCRVDMVT-NQLDRLIARQRAHGIQTLFFDHPCIA 421
QY 411 WTRGDSVANSGLAALITDPGAKRMVYGRONAGETMHDITGNRSEPVVINSGWGEF 470
Db 422 FSRSGTEE--NPGCVVVLNSNDDEKTLILLGDYANKTWRFSGNRDEYVVTNQGEATF 479
QY 471 HVGGSVSIYV 481
Db 480 FCNAGSVSVWV 490
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Search completed: October 7, 2004, 00:20:44
Job time : 15.8246 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 6, 2004, 23:46:32 ; Search time 8.47121 Seconds

(without alignments)
2968.867 Million cell updates/sec

Title: US-09-925-576C-8

Perfect score: 2666
Sequence: 1 ANANGTLMQYFEWYMPNDQ.....SEGKGEFHVNGGSVSIYQR 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2648	99.3	512 1 AMY_BACLI	P06278 bacillus 11
2	2184	81.9	514 1 AMY_BACAM	P00692 bacillus am
3	1879	70.5	518 1 AMT6_BACS7	P19571 bacillus sp
4	1776.5	66.6	549 1 AMY_BACST	P06279 bacillus st
5	1058	39.7	494 1 AMY2_SALTU	P26613 salmonella
6	1047	39.3	495 1 AMY2_ECOLI	P26612 escherichia
7	340	12.8	1196 1 AMYB_PABPO	P21543 penibacilli
8	311.5	11.7	421 1 AMYA_VIGMU	P17859 vigna mungo
9	304	11.4	440 1 AM3A_ORYSA	P27932 oryza sativ
10	300	11.3	437 1 AM3C_ORYSA	P27933 oryza sativ
11	298	11.2	713 1 CDGT_BAC8	P17692 bacillus sp
12	294	11.0	713 1 CDGT_BAC80	P05618 bacillus sp
13	292.5	11.0	413 1 AMY3_WHEAT	P08117 triticum ae
14	292	11.0	718 1 CDGT_BACCI	P30920 bacillus ci
15	291.5	10.9	718 1 CDGT_BACSS	P31747 bacillus sp
16	290	10.9	437 1 AM3E_ORYSA	P27934 oryza sativ
17	289	10.8	438 1 AM3B_ORYSA	P27937 oryza sativ
18	288	10.8	712 1 CDGT_BACS3	P09121 bacillus sp
19	286	10.7	713 1 CDGU_BACCI	P43379 bacillus ci
20	281	10.5	435 1 AM3D_ORYSA	P27933 oryza sativ
21	279	10.5	713 1 CDGT_BACSP	P30921 bacillus sp
22	277.5	10.4	710 1 CDGT_THERU	P26827 thermocae
23	276.5	10.4	718 1 CDGT_BACLI	P14014 bacillus 11
24	271.5	10.2	528 1 AMY_BACCI	P08137 bacillus ci
25	262	9.8	494 1 AMY1_SACRI	P21567 saccharomyc
26	259	9.7	368 1 AMY3_HORVU	P04747 hordeum vul
27	259	9.7	429 1 AMY2_HORVU	P04063 hordeum vul
28	259	9.7	429 1 AMY6_HORVU	P04750 hordeum vul
29	257	9.6	428 1 AMY1_ORYSA	P17654 oryza sativ
30	252.5	9.5	438 1 AMY1_HORVU	P00693 hordeum vul
31	247	9.3	441 1 MGTA_THENA	P80099 thermotoga
32	245.5	9.2	719 1 AMYM_BACST	P19531 bacillus st
33	242.5	9.1	443 1 AM2A_ORYSA	P27935 oryza sativ

ALIGNMENTS

RESULT 1	AMY_BACLI	STANDARD;	PRT;	512 AA.
AC	P06278; 084171;			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan			
DE	glucanohydrolase) (BLA).			
GN	AMYS OR AMYL.			
OS	Bacillus licheniformis.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
NCBI_TaxId=1402;				
LN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC 27811;			
RA	MEDLINE=6611694; PubMed=2418011;			
RA	Yunkel T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,			
RA	Teukagoshi N., Uda S.;			
RT	"Complete nucleotide sequence of a gene coding for heat- and			
RT	pH-stable alpha-amylase of Bacillus licheniformis: comparison of the			
RT	amino acid sequences of three bacterial liquefying alpha-amylases			
RT	deduced from the DNA sequences."			
RL	J. Biochem. 98:1147-1156(1985).			
LN	[2]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=66195857; PubMed=3009417;			
RA	Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,			
RA	Carmona C., Reguad C.;			
RT	"Structural genes encoding the thermophilic alpha-amylases of			
RT	Bacillus stearothermophilus and Bacillus licheniformis."			
RL	J. Bacteriol. 166:635-643(1986).			
LN	[3]			
RP	SEQUENCE FROM N.A.			
RC	Shahosseini M., Ziaei A.A., Ghaemi N., Pourbaei A.A.;			
RA	"An unusual DNA sequence encoded a hyperthermostable alpha-amylase."			
RT	submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
LN	[4]			
RP	SEQUENCE OF 1-104 FROM N.A.			
RC	MEDLINE=64185455; PubMed=6609154;			
RA	Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.;			
RT	"Nucleotide sequence of the 5' region of the Bacillus licheniformis			
RT	alpha-amylase gene: comparison with the B. amyloliquefaciens gene."			
RL	J. Bacteriol. 158:369-372(1984).			
LN	[5]			
RP	SEQUENCE OF 1-29 FROM N.A.			
RC	MEDLINE=69213924; PubMed=2540150;			
RA	Lacide B.M., Chambliss G.H., McConnell D.J.;			
RT	"Bacillus licheniformis alpha-amylase gene, amyL, is subject to			
RT	promoter-independent catabolite repression in Bacillus subtilis."			
RL	J. Bacteriol. 171:2435-2442(1989).			
LN	[6]			
RP	SEQUENCE OF 30-47.			
RC	MEDLINE=62098050; PubMed=6172418;			
RA	Kuhn H., Fietzek P.P., Lampen J.O.;			
RT	"N-terminal amino acid sequence of Bacillus licheniformis			

RT alpha-amylase: comparison with Bacillus amyloliquefaciens and
 RT Bacillus subtilis enzymes.";
 RL J. Bacteriol. 149:372-373(1982).
 RN [7]
 RP MAPPING OF SUBSTRATE-BINDING SITE.
 RX MEDLINE=21992788; PubMed=11997021.
 RA Kandra L., Gyemant G., Remyarik J., Hovanszki G., Lipcak A.;
 RT "Action pattern and subite mapping of Bacillus licheniformis
 RT alpha-amylase (BIA) with modified maltooligosaccharide substrates.";
 RL FEBS Lett. 518:79-82(2002).
 RN [8]
 RP MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
 RC STRAIN=ATCC 6598;
 RX MEDLINE=90368748; PubMed=2394736;
 RA Declerck N., Joyet P., Gallardin C., Maeson J.M.;
 RT "Use of amber suppressors to investigate the thermostability of
 RT Bacillus licheniformis alpha-amylase. Amino acid replacements at 6
 RT histidine residues reveal a critical position at His-133.";
 RL J. Biol. Chem. 265:15481-15488(1990).
 RN [9]
 RP MUTAGENESIS OF ALA-238.
 RC STRAIN=ATCC 6598;
 RX MEDLINE=96367070; PubMed=8771184;
 RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Gallardin C.;
 RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
 RT multiple amino acid replacements and molecular modelling.";
 RL Protein Eng. 8:1029-1037(1995).
 RN [10]
 RP MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
 RP ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359
 RP AND GLU-365.
 RC STRAIN=ATCC 6598;
 RX MEDLINE=20425100; PubMed=10966804;
 RA Declerck N., Machius M., Wiegand G., Huber R., Gallardin C.;
 RT "Probing structural determinants specifying high thermostability in
 RT Bacillus licheniformis alpha-amylase.";
 RL J. Mol. Biol. 301:1041-1057(2000).
 RN [11]
 RP MUTAGENESIS OF GLN-293 AND ASN-294.
 RC STRAIN=ATCC 6598;
 RX MEDLINE=22622182; PubMed=12736372;
 RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,
 RA Gallardin C.;
 RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and
 RT modulation of its stability over a 50 degrees C temperature range.";
 RL Protein Eng. 16:287-293(2003).
 RN [12]
 RP MUTAGENESIS OF TRP-292 AND VAL-315.
 RC STRAIN=ATCC 27811;
 RX MEDLINE=22797417; PubMed=12915728;
 RA Rivera M.H., Lopez-Munguia A., Soberon X., Saab-Rincon G.;
 RT "Alpha-amylase from Bacillus licheniformis mutants near to the
 RT catalytic site: effects on hydrolytic and transglycosylation
 RT activity.";
 RL Protein Eng. 16:505-514(2003).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RC STRAIN=ATCC 27811;
 RX MEDLINE=95182462; PubMed=7877175;
 RA Mechius M., Wiegand G., Huber R.;
 RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-
 RT amylase at 2.2-A resolution.";
 RL J. Mol. Biol. 246:545-559(1995).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=98212915; PubMed=9551551;
 RA Mechius M., Declerck N., Huber R., Wiegand G.;
 RT "Activation of Bacillus licheniformis alpha-amylase through a
 RT disorder-->order transition of the substrate-binding site mediated
 RT by a calcium-sodium-calcium metal triad.";
 RL Structure 6:281-292(1998).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 330-512.

RX MEDLINE=20384196; PubMed=10924103;
 RA Brozozewski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,
 RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
 RT "Structural analysis of a chemically modified bacterial alpha-amylase.
 RT High-resolution analysis of native and ligand complexes.";
 RL Biochemistry 39:9099-9107(2000).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
 RP H162V/N219F/A238V/Q293S/N294Y.
 RC STRAIN=ATCC 6598;
 RX MEDLINE=22538505; PubMed=12540849;
 RA Machius M., Declerck N., Huber R., Wiegand G.;
 RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through
 RT introduction of hydrophobic residues at the surface.";
 RL J. Biol. Chem. 278:11546-11553(2003).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
 CC -1- SUBUNIT: Monomer.
 CC -1- BIOTECHNOLOGY: Used in the food industry for high temperature
 CC liquefaction of starch-containing mashes and in the detergent
 CC industry to remove starch. Sold under the name termamyl by
 CC Novozymes.
 CC -1- MISCELLANEOUS: Able to work at relatively high (alkaline) pH
 CC values (up to pH 11) and at high temperatures (up to 100 degrees
 CC Celsius).
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 DR EMBL; X03236; CAA26981.1; -;
 DR EMBL; M38570; AAA22226.1; -;
 DR EMBL; M13256; AAA22240.1; -;
 DR EMBL; K01984; AAA22193.1; -;
 DR EMBL; AF438149; AA026743.1; -;
 DR EMBL; M26412; AAA22237.1; -;
 DR EMBL; A17930; CAA01355.1; -;
 DR PIR; A91997; ALBSL.
 DR PDB; 1BLI; 23-MAR-99.
 DR PDB; 1BPL; 17-AUG-96.
 DR PDB; 1E3X; 21-JUN-01.
 DR PDB; 1E3Z; 24-JUN-03.
 DR PDB; 1E40; 24-JUN-03.
 DR PDB; 1E43; 21-JUN-01.
 DR PDB; 1O80; 03-APR-97.
 DR PDB; 1VUS; 12-MAR-97.
 DR InterPro; IPR006589; Alp amyl cat. sub.
 DR InterPro; IPR006047; Alpha amyl cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase. 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR SMART; SM00642; Amyy. 1.
 KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KW Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 512 ALPHA-AMYLASE.
 FT ACT_SITE 260 260
 FT ACT_SITE 264 264
 FT ACT_SITE 357 357
 FT METAL 133 133
 FT METAL 190 190
 FT METAL 210 210 CALCIUM 2 AND SODIUM.
 FT METAL 212 212 CALCIUM 2 (VIA CARBONYL OXYGEN).
 FT METAL 223 223 CALCIUM 2 AND SODIUM.
 FT METAL 229 229 CALCIUM 1 AND SODIUM.
 FT METAL 231 231 CALCIUM 2.
 FT METAL 233 233 CALCIUM 2.

Query Match 99.3%; Score 2648; DB 1; Length 512;
 Best Local Similarity 99.2%; Pred. No. 9.5e-187;
 Matches 479; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ANLNGTMOYFEMWMPDQGHRLONDSATLAHGTTAWTPPAYKGTSGADVGYGAYD 60
DB 30 ANLNGTMOYFEMWMPDQGHRLONDSATLAHGTTAWTPPAYKGTSGADVGYGAYD 89
QY 61 LYDGEFHQGTATVTKYGTGELGSAIKSLHSRDINYGVDVINHKGAADTEVTAVEV 120
DB 90 LYDGEFHQGTATVTKYGTGELGSAIKSLHSRDINYGVDVINHKGAADTEVTAVEV 149
QY 121 DPADRNVI SEGHILKMTWHPFGSGSTYSDPFKMHVYHFDGTWDESRKLNRIYKFGK 180
DB 150 DPADRNVI SEGHILKMTWHPFGSGSTYSDPFKMHVYHFDGTWDESRKLNRIYKFGK 209
QY 181 AMDWVSNGNNDYLYMADIDYHPDVAARIKMGWYANELQDGFRLDAVHKIKFSF 240
DB 210 AMDWVSNGNNDYLYMADIDYHPDVAARIKMGWYANELQDGFRLDAVHKIKFSF 269
QY 241 LRDMVNVREKTKGEMPTVAEYMONDGALENYLNTKTNFNSVDPVPLHYQFHAASVQGG 300
DB 270 LRDMVNVREKTKGEMPTVAEYMONDGALENYLNTKTNFNSVDPVPLHYQFHAASVQGG 329
QY 301 GYDMRKLNGTVSKHPLKSVTPVNDHDTOPQSLSTVOTWPFPLAAYFLLTRESGYPO 360
DB 330 GYDMRKLNGTVSKHPLKSVTPVNDHDTOPQSLSTVOTWPFPLAAYFLLTRESGYPO 389
QY 361 VFYDMMYTKGDSQREIPALGHKLEPILKARKOYAYAGNDYFPHHDIVGWTREGDSVA 420
DB 390 VFYDMMYTKGDSQREIPALGHKLEPILKARKOYAYAGNDYFPHHDIVGWTREGDSVA 449
QY 421 NSGIALITDGPAGAKMTYGRONAGETWHDITGRSEPVYINSEGMGEFHVNGSVISY 480
DB 450 NSGIALITDGPAGAKMTYGRONAGETWHDITGRSEPVYINSEGMGEFHVNGSVISY 509
QY 481 VQR 483
DB 510 VQR 512

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RESULT 2

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ID AMY_BACAM STANDARD; PRT; 514 AA.
AC P00692;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amyase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
  glucanohydrolase).
OS Bacillus amylioliquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IH;
RX MEDLINE=83108808; PubMed=6185474;
RA Takkinen K., Petersson R.F., Kalkkinen N., Palva I., Soederlund H.,
  Kaasarijaenen L.;
RT "Amino acid sequence of alpha-amyase from Bacillus amylioliquefaciens
  deduced from the nucleotide sequence of the cloned gene.";
RL J. Biol. Chem. 258:1007-1013 (1983).
RN [2]
RP SEQUENCE OF 32-222.
RX MEDLINE=80241725; PubMed=6156671;
RA Chung H.S., Friedberg F.;
RT "Sequence of the N-terminal half of Bacillus amylioliquefaciens alpha-
  amyase.";
RL Biochem. J. 185:387-395 (1980).
RN [3]
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE=82051296; PubMed=6170539;

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RA Palva I., Petersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M.,
RA Soederlund H., Takkinen K., Kaasarijaenen L.;
RT "Nucleotide sequence of the promoter and NH2-terminal signal peptide
  region of the alpha-amyase gene from Bacillus amylioliquefaciens.";
RL Gene 15:43-51 (1981).
RN [4]
RP SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE=88137952; PubMed=2830166;
RA Ruohonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karaenen S.;
RT "Efficient secretion of Bacillus amylioliquefaciens alpha-amyase by
  its own signal peptide from Saccharomyces cerevisiae host cells.";
RL Gene 59:161-170 (1987).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.
RX MEDLINE=20384196; PubMed=10924103;
RA Brzozowski A.M., Lawson D.M., Turkmenburg J.P., Bisgaard-Frantzen H.,
  Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amyase.
  High-resolution analysis of native and ligand complexes.";
RL Biochemistry 39:9099-9107 (2000).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
  linkages in oligosaccharides and polysaccharides.
CC -1- COPFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC -----
DR EMBL; J01542; AAA22191.1; -
DR EMBL; V00092; CAA23430.1; -
DR EMBL; A20154; CAA01489.1; -
DR EMBL; M18424; AAA22192.1; -
DR PIR; A92389; ALBSN.
DR PDB; 1E3X; 21-JUN-01.
DR PDB; 1E3Z; 24-JUN-03.
DR PDB; 1E40; 24-JUN-03.
DR PDB; 1E43; 21-JUN-01.
DR InterPro; IPR005589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT CHAIN 1 31
FT ACT_SITE 32 514 ALPHA-AMYLASE.
FT ACT_SITE 262 262
FT ACT_SITE 292 292
FT ACT_SITE 359 359
FT METAL 133 133
FT METAL 190 190
FT METAL 212 212
FT METAL 214 214
FT METAL 225 225
FT METAL 231 231
FT METAL 233 233
FT METAL 235 235
FT METAL 266 266
FT METAL 331 331
FT METAL 438 438
FT METAL 461 461
FT CONFLICT 54 54
FT CONFLICT 64 64
FT CONFLICT 79 79
FT CONFLICT 84 84
BY SIMILARITY.
CALCIUM 1.
CALCIUM 2 AND SODIUM.
CALCIUM 2 (VIA CARBOXYL OXYGEN).
CALCIUM 3 (BY SIMILARITY).
CALCIUM 3 (VIA CARBOXYL OXYGEN).
CALCIUM 3 (BY SIMILARITY).
CALCIUM 3 (BY SIMILARITY).
L -> I (IN REF. 2).
I -> L (IN REF. 2).
S -> D (IN REF. 2).
G -> S (IN REF. 2).

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SEQ	SEQUENCE	514 AA;	58403 MW;	3D666B3FB5CDBE7E CRC64;
QY	Query Match	81.9%;	Score 2184;	DB 1; Length 514;
Db	Best Local Similarity	80.3%;	Pred. No. 9,8e-153;	
Matches	388;	Conservative 44;	Mismatches 49;	Indels 2; Gaps 1;
QY	3	LNGLTLMQVFEWYMPDQGMRLRLQNDLSAYLAEHGITATWITPRAYKGTSGQADVGCAAYLY	62	
Db	32	VNGLTLMQVFEWYTPPDQGMRLQNDASHLSDIGITAWIPPAKGLSOSNGGYPYLY	91	
QY	63	DLGEFHQGTGYRTKTKGTGSELQSAIKSLHSRDINVGQVVLNHKGADATEDVPAVEYDP	122	
Db	92	DLGEFHQGTGYRTKTKGTSELQDAIGSLHSRNVQYGVVVLNHKGADATEDVPAVEYDP	151	
QY	123	ADRRNVISGEHLIKAWTFHFPFGSGSTYSDFKMWVHPDGTWDSESRKLRIYK--QKG	180	
Db	152	ANRMOETSEYQIKAWTDFFRFPGRGNTYSDFKMHVYHFDGADWDSESRKISRIKFRGSGK	211	
QY	181	AMDEVSSENNQVYLMADIDYHPDPAAEIKRGTGYVANELODGRDLAVKIKSF	240	
Db	212	AMDEVSSENNQVYLMADYDVHPDPAAEIKRGTGYVANELODGRDLAVKIKSF	271	
QY	241	LRDWNHVRKTKGEMFTVAEYQWQNDLGALENVYLNKTFNHSVFPVPLHYQFHAASQGG	300	
Db	272	LRDWNVAQVRKTKGEMFTVAEYQWQNDLGALENVYLNKTFNHSVFPVPLHYQFHAASQGG	331	
QY	301	GYDKRKLNGTVSGKHPPLKSTVFDVNDHTOPQGSLSFTVQTFKPLAAYFLITRESGYPQ	360	
Db	332	GYDKRRLDGTGVSHPEKAVTPEVNHDTQGGSLSTVQTFKPLAAYFLITRESGYPQ	391	
QY	361	VFYGDWMTKQDSQREIPALNKHKEPIILKARKQVAYGQHDYFPDHHIVGWTREGDSVA	420	
Db	392	VFYGDWMTKQDSQREIPALNKHKEPIILKARKQVAYGQHDYFPDHHIVGWTREGDSVA	451	
QY	421	NSGLAALITDPPGAKKMYVGRQVAGETWHTITGRSEHPVYINSRGMEFPVNGGSVITY	480	
Db	452	KSLAALITDPPGAKKMYVGRQVAGETWHTITGRSEHPVYINSRGMEFPVNGGSVITY	511	
QY	481	VQR 483		
Db	512	VQR 514		
RESULT 3				
ID	AMT6_BACS7			
AC	AMT6_BACS7	STANDARD;	PRT;	518 AA.
AC	PI9571;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Glucan 1,4-alpha-maltohexosidase precursor (EC 3.2.1.98) (66-amy-lase)			
DE	(Maltotetraose-producing amylase) (Exo-maltohexohydrolase).			
OS	Bacillus sp. (strain 707)			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1416;			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.			
RX	MEDLINE=88162814; PubMed=3258152;			
RA	Takamato A., Kimura K., Ishii Y., Takano T., Yamane K.;			
RT	"Nucleotide sequence of the maltotetraose-producing amylase gene from			
RT	an alkaliphilic Bacillus sp. #707 and structural similarity to			
RT	liquefying type alpha-amylases."			
RL	Biochem. Biophys. Res. Commun. 151:25-31(1988).			
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages			
CC	in amyloseous polysaccharides so as to remove successive			
CC	maltotetraose residues from the non-reducing chain ends.			
CC	-1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By			
CC	similarity).			
CC	-1- PATHWAY: Starch degradation.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Belongs to Family 13 of glycosyl hydrolases.			
CC	-----			
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CC	EMBL_M18662; AAA22231.1; -.	
DR	PIR; A27705; A27705.	
DR	HSSP; P06278; IVUS.	
DR	InferPro; IPR006589; Alp_amy1_cat_sub.	
DR	InferPro; IPR006047; Alpha_amy1_cat.	
DR	InferPro; IPR006046; Glyco_hydro_13.	
DR	Pfam; PF00128; alpha-amyase.1.	
DR	PRINTS; PR00110; ALPHAAMYLASE.	
KW	SMART; SMO0642; Amyy; 1.	
RN	Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.	
FT	SIGNAL	1 33
FT	CHAIN	34 518 GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE.
FT	ACT_SITE	269 269 BY SIMILARITY.
FT	ACT_SITE	273 273 BY SIMILARITY.
FT	ACT_SITE	366 366 BY SIMILARITY.
FT	METAL	139 139 CALCIUM 1 (BY SIMILARITY).
FT	METAL	196 196 CALCIUM 2 AND SODIUM (BY SIMILARITY).
FT	METAL	219 219 CALCIUM 2 (VIA CARBOXYL OXYGEN) (BY SIMILARITY).
FT	METAL	221 221 CALCIUM 2 AND SODIUM (BY SIMILARITY).
FT	METAL	232 232 CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT	METAL	238 238 CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT	METAL	240 240 CALCIUM 2 (BY SIMILARITY).
FT	METAL	242 242 CALCIUM 2 (BY SIMILARITY).
FT	METAL	273 273 CALCIUM 1 (VIA CARBOXYL OXYGEN) (BY SIMILARITY).
SQ	SEQUENCE	518 AA; 59009 MW; 3A961E21612682C4 CRC64;
Query Match	Best Local Similarity	70.5%; Score 1879; DB 1; Length 518; Matchee 329; Conservative 67; Mismatches 79; Indels 10; Gaps 4;
Dn	NGTLMQYEWMPNDGOHMRLONSDAVLAEHGITAWIPRAYKGSQADYGAYDLYD	63
Dn	39 NGTMQYEWMLPDGDNHRNLINDASLSKGITAWIPRAMKGAQNVDYGYATDYLD	98
Dn	64 LGEPFQKGTAVTKYTGKGLDSAIKSLSHRSDINYYGDVINHKSGADATEDVTAVEYPA	123
Dn	99 LGEFNQGKTAVTKYTGTSQLQAIVTSLKNNGIQYUGDVVMNHKGGADATEWRAVEVPN	158
Dn	124 DNRNVISGEHLIKAWTHHFPGRGSTYSDFPMWHYHERDTGWDESRKL-NRIYFQ-GX	180
Dn	159 NRNOEVLTSEYTIEMTFEDFPGRGNHTSSFEMRWYHFGGVMDOSRRLNIRNYKFRGHGX	218
Dn	181 AMDEVSNENENNYLIWADI DYDHPPVAELIKMGTWYANELDDGERLLAVAHIKPSF	240
Dn	219 AMDWEVDTENENYLIWMADTDIMHPERYNNLRMVGWYTNTLGDERRDDVAVALIKFSF	278
Dn	241 LRDWVNHYREKTGEMEFTVAEYMONDGALENIYNKTNFHNHSVEDVPLAHYOFHAASTOGS	300
Dn	279 TRDMINVRYRSATGGMFAVAEFMNDDGALIENTYOKTNMHNSVDPRLHYNLNAASCGG	338
Dn	301 GYDKRKLLINGTVASKPKSVTPVDNHDTOPGSLGSTVOQTWRPLAVALTLRESGPQ	360
Dn	339 NYDKRNIFNGTVQRHSHAVTFPDNHDSCGEFEALSFEVEWPFKPFLAVALTLTREOGYPVS	398
Dn	361 VFEGDMMG--TKGSQEERIALKKIEPKLKARQYAUGAOHDFRDHDIUIGMRBGDSS	418
Dn	399 VFYADVYGIPLHG----VPARKSKDLPLEAKCKYAYGKONDYLDHHNIIIGWTREGNTA	453
Dn	419 VANGSLAALTIDPGGAKRMVFVQONGETWNHDTGKRSEPVVINSGEWGCFHNAGSVS	478
Dn	454 HPNSGLATINSDGAGSKMFVGNKAAGQWMSDLITNKRTGITVTINADOMGFNVSNGGSVS	513
Dn	479 IYVOR 483 : :	

Db 514 IWVWK 518

RESULT 4

AMY_BACST STANDARD; PRT; 549 AA.

AC P06279; Q45519; (1)

DT 01-JAN-1998 (Rel. 06, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Alpha-amylose precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).

GN AMYS.

OS Bacillus stearothermophilus.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.

OX NCBI_TaxID=1422;

RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.

RX MEDLINE=65234394; PubMed=3924897;

RA Nakajima R., Imanaka T., Alba S.;

RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylose gene";

RT active sites.";

RL J. Bacteriol. 163:401-406(1985).

RP [2]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=DY5/PHI300;

RX MEDLINE=86008166; PubMed=3876333;

RA Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Uda K.S.;

RT "Complete nucleotide sequence of a thermophilic alpha-amylose gene: homology between prokaryotic and eukaryotic alpha-amyloses at the active sites.";

RL J. Biochem. 98:95-103(1985).

RP [3]

RP SEQUENCE FROM N.A.

RC STRAIN=NZ-3;

RX MEDLINE=86195857; PubMed=3009417;

RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L., Carmona C., Regardt C.;

RT "Structural genes encoding the thermophilic alpha-amyloses of Bacillus stearothermophilus and Bacillus licheniformis.";

RL J. Bacteriol. 166:635-643(1986).

RP [4]

RP SEQUENCE FROM N.A.

RA Suominen I., Kari M., Lautamo J., Knowles J., Mantsaenla P.;

RT "Reversible alpha-amylose of Bacillus stearothermophilus: cloning, expression, and secretion by Escherichia coli.";

RL (in) Chaloupka J., Krumpal V. (eds.);

RL Extracellular enzymes of microorganisms, pp.129-137, Plenum Press, New York (1987).

RP [5]

RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.

RC STRAIN=DY-5;

RX MEDLINE=86059211; PubMed=2999073;

RA Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H., Ido T., Yamagata H., Uda K.S.;

RT "Efficient synthesis and secretion of a thermophilic alpha-amylose by protein-producing Bacillus brevis 47 carrying the Bacillus stearothermophilus amylose gene.";

RL J. Bacteriol. 164:1182-1187(1985).

RP [6]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=21125602; PubMed=11226887;

RA Suvd D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;

RT "Crystal structure of Bacillus stearothermophilus alpha-amylose: possible factors determining the thermostability.";

RL J. Biochem. 129:461-468(2001).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.

CC -1- SUBUNIT: Monomer.

CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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CC -----

DR EMBL; M11450; AAA2235.2; -

DR EMBL; X02769; CAA26547.1; -

DR EMBL; M57457; AAA2227.1; -

DR EMBL; M13255; AAA2224.1; -

DR PIR; A24436; A24436.

DR PIR; A91999; ALBSF.

DR PDB; 1HVX; 05-ANG-03.

DR InterPro; IPR006589; Alp_amy1_cat_sub.

DR InterPro; IPR006047; Alpha_amy1_cat.

DR InterPro; IPR006046; Glyco_hydro_13.

DR Pfam; PF00128; alpha-amylose; 1.

DR PRINTS; PR00110; ALPHAMYLASE.

DR SMART; SM00642; Amy; 1.

KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.

FT CHAIN 1 34

FT FT SIGNAL 35 549

FT ACT_SITE 268 268

FT ACT_SITE 272 272

FT ACT_SITE 365 365

FT METAL 139 139

FT METAL 196 196

FT METAL 218 218

FT METAL 220 220

FT METAL 231 231

FT METAL 237 237

FT METAL 238 238

FT METAL 239 239

FT METAL 272 272

FT METAL 337 337

FT METAL 339 339

FT METAL 440 440

FT METAL 441 441

FT METAL 464 464

FT CONFLICT 13 13

FT CONFLICT 19 19

FT CONFLICT 23 23

FT CONFLICT 31 31

FT CONFLICT 107 107

FT CONFLICT 167 167

FT CONFLICT 179 179

FT CONFLICT 251 251

FT CONFLICT 260 260

FT CONFLICT 284 284

FT CONFLICT 312 312

FT CONFLICT 338 338

FT CONFLICT 342 342

FT CONFLICT 346 346

FT CONFLICT 376 376

FT CONFLICT 526 527

FT CONFLICT 527 527

FT CONFLICT 535 535

FT CONFLICT 549 549

SEQUENCE 549 AA; 62670 MW; 3A2DD93A955E79D3 CRC64;

Query Match 66.6%; Score 1776.5; DB 1; Length 549;

Best local similarity 64.7%; Pred. No. 7.9e-123;

Matches 314; Conservative 66; Mismatches 100; Indels 5; Gaps 2;

Qy 1 ANLNGTLMQYFEMWMPNDGQHWRLQNDLSAVLAHGTTAVWIPPAKYGTSQADVGYAYD 60

Db 36 APFNGTMMQYFEMWLPDGLTMTKVNANNTSLGITLMLPRAYVGTGRSDVGYGYD 95

Qy 61 LYDGFPHQGTGVTGKYGELQSAIKSLHSDINVGIVINHGGAADTEVYAVEV 120

Db 96 LYDGFPHQGTGVTGKYGELQSAIKSLHSDINVGIVINHGGAADTEVYAVEV 155

[illegible]

```

RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions i1a and i1b, including a
RT large non-coding region."
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL, L01643; AAA27110.1; -.
DR EMBL, AE008787; AAL20875.1; -.
DR EMBL, M85241; AAA27079.1; -.
DR EMBL, L13280; AAA71970.1; -.
DR PIR, B45738; B45738.
DR HSSP, P06278; 1V0S.
DR StyGene; SG10011; amYA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR SMART; SM00644; Aamy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Complete proteome.
FT ACT_SITE 235 BY SIMILARITY.
FT ACT_SITE 265 BY SIMILARITY.
FT ACT_SITE 332 BY SIMILARITY.
FT METAL 104 CALCIUM (BY SIMILARITY).
FT METAL 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 462 L -> S (IN REF. 1).
SQ SEQUENCE 494 AA; 5652 MW; 5C1B62FEDDB5E47C CEC64;
Query Match 39.7%; Score 1058; DB 1; Length 494;
Best Local Similarity 42.4%; Pred. No. 3.2e-70;
Matches 208; Conservative 87; Mismatches 180; Indels 16; Gaps 6;
QY 4 NGTLMQYEWMTMPDQGHWRRLQNDSDAYLAHGTITAWIPRAYKGTSGA-DVYGADYLY 62
DB 3 NPTLLQYHMYWPPGGKLMSELAEARADGLNDIGINMWLPRACKGASGYSVGYDTYDLF 62
QY 63 DLGEFHQGVYRTYKTKGELQSAIKLSHRDINWGDVYVNNHKGADATEDYVAVEDP 122
DB 63 DLGEEDQGGTATYATYGGDRQLLTALIDAKKNINAVLLDVVNNHKGADAEKRIRVQVNO 122
QY 123 ADRRRVISGEHLIAYMTFHFPFGSGTSDSEKMYHFPDGTDMDESRLANLYK----FQ 178
DB 123 DDRQIQIDNIIIECGWTRTYTPPAAAGQSNRTIMWHCSGSDIHNENPEDDIFKIVNDYT 182
QY 179 GKAMDWEYSNENGVYDILMYADIDYDHDVYAAEIKRWGTWYANBELQDGFRLDAVKHIF 238
DB 183 GDGNWDDQYDDMDGNFYDLMGENIDIFRNHAYTEEIKYVARWMEQTHCDGFRLDVAKHIPA 242
QY 239 SFPLADVNNHAEKTKGKEMFTYAAEAWQNDGLALENTYLNKTNHNSVDFVPLHYQFHAASQ 298
DB 243 WFEYKEWIEHQAVALPKPLFTIYVAEYWSHEVDLQTYIIQVVDKTYLFPAPLQMKFHEASRQ 302
QY 299 GGGYDMRKLTNGTAVVSKPLSKSVFVNNDHPQPGSLESYQTFMKPLAYAFILTRREGY 358
DB 303 GAETDMRKRTIFGLTVEADPFPAVTLVANNDQPLQALADAPYEPFKPLAYALLIRKNGV 362
QY 359 PQQVYGDMYG-----KQDSQR-EIPALGKLEPLIKAKQAYAGQNDYFDHNDIVG 410

```

Db 363 PSVFPDLYGASVDSGNGETCKVMDPI-NQDLRLIARQRPAHGIQTLFDPHNCIA 421
Qy 411 WTRBGSSVANSGLAALITDGPAGAKMYVGRONAGETWHDITGNSEPVINSEKGEF 470
Db 422 FSRSGTEB--NPGCVVVLNSNDDDEKTLTLGDVYANKTWDFLGNRDEYVYVNDQGSATF 479
Qy 471 HVNGGSVSIYV 481
Db 480 FCNAGSVSVWV 490

RESULT 6
AMY2_ECOLI
ID AMY2_ECOLI STANDARD; PRT; 495 AA.
AC P26612; P78072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMYA OR B1927.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL1;
RX MEDLINE=93015717; PubMed=1400215;
RA Rana M., Kawagishi I., Mueller V., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA";
RL J. Bacteriol. 174:6644-6652(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Siao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Maki T., Mizobuchi K., Mori H., Motoki T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampaio G., Seki Y., Sivasubraman S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horikuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map";
RL DNA Res. 3:379-392(1996).
RN [4]
RP SEQUENCE OF 1-5 FROM N.A.
RC STRAIN=JAL1;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes";
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [5]
RP SEQUENCE OF 475-495 FROM N.A.
RC STRAIN=JAL1;
RX MEDLINE=93381452; PubMed=8371104;
RA Rana M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIA and IIB, including a
RT large non-coding region";
RL J. Gen. Microbiol. 139:1401-1407(1993).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL; L01642; AAA23810.1; -.
DR EMBL; AEO00285; AAC74994.1; -.
DR EMBL; D90833; BAA15755.1; -.
DR EMBL; M85240; -; NOT_ANNOTATED_CDS.
DR EMBL; L13279; AAA82575.1; -.
DR PIR; D64956; A45738.
DR HSSP; P06278; IVUS.
DR EcoGene; EG11387; amyA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Complete proteome.
FT ACT_SITE 235 235 BY SIMILARITY.
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 332 332 BY SIMILARITY.
FT METAL 104 104 CALCIUM (BY SIMILARITY).
FT METAL 239 239 CALCIUM (VIA CARBOXYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 19 20 KL -> SS (IN REF. 1).
FT CONFLICT 109 109 A -> V (IN REF. 1).
FT CONFLICT 149 149 Q -> E (IN REF. 1).
FT CONFLICT 234 234 L -> I (IN REF. 1).
SQ SEQUENCE 495 AA; 56639 MW; 26AF6797DDA54D6 CRC64;
Query Match 39.3%; Score 1047; DB 1; Length 495;
Best local Similarity 42.2%; Pred. No. 2,1e-69;
Matches 208; Conservative 86; Mismatches 179; Indels 20; Gaps 8;
Qy 4 NGTLMQYFWMYRNDQGMRLQNDLSAYLAHGTAVNIPYAKGTSQA-DVCGAADVLY 62
Db 3 NPTLLQCFHYTYPEGGLWPELBERADGFNDIGINWMLPPAYKASGGYSGVDYDLF 62
Qy 63 DLGFFHDKGVTRPKYVGTGKGLQSAIKSLHSRDINNVYGVYINHGKADATEDVTAVEVP 122
Db 63 DLGFFDQKSGIPKYGKQALLAIDLKRNDAVLADVVVNHKMGDEKALRVQVNA 122
Qy 63 ADRNRVYSGEHLI-KAMTFHPFGSGTYSDFKMWHYHFGDWDSEKRLNRYK---- 176
Db 123 DDRITQI--DEIIIECBETRYTTPPARAGQYSQFIWDFKCSGDIHINPDEGIFKLVND 180
Qy 177 FQKAMPWEVSNENQDYIMADIDYDHPVAAEIRKGTWYANEQLDGFRLDAVKHI 236
Db 181 VTGSGMNDQYDDELGNEDYLMGEIDIFRNHAYVEIRYKRWARWMEQTCGGRFLDAVKHI 240
Qy 237 KFSFLRWNVNHYVEKQKEMFTVAEYQNDGLNENTNPNHVSFVDPLHYQPHAS 296
Db 241 PAMFYKWIHVQVAVKPLFIYAEVYSHEDKQYIYIDVQEGKTMFLDAPLQKFEAS 300
Qy 297 TQGGYDMRKLNGTVVSKPLKSVTFVNDNDTOPQGSLESTVQTWKPLAYAFILTRRS 356
Db 301 RMGRDYDMTQIFGTLVADPFAHVTLVANHDTPQLQALBAPVBPWPKPLAYALLILREN 360
Qy 357 GYPOVYFGDMYGTK----GDSQR--EIPALKKIEPILKARQVAYGQHYFDHNDI 408
Db 361 GVPSVFPDLYGAHYEDVGDVGQYTPIDMPIE-QDELILARQFAHGVQTLFDPHNC 419

```

Qy 409 VGMTRGDSVANSGLAALITDPCGAKMYVGRONAGETWHDITGNSEPVINSBGWG 468
Db 420 IAFRSSTGDEF--PCVYVMSNGSDGDEKTHILGSEYNGKTRDPLNGRQERVVDNCEA 477
Qy 469 EFHVNQGSVSIVY 481
Db 478 TFCNGSGSVSYVW 490

RESULT 7
AMYB_PAPEO STANDARD; PRT; 1196 AA.
ID AMYB_PAPEO
AC P21543;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Beta/alpha-amyase precursor [includes: Beta-amyase (EC 3.2.1.2);
OS Paenibacillus polymyxa (Bacillus polymyxa)].
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxId=1406;

RN [1]
RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=87165765; PubMed=2435707;
RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,
RT "Cloning and nucleotide sequence of the gene coding for enzymatically
active fragments of the Bacillus polymyxa beta-amyase."
RL J. Bacteriol. 169:1564-1570(1987).
RN [2]
RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=89123046; PubMed=2464578;
RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
RT "A single gene directs synthesis of a precursor protein with beta-
and alpha-amyase activities in Bacillus polymyxa."
RL J. Bacteriol. 171:375-382(1989).
RN [3]
RP SEQUENCE OF 1-776 FROM N.A.
RC STRAIN=ATCC 8523;
RX MEDLINE=87231094; PubMed=2438660;
RA Rhodes C., Strasser J., Friedberg F.;
RT "Sequence of an active fragment of B. polymyxa beta amyase."
RL Nucleic Acids Res. 15:3934-3934(1987).
RN [4]
RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
RX MEDLINE=91215008; PubMed=1827035;
RA Uozumi N., Matsuda T., Tsukagoshi N., Uda S.;
RT "Structural and functional roles of cysteine residues of Bacillus
polymyxa beta-amyase."
RL Biochemistry 30:4594-4599(1991).
CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
PRODUCE MULTIFORM BETA-AMYLASES AND A 48 kDa ALPHA-AMYLASE AFTER
SECRETION.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
polysaccharides so as to remove successive maltose units from the
non-reducing ends of the chains.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: In the N-terminal section, belongs to family 14 of
glycosyl hydrolases.
CC -1- SIMILARITY: In the C-terminal section, belongs to family 13 of
glycosyl hydrolases.
CC -----
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CC -----
CC EMBL; M15817; AA85446.1; -.
CC EMBL; Y00150; CA68344.1; -.
CC PIR; A29130; A29130.
CC HSSP; P36924; 1B92.
CC InterPro; IPR006589; Alp_ami_cat_sub.
CC InterPro; IPR006048; Alpha_ami1_C.
CC InterPro; IPR006047; Alpha_ami1_cat.
CC InterPro; IPR005085; CBM_25.
CC InterPro; IPR006046; Glyco_hydro_13.
CC InterPro; IPR001554; Glyco_hydro_14.
CC Pfam; PF00128; alpha-amyase; 1.
CC Pfam; PF02806; alpha-amyase_C; 1.
CC Pfam; PF01373; Glyco_hydro_14; 1.
CC PRINTS; PR00110; ALPHAMYLASE.
CC SMART; SM00642; Amyy; 1.
CC SMART; SM00632; Amyy_C; 1.
CC PROSITE; PS00506; BETA_AMYLASE_1; 1.
CC PROSITE; PS00679; BETA_AMYLASE_2; 1.
CC Multicatalytic enzyme; Hydrolase; Glycosidase; Signal;
KW Polysaccharide degradation; Repeat.
FT SIGNAL 1 35
FT CHAIN 36 1196
FT DOMAIN 36 454
FT REPEAT 435 558
FT REPEAT 565 668
FT DOMAIN 669 1196
FT DISULFID 118 126
FT ACT_SITE 198 198
FT ACT_SITE 394 394
FT MOTIFAN 118 118
FT MOTIFAN 126 126
FT MOTIFAN 116 116
FT MOTIFAN 358 358
FT CONFLICT 1 1
FT CONFLICT 67 67
FT CONFLICT 100 100
FT CONFLICT 154 154
FT CONFLICT 177 177
FT CONFLICT 227 228
FT CONFLICT 330 330
FT CONFLICT 425 425
FT CONFLICT 493 493
FT CONFLICT 532 532
FT CONFLICT 559 559
FT CONFLICT 665 665
FT CONFLICT 681 681
FT CONFLICT 686 686
FT CONFLICT 725 728
FT CONFLICT 736 736
FT CONFLICT 741 741
FT CONFLICT 758 758
SQ SEQUENCE 1196 AA; 130893 MW; A41BA6B70F257064 CRC64;

Query Match 12.8%; Score 340; DB 1; Length 1196;
Best Local Similarity 23.1%; Pred. No. 4,2e-17;
Matches 119; Conservative 64; Mismatches 175; Indels 158; Gaps 22;

Qy 12 EWMTPMDGQHRRLQNDASVLAHNGITAVIPRAYKTSQ-ADVCGAYDIVLGEFHOK 70
Db 779 KWH-----GGDFQGITINKLDYIKMGFTAWITPVTKSEYAVGHYTFDVF----- 826
Qy 71 GYRTKYGTGKGLQSAIKLSHRSDINVGDVVINKGADATEDVAVVEVDPADRRRVIS 130
Db 827 -ANDGILGTMDKQLQELVRKAHDKNIAVMDVVVNHGDPQ----- 865
Qy 131 GEHLIAWTHFHPGSGSTYSDF-KWHMYHPDGTMDSESRKLNRIYKFGQKAMDEVSNE 189
Db 866 -----PGNGFAKAPFDKADWYHHNGDITDGGYNSNN-----QWRI--E 901
Qy 190 NGNYDVIAMVDADIDYDHPDAELIKRWGTYVAMELDQGRLDVAVVKIKRPSFLRDVNVNHR 249

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Db 902 NG--DVAGLDLNNENPATNELKMWIKMLNENGIDGLRLDTYKHPKGLDF-----954
Qy 250 EKTKEMETVAEYQNDLGLALNTNTNFNSFEDVLYHQFLAASOGGYDMRL--307
Db 955 -DQANTFTMGELTFHGPAYVGD--TRYDALDLPMTYTT--KVFHGDSMRKIKD 1008
Qy 308 -----LNGTVSSKHPKLVTFVDNHDPOQSLESTVQTFKPLAVAFILTR 355
Db 1009 RYSDRRYRDAQNTGVLIDNHDK--RFLNDASGKPAANDKMPQL--KALGFLTL-S 1062
Qy 356 SGTPQVFTGYMGYTKGDSQREIPALKKIEPIKARKQVYAGQHYFDHHDVGMTR 415
Db 1063 RGPIITVYQTEQYSGGDD--PA-----NRENMFNANHDLQYIATKLIVYRNN 1109
Qy 416 DSVANGGLAALITDGGCGAKMYVGRQNGETHD-----ITGRSEPVYINSEGW- 467
Db 1110 HPALQN-----GSGR-----EKWVDSTFSFORSKNGDEALIVFINSWN 1148
Qy 468 -----GEF-----HVGGSVSI 479
Db 1149 SQRTTGNFNLNGTGLTNGLNSDVSQINNGSITV 1164

RESULT 8
AMYA_VIGMU STANDARD; PRT; 421 AA.
AC P17859;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amyase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMY1.1.
OS Vigna mungo (Rice bean) (black gram).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid1; Fabales; Fabaceae; Papilionoideae; Phaseolae; Vigna.
OC NCBI_TaxID=3915;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RX MEDLINE=90332425; PubMed=2377468;
RA Yamauchi D., Minamikawa T.;
RL "Nucleotide sequence of cDNA for alpha-amyase from cotyledons of
RT germinating Vigna mungo seeds.";
RL Nucleic Acids Res. 18:4250-4250(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94120017; PubMed=8290640;
RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
RL "Nucleotide sequence of the alpha-amyase gene from Vigna mungo.";
RL Plant Physiol. 103:1459-1459(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X53049; CA37217.1; -
DR EMBL; X73301; CA31734.1; -
DR PIR; S10514; S10514.
DR HSSP; P04063; IAVA.
DR InterPro; IPR006047; Alp_amy1_cat.
DR InterPro; IPR006047; Alp_amy1_cat.

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DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAAMYLA.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal.
FT SIGNAL 1 23
FT CHAIN 24 421
FT ACT_SITE 201 201
FT ACT_SITE 309 309
FT METAL 113 113
FT METAL 130 130
FT METAL 133 133
FT METAL 135 135
FT METAL 139 139
FT METAL 149 149
FT METAL 160 160
FT METAL 168 168
FT METAL 170 170
SQ SEQUENCE 421 AA; 4688 MW; 15CA0DABA3DB4656 CRC64;
Query Match 11.7%; Score 311.5; DB 1; Length 421;
Best Local Similarity 27.2%; Pred. No. 1,4e-15;
Matches 126; Conservative 48; Mismatches 159; Indels 131; Gaps 22;
Qy 7 LMQPEWYMNDDQHRRRLONDSAYLAEGITVWIPPAVKGSQADVGAYDYLDTGE 66
Db 26 LFGQFNWSSKKQGWNLNSIPDLANNAGITVWLPSPQSVPPE--GLPGRLYLD- 82
Qy 67 FHKQGVTRTKYTKGELQSAIKSLHSRDINVDVIVNHKGADATEDVAVEDVPADRN 126
Db 83 -----ASKYGSKNELKSLIAAFHEKGICLADIVINHR-----TAERKD----- 121
Qy 127 RVISGEHLIKAWTHFHPGSGSTYSDFKWHVHFDGT-----DWDSRKLNRITYKFGKA 181
Db 122 -----GRG-IYCIFFE-----GGTPDSRQDW-----GPS 143
Qy 182 W-----DWEVSENGENVYD-----YLMVADIDVDHDDVAIEIRKGTWYANELQDGFRLDAV 233
Db 144 FICRDPYASVDGNGNDGSGGYDAAPDIDHLPQVORELEMMNWLKTEIGFGMRPDEV 203
Qy 234 KHIKFSFLRDMNVNHEKTEKEMFTVAEYV-----QNDLGLAENYLNKTN 278
Db 204 KGYAPSSISKTYM-----EGT-KPDPFAVEKMDSTISYGDDKPKNNQDSHRGALVWVBSAG 258
Qy 279 FNSHVPDVLHYQFPAASTGQGGYDMRKLL--NGT--VVSKHPLKSVTFVDNHDTPQ 333
Db 259 GAITAFDFTTKGILQAA-VQG--ELWRLLDPNGKPGMGIVKPENAVTFIDNHD- 310
Qy 334 SLSTVQVWPKP-----LAAFLITRESGYQVFGYGMGTGKDSQREIPALKKIEPIL 388
Db 311 --GSTQRLMPFPDPDKWQGYAVYILT-HPGTPSIFYDHFPM-----GLKEQLAKLS 358
Qy 389 KARKQVYAGQHYFDHHDVGMTRBGDSVANSGLAALTDPG 432
Db 359 SIR-----LNGINEKSTYKYNASBDLYAAIKDKIMKIKGP 396

RESULT 9
AM3A_ORYSA STANDARD; PRT; 440 AA.
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amyase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
glucan glucanohydrolase).
GN AMT1.2 OR AMT3A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzeae; Oryza.

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NCBI_TaxId=4530;
 (1)
 SEQUENCE FROM N.A.
 STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
 MEDLINE=91329692; PubMed=1714318;
 RA Sutcliffe T.D., Huang N., Lites J.C., Rodriguez R.L.;
 "Characterization of an alpha-amylose multigene cluster in rice.";
 RL Plant Mol. Biol. 16:579-591(1991).
 CC - FUNCTION: Important for breakdown of endosperm starch during
 CC germination.
 CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC - COFACTOR: Binds 3 calcium ions per subunit (By similarity).
 CC - SUBUNIT: Monomer.
 CC - TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.
 CC - DEVELOPMENTAL STAGE: Expressed at a high level during germination
 CC in the aleurone cells under the control of the plant hormone
 CC gibberellic acid and in the developing grains at a low level.
 CC - SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC or send an email to license@ebi.ac.uk).
 CC
 CC -----
 CC EMBL: X56336; CAA39776.1; -.
 CC PIR: S14958; S14958.
 CC HSP: P04063; IAVA.
 CC Gramene: P27932; -.
 CC InterPro: IPR006589; ALP_amy1_cat_sub.
 CC InterPro: IPR006047; Alpha_amy1_cat.
 CC InterPro: IPR006046; Glyco_hydro_13.
 CC Pfam: PF00128; alpha-amylose; 1.
 CC PRINTS: PR00110; ALPAMYLYASE.
 CC SMART: SM00642; Aamy; 1.
 CC K01 Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 CC KW Signal, Multigene family.
 CC FT SIGNAL 1 26 POTENTIAL.
 CC FT CHAIN 27 440 ALPHA-AMYLASE ISOZYME 3A.
 CC FT ACT_SITE 207 307 BY SIMILARITY.
 CC FT ACT_SITE 315 315 BY SIMILARITY.
 CC FT METAL 119 119 CALCIUM 1 (BY SIMILARITY).
 CC FT METAL 145 145 CALCIUM 2 (BY SIMILARITY).
 CC FT METAL 155 155 CALCIUM 3 (BY SIMILARITY).
 CC FT METAL 166 166 CALCIUM 3 (BY SIMILARITY).
 CC FT METAL 169 169 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
 CC SIMILARITY).
 CC FT METAL 170 170 CALCIUM 1 (BY SIMILARITY).
 CC FT METAL 171 171 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
 CC SIMILARITY).
 CC FT METAL 174 174 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
 CC SIMILARITY).
 CC FT METAL 176 176 CALCIUM 1 AND 3 (BY SIMILARITY).
 CC SQ SEQUENCE 440 AA; 48872 MW; 5E9B78C29AA91C2B CRC64;
 Query Match 11.4%; Score 304; DB 1; Length 440;
 Best Local Similarity 27.0%; Pred. No. 5.2e-15;
 Matches 115; Conservative 46; Mismatches 149; Indels 116; Gaps 19;
 QY 7 LMOYFEW-YMENDGQWRRRLNDSDAAYLAEHGITAIVIPPAVKGNISQADVCGAYDLVDLG 65
 Db 31 LFGGNDMSWKKGQGWYNNMLKDQVGDIIASAETHVWLEPPHYSVPO-GIMPGRLVDLN 88
 QY 66 EFHOKGVTRKYKGTGKGLQSAIKSLHSRDINVDGVDVINHKGADATEDVYAVEVDADR 125
 Db 89 -----ASKYKTKAELKSLIAFPAHAKGICVADIYNNRCADK----- 126
 QY 126 NRVISGEHLIAKMTFHPHPPGSGTSDPKFWWHFDG-----TWDSRKLNRIYFQKG 180
 Db 127 -----DGRG-VYCIYFK-----GGGPRGCLIMGSMTC----- 152

Qy	161	AMDESVSNENGN-----YYLMTADIDYHPDYVAEIKRWGMYVANELOLDSGRDLAVGHI	236
Db	153	CDVYQYSDGTGHRDTGADFAAPARDIDHNLPLVQRELSDMLWRDLRGDFDGRDLDPAGY	212
Qy	237	KSFPLRDVWNRHREKTKGEMFTVAEYWMQNDLG-----ALENYLNKTNFN	280
Db	213	SAAVARTYVQNAARBS-----FVVAIEIW-NSLSYDSODGKPAANQSGROELVNMWQVGGP	266
Qy	261	HSVPDVLPHYOPHAASVGGGYDMRKLIENG--VSKHPLKSVTFVNDHDTOPGQSILES	337
Db	267	ATAFPTTKGILQSA-VQGEILMRARD-KDGKAPGMIQWPEKATVFDNHDT-----GS	318
Qy	338	TVQWTFK-----LAFATILRESGYPQVFGDMWGTGDSQREILPAKHIEPILKARK	392
Db	319	TQRMPPSPDSKVLIGYATILY-HPEVPCIFYDQVDFWN-----LKQEINLAATRK	368
Qy	393	QYAYGA	398
Db	369	RNGINA	374
RESULT 10			
AM3C	ORYSA		
ID	_AM3C_ORYSA	STANDARD;	PRT; 437 AA.
AC	P27939;		
DT	01-AUG-1992	(Rel. 23, Created)	
DT	01-AUG-1992	(Rel. 23, Last sequence update)	
DT	15-MAR-2004	(Rel. 43, Last annotation update)	
DE	Alpha-amylase isozyme 3C precursor (EC 3.2.1.1) (1,4-alpha-D-glucan		
DE	glucanhydrolase).		
GN	AMY1.7 OR AMY3B.		
OS	Oryza sativa (Rice).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartoideae; Oryzaeae; Oryza.		
OX	NCBI_TaxID=4530;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;		
RA	MEDLINE=91329692; PubMed=1714318;		
RX	Sutcliffe T.D., Huang N., Latts J.C., Rodriguez R.L.;		
RT	"Characterization of an alpha-amylase multigene cluster in rice.";		
RL	Plant Mol. Biol. 16:579-591 (1991).		
CC	-1- FUNCTION: Important for breakdown of endosperm starch during		
CC	germination.		
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic		
CC	linkages in oligosaccharides and polysaccharides.		
CC	-1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).		
CC	-1- SUBUNIT: Monomer.		
CC	-1- TISSUE SPECIFICITY: Germinating seeds.		
CC	-1- DEVELOPMENTAL STAGE: Expressed at a high level during germination		
CC	in the aleurone cells under the control of the plant hormone		
CC	gibberellic acid and in the developing grains at a low level.		
CC	-1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.		
CC	-----		
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CC	use by non-profit institutions as long as its content is in no way		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; X56338; CAA39778.1; -.		
DR	PIR; S14956; S14956.		
DR	HSSP; P04063; IAVA.		
DR	Greene; P27939; -.		
DR	InterPro; IPR006589; Alp_amy1_cat_sub.		
DR	InterPro; IPR006047; Alpha_amy1_cat.		
DR	InterPro; IPR006046; Glyco_hydro_13.		
DR	Pfam; PF00128; alpha-amylase; 1.		
DR	PRINTS; PR00110; ALPHAMYLASE.		

```

RESULT 10
AM3C_ORYSA STANDARD; PRT; 437 AA.
ID AM3C_ORYSA P27939;
AC P27939;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DR 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3C precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
  glucanohydrolase).
GN AMYL.7 OR AMY3B.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Buzbarioidae; Oryzaceae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
RA MEDLINE=91328692; Pubmed=1714318;
RA Sutcliffe T.D., Huang N., Lites J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amylase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).
CC -1- FUNCTION: Important for breakdown of endosperm starch during
  germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
  linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (by similarity).
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Germinating seeds.
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
  in the aleurone cells under the control of the plant hormone
  gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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  CC -----
CC EMBL; X56338; CA939778.1; -.
CC PIR; S14956; S14956.
CC HSSP; P04063; IAVA.
CC Gramene; P27939; -.
CC InterPro; IPR006589; Alp_ami1_cat_sub.
CC InterPro; IPR006047; Alpha_ami1_cat.
CC InterPro; IPR005046; Glyco_hydro_13.
CC Pfam; PF00128; alpha-amylase/1.
CC PRINTS; PR00110; ALPHAMYLASE.

```


DR SMART; SM00642; Aamy; 1.
 KM Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
 KW Signal; Multigene family.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 437 ALPHA-AMYLASE ISOZYME 3C.
 FT ACT_SITE 205 205 BY SIMILARITY.
 FT ACT_SITE 313 313 BY SIMILARITY.
 FT METAL 117 117 CALCULUM 1 (BY SIMILARITY).
 FT METAL 134 134 CALCULUM 2 (BY SIMILARITY).
 FT METAL 137 137 CALCULUM 2 (BY SIMILARITY).
 FT METAL 139 139 CALCULUM 2 (BY SIMILARITY).
 FT METAL 143 143 CALCULUM 2 (BY SIMILARITY).
 FT METAL 153 153 CALCULUM 3 (BY SIMILARITY).
 FT METAL 164 164 CALCULUM 3 (BY SIMILARITY).
 FT METAL 167 167 CALCULUM 3 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT METAL 168 168 CALCULUM 1 (BY SIMILARITY).
 FT METAL 169 169 CALCULUM 1 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT METAL 172 172 CALCULUM 3 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT METAL 174 174 CALCULUM 1 AND 3 (BY SIMILARITY).
 FT SEQUENCE 437 AA; 48637 MW; B0304250B40C7AAB CRC64;
 Query Match 11.3%; Score 300; DB 1; Length 437;
 Best Local Similarity 25.8%; Pred. No. 1e-14;
 Matches 109; Conservative 48; Mismatches 146; Indels 120; Gaps 16;
 QY 7 LM0YFWMYPMNDGQHMRR-LONDSAYLAHEGITAVMIPPAKGTSGADVGYGAYDLYDLG 65
 DB 29 LFQGFNMESNMKQCGWYFLLSHVDYLAATGVTVMLEPP-PSHSAVAPQGYMPEGLYDL 86
 QY 66 EFHOKGTRTKYTKGELQSAIKSLHSRDINVDVYNHKGADADIEDYVAEVDPADR 125
 DB 87 -----ASKYGTGAELRSLIAFHSHKICVADIVINH----- 118
 QY 126 NRVISGEHLKAWTHFHPGSGSTYSDPKMWHFPGD-----TDWDESKLNTIYKRG 179
 DB 119 -----RCADYKDSRGTYCIFEGETPSPRLDMPDMICSD----- 152
 QY 180 KAMPMEVSENENGN-----YDLYMTADIDYDHPDVAEIKRWGTWYANLELDGFFRLDAVKH 235
 DB 153 ---DTQVNSNGRGRHDYTGADFGAAPPIDHILNRTVTELSDMNLAKSDVGFQGMRLDFAKG 209
 QY 236 IKPSFLRWVNVHVBKTKGEMFTVAETYN-----DGLALENYLANKNTNEN 280
 DB 210 YSATVLAITYVNT-----DPSFVVAEISNMRYDNGNGSPWNOGDGDELVNMAQAAGCP 264
 QY 281 HSVFDVPLHYGFHASQGGYDMRKLNGT-----VVSXKPLKSYTFVDNHDTPQPSL 335
 DB 265 ASAFDPTTKGELQA-VQG---ELWRMKDNGKAPGMGLPEKAVTFIDNHD----- 314
 QY 336 ESTVQWTFKP-----LAFAFLITRESGPVGFYGMGYTKGDSQREIPALKHKEPILKA 390
 DB 315 GSTONSNWPFDPDKWQRYAYILT-HPGVPCIFIDHVPWN-----LQGEISTLAANV 364
 QY 391 RKQ 393
 DB 365 RSR 367
 RESULT 11
 CDGT_BACS8 STANDARD; PRT; 713 AA.
 AC P17692;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclomaltohextrin glucanotransferase precursor (EC 2.4.1.19)
 DE (Cyclodextrin-glycosyltransferase) (CGTase) (Raw-starch-digesting amy1ase).
 OS Bacillus sp. (strain B1018).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1417;
 RN [1].
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
 RX MEDLINE=9014765; PubMed=1689153;
 RA Iktor P., Teukogoshi N., Udaoka S.;
 RT "Nucleotide sequence of the raw-starch-digesting amy1ase gene from Bacillus sp. B1018 and its strong homology to the cyclodextrin RT glucanotransferase genes."
 RL Biochem. Biophys. Res. Commun. 166:630-636(1990).
 CC -1- FUNCTION: This endo-type adsorbable amy1ase is capable to digest raw starch.
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.
 CC -1- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC -----
 DR EMBL; M33302; AAA22329.1; -
 DR EMBL; D90112; BAA1440.1; -
 DR PIR; S09196; S09196.
 DR HSSP; P43379; ICDG.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006048; Alpha_amy1_C.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR002044; CBD_4.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR InterPro; IPR007110; 1g-1like.
 DR InterPro; IPR002909; IPT_TIG.
 DR Pfam; PF00128; alpha-amy1ase; 1.
 DR Pfam; PF02806; alpha-amy1ase_C; 1.
 DR Pfam; PF00686; CBM_20; 1.
 DR Pfam; PF01833; TIG; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR PRODOM; PD001568; CBD_4; 1.
 DR SMART; SM00642; Aamy; 1.
 DR SMART; SM00632; Aamy; C; 1.
 KM Transferase; Glycosyltransferase; Calcium-binding; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 713 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
 FT ACT_SITE 256 256 BY SIMILARITY.
 FT ACT_SITE 284 284 BY SIMILARITY.
 FT ACT_SITE 355 355 BY SIMILARITY.
 FT METAL 54 54 CALCULUM 1 (BY SIMILARITY).
 FT METAL 56 56 CALCULUM 1 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT METAL 59 59 CALCULUM 1 (BY SIMILARITY).
 FT METAL 60 60 CALCULUM 1 (BY SIMILARITY).
 FT METAL 80 80 CALCULUM 1 (BY SIMILARITY).
 FT METAL 166 166 CALCULUM 2 (BY SIMILARITY).
 FT METAL 217 217 CALCULUM 2 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT METAL 226 226 CALCULUM 2 (BY SIMILARITY).
 FT METAL 260 260 CALCULUM 2 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT SEQUENCE 713 AA; 77420 MW; 85FB616DA687B888 CRC64;
 Query Match 11.2%; Score 298; DB 1; Length 713;
 Best Local Similarity 23.8%; Pred. No. 2.6e-14;
 Matches 113; Conservative 86; Mismatches 175; Indels 100; Gaps 20;
 QY 19 GQMRRLQN--DSAYLAHEGITAVMIP-----AYKGTSGADVGYGAYDLYDLGFEHOKGT 72
 DB 78 GSDWQGIINKINGQYTLGKMGVTAIWISQPVENIYSINYGWNVTAHGWARDPKK--- 134
 QY 73 VRTKYGKGELOSAIKSLHSRDINVDVYNHKGADADIEDYVAEVDPADRRRVISGE 132

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Db 135 TNPAYGTADPQNIIAAHAKIKVILDFAPNH-----TSPASSDQPSFAENGLYDNG 188
Qy 133 HLIAAMTHFHHFGSGTYSDSKMKMYHEDGDMDESRKLNIFYFGGKAMWEVSNENGN 192
Db 189 TLLGGYT-----NDTQNLFFHNAGTDFP-----TTTNGI 217
Qy 193 YDYVYMAIDYDHPDVAAE-----IKRWGTVYANIELQDGFRLDAVGHKESFLRDMVN 246
Db 218 YKNL-YDLADLNHNNSISDYVLKDAIKW-----LDLGIDDIRDAVGHMFQKQSMMA 271
Qy 247 HVREKTEKEMFTVAEYV--QNDLGALENYLKNTPNHSVDFVPLHYQFHAATG----- 298
Db 272 AVNNY--KPVFTFPEMFVAGVNEGP-ENHKRANESGMSILD-----FPFAQVRQVFRDNT 324
Qy 299 CGGDMKRLNGTVVSHHPL-KSTFVNDHDTQGGQSLSEVQVQWFKPLAFLITSESG 357
Db 325 DNMVGLKAMEGSAADVAQVDDQVTFIDNHMERFPHASNARRLKLOALATLLAR--- 381
Qy 358 YPOVYFG-DWY--GTKGDSQREIIPALK-----HKIRPILKARKQVYGAQHDFD 404
Db 382 VPATYYGTEQYMSGTDPDNARIPSPSTTANQVLYOKLAPLKSNPAIAYSGSTQERMT 441
Qy 405 HHDIWGTREGDSV-----ANSGLAALITDGPQAKMYVGRQNAGET 448
Db 442 NNDVLIYERKFGSNVAVVAVNRNLNAPASISGLVTSIPQSGYNDVLGGLNGNT 495

RESULT 12
CDGT_BACSO STANDARD; PRT; 713 AA.
ID CDGT_BACSO STANDARD; PRT; 713 AA.
AC P05618;
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltohextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase).
GN CGT.
OS Bacillus sp. (strain 1011).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=47308036; PubMed=2957361;
RA Kimura K., Kataoka S., Ishii Y., Takano T., Yamane K.;
RT "X-ray structure of cyclodextrin glucanotransferase from alkalophilic
RT of alkalophilic Bacillus sp. strain 1011 and similarity of its amino
RT acid sequence to those of alpha-amylases."
RT J. Bacteriol. 169:4399-4402(1987).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RA Harata K., Haga K., Nakamura A., Aoyagi M., Yamane K.;
RT "X-ray structure of cyclodextrin glucanotransferase from alkalophilic
RT Bacillus Sp. 1011. Comparison of two independent molecules at 1.8-A
RT resolution."
RT Acta Crystallogr. D 52:1136-1145(1996).
CC -i- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.
CC -i- COFACTOR: Binds 2 calcium ions per subunit.
CC -i- SUBUNIT: Monomer.
CC -i- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC MALTOLOGOSACCHARIDE PRODUCED.
CC -i- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
Db EMBL; M17366; AAA22308.1; -.
DR PIR; A26678; ALBSG1.
DR PDB; 1D7F; 17-MAR-00.
DR PDB; 1DED; 07-APR-00.
DR PDB; 1I75; 11-APR-01.
DR PDB; 1PAM; 11-JAN-97.
DR InterPro; IPR006589; Alp_ami_cat_sub.
DR InterPro; IPR006048; Alpha_ami1_C.
DR InterPro; IPR006047; Alpha_ami1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; Ig-1ike.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR Pfam; PF02806; alpha-amy1ase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR PRODOM; PD001568; CBD_4; 1.
DR SMART; SM00642; Amyy; 1.
DR SMART; SM00632; Amyy_C; 1.
KW Transferase; Glycosyltransferase; Calcium-binding; Signal;
KW 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 713 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT DOMAIN 28 165 A1.
FT DOMAIN 166 229 B.
FT DOMAIN 230 433 A2.
FT DOMAIN 434 522 C.
FT DOMAIN 523 609 D.
FT DOMAIN 610 713 E.
FT ACT_SITE 256 256
FT ACT_SITE 284 284
FT ACT_SITE 355 355
FT METAL 54 54 CALCIUM 1.
FT METAL 55 55 CALCIUM 1 (VIA CARBONYL OXYGEN).
FT METAL 56 56 CALCIUM 1.
FT METAL 59 59 CALCIUM 1.
FT METAL 60 60 CALCIUM 1.
FT METAL 80 80 CALCIUM 1.
FT METAL 166 166 CALCIUM 2.
FT METAL 217 217 CALCIUM 2 (VIA CARBONYL OXYGEN).
FT METAL 226 226 CALCIUM 2.
FT METAL 260 260 CALCIUM 2 (VIA CARBONYL OXYGEN).
FT DISULFID 70 77
FT TURN 30 31
FT TURN 33 34
FT TURN 40 41
FT STRAND 44 46
FT HELIX 49 51
FT HELIX 52 52
FT HELIX 57 59
FT HELIX 63 65
FT STRAND 66 66
FT STRAND 68 69
FT TURN 73 74
FT STRAND 76 76
FT HELIX 81 89
FT TURN 90 93
FT HELIX 94 96
FT TURN 97 97
FT STRAND 100 103
FT STRAND 107 109
FT STRAND 114 116
FT TURN 117 118
FT TURN 119 121
FT STRAND 124 125
FT STRAND 129 135
FT TURN 137 139
FT HELIX 142 154
FT TURN 155 156

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FT STRAND 158 163
FT TURN 165 166
FT STRAND 167 170
FT TURN 176 177
FT TURN 179 182
FT STRAND 184 186
FT TURN 187 188
FT STRAND 189 192
FT TURN 195 196
FT TURN 198 199
FT STRAND 202 202
FT STRAND 207 207
FT HELIX 213 218
FT STRAND 220 220
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FT STRAND 224 227
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FT HELIX 232 247
FT TURN 248 249
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FT TURN 422 423
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FT TURN 453 454
FT STRAND 455 462
FT STRAND 469 471
FT STRAND 475 475
FT STRAND 481 483
FT TURN 486 491
FT STRAND 496 498
FT HELIX 500 502
FT STRAND 503 504
FT STRAND 507 509
FT TURN 511 512
FT STRAND 514 519
FT STRAND 527 532
FT STRAND 535 536
FT TURN 538 539
FT STRAND 541 547
FT STRAND 555 558
FT TURN 559 560
FT STRAND 561 563
FT HELIX 565 567
FT STRAND 568 571
FT STRAND 575 579
FT STRAND 586 593
FT TURN 595 596
FT STRAND 599 599

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FT STRAND 603 608
FT STRAND 613 621
FT TURN 627 628
FT STRAND 630 635
FT HELIX 638 640
FT TURN 641 643
FT HELIX 645 647
FT STRAND 649 649
FT STRAND 653 653
FT TURN 660 661
FT STRAND 663 670

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Query Match 11.0%; Score 294; DB 1; Length 713;

Best Local Similarity 23.0%; Pred. No. 5.2e-14; Matches 127; Conservative 89; Mismatches 173; Indels 164; Gaps 29;

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QY 19 GQHWRRLQV--DSAYLAHSGITAWIIPP---AYKGTSGADVGYGAYDLYDLSEFHOKGT 72
DB 78 GGDWOGIINKINDGYLGMGITAIVISQPVENIVSVINSGVNNVTAHYGWARDPFKK--- 134
QY 73 VRTKYGTELOSAISLHSRDINVGDVVINKSGADATEDVTAVEVP--ADRNKVIS 130
DB 135 TNPAYGTMDPFKNLIDPAHANIKVLIIDPAPNHTSPASSD-----DSFANGRLYD 186
QY 131 GEHLIKAMTHFHFPGSGSTYSDFKMWYHFDGTDWDSRLNRIYKFGKAMDEYSENEN 190
DB 187 NGNLLGGYT-----NDTONLFHHYGTDFS-----TIEN 215
QY 191 GNYDYIM-VADIDYDHDVAA---EIKRWGTVANELQDGRRLDAVKIKFSFLDMV 245
DB 216 GIYKNLYDLADLNHNNSVDVYLDKDAIKMW-----LDLGVGDIRVDAVKHMPFGMCKSF 270
QY 246 NHVREKTKEMFTVAEYWDNLGALF-----NYLNTKTNHNSVFDVPLHYQFAASTO- 298
DB 271 ATINNV--KPVFTGEWF--LGVNESPEYHOFANESGMS-----LDFRFAQKARQV 319
QY 299 -----GGGYDMRKLLNGTVVSKHPLK-SYTFVNDH-----TOPG--QSESTVQWFKP 345
DB 320 FRDNTDMYGLKAMLESEVDYAVQVDFIINHDERFHTNSGDRKLEQ----- 371
QY 346 LAYAFILTRSGYPQVFG-DMY---GTKGDSQREIPALK-----HKIEPILKARK 392
DB 372 -ALAFITLT-SRGVPAIYVSGEQWMSGNDPDNRARLPFSYTTAYAVIOKLAPLRKSNP 429
QY 393 QYAYGAQHDYFDHHDIVGWTREBGSVA-----NSGLAA 426
DB 430 AIAVGSHTHERMINNDVILYERKFGNNVAVAINRNMTPTASITGLVTSLRASINDVLCG 489
QY 427 L-----ITDPPGAKRMVYGRQNAGETWH-----DITGN---RSEP---VVINSEGW 467
DB 490 ILANGTILTVAGAGGAASFTLAPGTAVWQYTTDATTPILIGNVGPMMAKPGVTITIDGRGF 549
QY 468 GEFHVGGSVSIV 480
DB 550 G-----SGKGTIV 557

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RESULT 13

AMY3 WHEAT

ID AMY3 WHEAT STANDARD; PRT; 413 AA.

AC P08117;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Alpha-amylase AMY3 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan

glucanohydrolase).

GN AMY1.1 OR ALPHA-AMY3.

OS Triticum aestivum (Wheat).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;

OC Triticaceae; Triticum.

OX NCBI_Taxid=4565;

RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=CV, Chinese Spring;
RA Baulcombe D.C., Huttly A.K., Martienssen R.A., Barker R.F.,
RT Jarvis M.G.;
RL Mol. Gen. Genet. 209:33-40(1987).
CC -1- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurone cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC or send an email to license@isb-sib.ch).
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DR EMBL, X05809, CAA29252.1; -.
DR EMBL, M16991, AAA34259.1; -.
DR PIR, S06357, ALMT3.
DR HSSP, P04063, IAVA.
DR InterPro, IPR006589, Alp_amy1_cat_sub.
DR InterPro, IPR006047, Alpha_amy1_cat.
DR InterPro, IPR006046, Glyco_hydro_13.
DR Pfam, PF00128, alpha-amy1ase; 1.
DR PRINTS, PR00110, ALPHAMYLASE.
DR SMART, SM00642, Amy; 1.
KM Germination; Carbohydrate metabolism; Hydrolase; Glycosidase; Seed;
KM Calcium-binding; Signal; Multicene family.
FT SIGNAL 1 24
FT CHAIN 25 413
FT ACT SITE 203 203
FT METAL 115 115
FT METAL 132 132
FT METAL 135 135
FT METAL 137 137
FT METAL 141 141
FT METAL 151 151
FT METAL 162 162
FT METAL 167 167
FT METAL 170 170
FT METAL 172 172
SQ SEQUENCE 413 AA; 45370 MW; C262BCALC54FC64 CRC64;
Query Match 11.0%; Score 292.5; DB 1; Length 413;
Best Local Similarity 25.7%; Pred. No. 3,4e-14;
Matches 121; Conservative 56; Mismatches 155; Indels 139; Gaps 22;
QY 7 LMQYFEN-YMPNDQGHRRRLONDSAYLAHGTIAVMPYPAYKGTSGADVGYAYDYDLG 65
DB 28 LFGGFNWSWKTOGQWKFQGVKEEYASTGATHVMWLPSPQSQSPPE--GYLPGQLYNL- 84
QY 66 BFGQKGVTRTKYKGLQSAIKSLHSRDINVYGDVIVNKGADNEDVTVAEVPADK 125
DB 85 -----NKRYSGADLKSLIQFGRKNISCVADIVNHR-----CADK 121
QY 126 NRVIQGHILKAWTHFHPGRGTYSDPKXMYHFDGT-----DMDSRRLNRIYFGQK 180
DB 122 K-----DGRG-VYCIFF-----GGSINRMDWGDDEICSD----- 150
QY 181 AMWQVSNENGNND-----YLMYADIDYDHPDVAAEIKRGTWTYANELQDLGFLDAVKHI 236
DB 151 --DTKYSNGRHDPDTGGGFAADBDIHLNPRVORELSAWMLNKLTLGFGWRLDPAKGV 208

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QY 237 KESFLRDMVNHVAREKTEKEMETVAEYQNDLGALENYLNTKTNHNSVDPVPLHYQFAAS 296
DB 209 SAAPAKTYVDN-----SKPAFVVGELYDRDRLQALWVRGVGPATAPFPYTGVLQEA- 262
QY 297 TOGGGGYDMRLKLNGT-----VSKHPLKSVTFVNDHDTPGQSLBSTVQTFKPE-----L 346
DB 263 VQG---DLGMRSDSGKAPKPMIGMPEKTYTFIDNNDT-----GSTQRLMPFSPDKWQ 313
QY 347 AYAFILTBESGYQVRYGDMYGTGKDSQREIPL-----KHKIEP-----ILKARQYAV 396
DB 314 GYAVIIL-HPGICPIFYDHFVWK--LKQETLALATVRSNCHIPGSTLDILKA----- 364
QY 397 GAGHDYVDHHDIDYGMWRREGDSSVANSGLAALIDGSGKAKMYGVQONAGE 447
DB 365 -----EGDLVYAKIGKVTYKIG-----SHYNIGD 389

RESULT 14
CDGT_BACCI
ID_CDGT_BACCI STANDARD; PRT; 718 AA.
AC P30920;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomalodextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase).
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8;
RX MEDLINE=91103970; PubMed=1368573;
RA Nitschke L., Heeger K., Bender H., Schulz G.E.;
RT "Molecular cloning, nucleotide sequence and expression in Escherichia
RT coli of the beta-cyclodextrin glycosyltransferase gene from Bacillus
RT circulans strain no. 8."
RL Appl. Microbiol. Biotechnol. 33:542-546(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE=91171298; PubMed=1826034;
RA Klein C., Schulz G.E.;
RT "Structure of cyclodextrin glycosyltransferase refined at 2.0-A
RT resolution."
RL J. Mol. Biol. 217:737-750(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE=90064533; PubMed=2531228;
RA Hofmann B.E., Bender H., Schulz G.E.;
RT "Three-dimensional structure of cyclodextrin glycosyltransferase from
RT Bacillus circulans at 3.4-A resolution."
RL J. Mol. Biol. 209:793-800(1989).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE=98226626; PubMed=9558324;
RA Schmidt A.K., Cottaz S., Drigues H., Schulz G.E.;
RT "Structure of cyclodextrin glycosyltransferase complexed with a
RT derivative of its main product beta-cyclodextrin."
RL Biochemistry 37:5909-5915(1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE=98409292; PubMed=9738912;
RA Parsiegla G., Schmidt A.K., Schulz G.E.;
RT "Substrate binding to a cyclodextrin glycosyltransferase and
RT mutations increasing the gamma-cyclodextrin production."
RL Eur. J. Biochem. 255:710-717(1998).
CC -1- CATALYTIC ACTIVITY: Degradates starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.

```

CC -1- COFACTOR: Binds 2 calcium ions per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC MALTOOLIGOSACCHARIDE PRODUCED.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X68326; CAA48401.1; -.
DR PIR; S23674; ALBSCG.
DR PDB; 1CGT; 31-JAN-94.
DR PDB; 1CGU; 31-JAN-94.
DR PDB; 3CGT; 27-MAY-98.
DR PDB; 4CGT; 12-AUG-98.
DR PDB; 5CGT; 12-AUG-98.
DR PDB; 6CGT; 14-OCT-98.
DR PDB; 7CGT; 12-AUG-98.
DR PDB; 8CGT; 14-OCT-98.
DR PDB; 9CGT; 14-OCT-98.
DR InterPro; IPR006589; Alp_ami1_cat_sub.
DR InterPro; IPR006048; Alpha_ami1_C.
DR InterPro; IPR006047; Alpha_ami1_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR02909; IPT_TIG.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR Pfam; PF02806; alpha-amy1ase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAMYLAASE.
DR ProDom; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy1; 1.
DR SMART; SM00632; Amy1_C; 1.
KW Transferrase; Glycosyltransferase; Calcium-binding; Signal;
KW 3D-structure.
FT SIGNAL 1 34
FT CHAIN 35 718 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT DOMAIN 35 172 A1.
FT DOMAIN 173 236 B.
FT DOMAIN 237 440 A2.
FT DOMAIN 441 528 C.
FT DOMAIN 529 614 D.
FT DOMAIN 615 718 E.
FT DISULFID 77 84
FT ACT_SITE 258 258
FT ACT_SITE 291 291
FT ACT_SITE 362 362
FT METAL 61 61
FT METAL 63 63 CALCULUM 2. (VIA CARBONYL OXYGEN).
FT METAL 66 66 CALCULUM 2. (VIA CARBONYL OXYGEN).
FT METAL 67 67 CALCULUM 2.
FT METAL 85 85 CALCULUM 2. (VIA CARBONYL OXYGEN).
FT METAL 87 87 CALCULUM 2.
FT METAL 173 173 CALCULUM 1. (VIA CARBONYL OXYGEN).
FT METAL 224 224 CALCULUM 1. (VIA CARBONYL OXYGEN).
FT METAL 233 233 CALCULUM 1.
FT METAL 267 267 CALCULUM 1 (VIA CARBONYL OXYGEN).
FT TURN 37 38
FT TURN 40 41
FT TURN 43 44
FT TURN 47 48
FT STRAND 51 53

FT HELIX 56 59
FT HELIX 64 66
FT HELIX 70 72
FT STRAND 73 73
FT TURN 75 76
FT TURN 80 81
FT STRAND 83 83
FT HELIX 88 96
FT TURN 97 98
FT HELIX 99 103
FT TURN 104 104
FT STRAND 107 110
FT STRAND 114 116
FT STRAND 121 123
FT TURN 124 125
FT STRAND 126 128
FT TURN 131 132
FT STRAND 136 142
FT TURN 144 146
FT HELIX 149 161
FT TURN 162 163
FT STRAND 165 170
FT TURN 172 173
FT STRAND 174 177
FT TURN 180 181
FT TURN 183 184
FT TURN 186 189
FT STRAND 191 193
FT TURN 194 195
FT STRAND 196 199
FT TURN 202 203
FT TURN 205 206
FT STRAND 209 209
FT STRAND 214 214
FT HELIX 220 225
FT STRAND 227 228
FT TURN 229 230
FT STRAND 231 234
FT TURN 236 237
FT HELIX 239 254
FT TURN 255 256
FT STRAND 259 262
FT HELIX 265 267
FT HELIX 270 283
FT STRAND 287 290
FT HELIX 301 309
FT STRAND 313 315
FT TURN 317 327
FT HELIX 328 328
FT HELIX 334 347
FT TURN 349 350
FT HELIX 351 353
FT STRAND 355 356
FT TURN 361 362
FT TURN 369 370
FT TURN 373 385
FT STRAND 389 393
FT TURN 394 395
FT TURN 396 398
FT TURN 399 399
FT TURN 405 406
FT HELIX 407 409
FT HELIX 420 428
FT TURN 429 430
FT TURN 431 434
FT HELIX 436 440
FT STRAND 442 448
FT STRAND 452 459
FT TURN 460 461
FT STRAND 462 469
FT STRAND 476 478
FT STRAND 482 482
FT STRAND 488 490

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FT      TURN      493      498

Query Match      11.0%; Score 292; DB 1; Length 718;
Best Local Similarity 23.6%; Pred. No. 7.3e-14;
Matches 110; Conservative 82; Mismatches 163; Indels 112; Gaps 21;

QY 19 GQHWRLON--DSAVLAHGITAAMIIPA-----YKG-TSQADVGYGYLDYDGE 66
DB 85 GGDWGLINKINDVNFSDGLVLTALMISCPVENIFATINYSVTWTAHNGYAKRPFKKTNP 144
QY 67 FHQKGTVTKYGTGKELSAIKSLHSRDINVGDVVNHKSGADATEDVTAVEVDP--AD 124
DB 145 Y-----FGTMADFQNLITTAHAKGIKIIDFAPNHTS-----PAMETDTSFAE 187
QY 125 RNRVYSGEHLIAKMTWHFHPGSGTSPDKMWHFPGTDWDESKLRIRIYFQSGKAMDW 184
DB 188 NGRLYDNGTLVGGYT-----NDTNGYFHHNGSDFS----- 218
QY 185 EVSNENGVYDYAMYADIDYHPDVAAE-----IKRWGTWYANELQDGFRLDAVKHIF 238
DB 219 --SLENGITYKNL-YDLADFNHNNATIDKYFKDAIKLM-----LDMGVDSIRVDAYKAMPL 270
QY 239 SFRLDVMVNHVEKTKGEMFTVAEYQNDLGALENYLNKTNFNSHVPVPLHYQFHAA--- 295
DB 271 GWOXSMWSSI--YAHKVPVFTGEWF---LGSASADADNTDFANKSGMGLDPRFSAVRN 325
QY 296 ---STGGGVYMRLLNGTGVVSKHPLK-SYTFVNNHDTQPGQSLSESTVQWTFKPLAFAFI 351
DB 326 VFRDNTSMATLDSMINSTATDYNQVNDQVTFDHNHMDRPKT--SAVNNRRLRQALAFI 383
QY 352 LTRBSGYPOVFGY-DMYGTGK---DSORELPALK-----HKIPILKARKQAYGA 398
DB 384 LT-SRGVPAIYGYEQVLTNGDPDNRKXKPSFKSTTAENVISKAPLRKSNALAYGS 442
QY 399 QHDFPDHHDVGMTRBGDSVA-----NSGLALITDGGGA 435
DB 443 TOGRMINNDVYVERKFKGSVAVAVNRNLSTSGSLSTLPTGS 489

RESULT 15
CDGT_BACSS
ID      CDGT_BACSS      STANDARD;      PRT;      718 AA.
AC      P31747;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Cyclomalto-dextrin glucanotransferase precursor (EC 2.4.1.19)
DE      (Cyclodextrin-glycosyltransferase) (CGTase).
GN      CGT.
OS      Bacillus sp. (strain 6.6.3).
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=29335;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Ahmedzhanov A.A.;
RL      Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
CC      -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC      of a 1,4-alpha-D-glucosidic bond.
CC      -1- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
CC      -1- SUBUNIT: Monomer.
CC      -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC      IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC      IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC      ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC      ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC      MALTOOLIGOSACCHARIDE PRODUCED.
CC      -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial

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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; X66106; CAA46901.1; -.
DR      PIR; S21532; ALBSG6.
DR      HSSP; P30920; 1CGT.
DR      InterPro; IPR006589; Alp_amy1_cat_sub.
DR      InterPro; IPR006048; Alpha_amy1_C.
DR      InterPro; IPR006047; Alpha_amy1_cat.
DR      InterPro; IPR002044; CBD_4.
DR      InterPro; IPR006046; Glyco_hydro_13.
DR      InterPro; IPR007110; 1g-1ike.
DR      InterPro; IPR002909; IPT_TIG.
DR      Pfam; PR00128; alpha-amy1ase; 1.
DR      Pfam; PF02806; alpha-amy1ase_C; 1.
DR      Pfam; PF00686; CBW_20; 1.
DR      Pfam; PF01833; TIG; 1.
DR      PRINTS; PR00110; ALPHAMYLIASE.
DR      ProDom; PD001568; CBD_4; 1.
DR      SMART; SM00642; Amyy_1.
DR      SMART; SM00632; Amyy_C; 1.
KW      transferase; Glycosyltransferase; Calcium-binding; Signal.
KW      TRANSFERASE; GLYCOSYLTRANSFERASE; POTENTIAL.
KW      CHAIN 1 34
FT      DOMAIN 35 718
FT      DOMAIN 35 172
FT      DOMAIN 173 236
FT      DOMAIN 237 440
FT      DOMAIN 441 528
FT      DOMAIN 529 614
FT      DOMAIN 615 718
FT      ACT_SITE 263 291
FT      ACT_SITE 291 291
FT      ACT_SITE 362 362
FT      METAL 61 61
FT      METAL 63 63
FT      METAL 66 66
FT      METAL 67 67
FT      METAL 85 85
FT      METAL 87 87
FT      METAL 173 173
FT      METAL 224 224
FT      METAL 233 233
FT      METAL 267 267
FT      DISULFID 77 84
SQ      SEQUENCE 718 AA; 78014 MW; 7644096D402707B5 CRC64;

Query Match      10.9%; Score 291.5; DB 1; Length 718;
Best Local Similarity 23.0%; Pred. No. 8e-14;
Matches 118; Conservative 91; Mismatches 180; Indels 123; Gaps 24;

QY 19 GQHWRLON--DSAVLAHGITAAMIIPA-----YKG-TSQADVGYGYLDYDGE 66
DB 85 GGDWGLINKINDVNFSDGLVLTALMISCPVENIFATINYSVTWTAHNGYAKRPFKKTNP 144
QY 67 FHQKGTVTKYGTGKELSAIKSLHSRDINVGDVVNHKSGADATEDVTAVEVDP--AD 124
DB 145 Y-----FGTMADFQNLITTAHAKGIKIIDFAPNHTS-----PAMETDTSFAE 187
QY 125 RNRVYSGEHLIAKMTWHFHPGSGTSPDKMWHFPGTDWDESKLRIRIYFQSGKAMDW 184
DB 188 NGRLYDNGTLVGGYT-----NDTNGYFHHNGSDFS----- 218
QY 185 EVSNENGVYDYAMYADIDYHPDVAAE-----IKRWGTWYANELQDGFRLDAVKHIF 238
DB 219 --SLENGITYKNL-YDLADFNHNNATIDKYFKDAIKLM-----LDMGVDSIRVDAYKAMPL 270
QY 239 SFRLDVMVNHVEKTKGEMFTVAEYQNDLGALENYLNKTNFNSHVPVPLHYQFHAA--- 295
DB 271 GWOXSMWSSI--YAHKVPVFTGEWF---LGSASADADNTDFANKSGMGLDPRFSAVRN 325

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QY 296 ---STGGGYDMRKLNGIVVSKHPLK-SYFVNDHDTQGSLESTVQTFKPLAVAFI 351
Db 326 VFRDNTSNMYALDSMINSTATDYNOVDQYTFIDNHMDRFT--SAVNNRRLQALAFI 383
QY 352 LTRBSGYPQVFG--DMYGTG---DSQREIPLAK-----HKLEPILKARKQYAYGA 398
Db 384 LT-SRGVPAIYYGTBOYLITNGDNDNRKMPSPSKSTTAPNVI SKLAPLRKSNPAIAYGS 442
QY 399 QHDYFDHHDIVGWTREGDSVA-----NSGLAALITDGPQGAKRMVYGRQUNGET 448
Db 443 TQQRWINDVYVYERKFKGSAVAVVAVNNRNLSTPANITGLSTLPTGSYTDVYLGGLANG-- 500
QY 449 MHDITGNRSEPPVYINSEGMGEFHVNGGSVSIY 480
Db 501 -NNITSNNGS---VNS-----FTLAGATAVW 523

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Search completed: October 7, 2004, 00:13:22
 Job time : 10.4712 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.3093 Seconds
(without alignments)
3290.816 Million cell updates/sec

Title: US-09-925-576C-8
Perfect score: 2666
Sequence: 1 ANLNGTLNQPEWYMPNDQ.....SEGNGEPHYNGSVSYVQR 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

```

```

1:  sp:archaea:25:*
2:  sp:bacteria:3:
3:  sp:fungi:3:
4:  sp:funghi:*
5:  sp:invertebrate:*
6:  sp:mammal:*
7:  sp:mhc:7:
8:  sp:organelle:
9:  sp:phage:*
10: sp:plant:*
11: sp:rodent:*
12: sp:virus:*
13: sp:vertebrate:*
14: sp:unclassified:*
15: sp:tvirus:*
16: sp:bacteriap:*
17: sp:archaeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2025	76.0	513	16	Q081A54	Q081A4 bacillus cere
2	2021	75.8	519	2	Q09RT8	Q09RT8 cytophaga s
3	2021	75.8	533	2	Q09A054	Q09A054 bacillus me
4	1991	74.7	513	16	Q081Yt4	Q081Y4 bacillus ana
5	1909	71.6	516	2	Q082839	Q082839 bacillus sp
6	1789.5	67.1	549	2	Q031193	Q031193 bacillus sp
7	1784.5	66.9	521	2	P71034	P71034 bacillus sp
8	1784.5	66.9	549	2	Q09KW6	Q09KW6 bacillus sp
9	1755.5	65.8	613	2	Q059222	Q059222 bacillus sp
10	1723.5	64.6	501	2	Q093148	Q093148 bacillus sp
11	1502.5	56.4	507	16	Q087H6	Q087H6 vibrio parv
12	1336	50.1	481	16	Q089Yp1	Q089Yp1 bacteroides
13	1262	46.7	493	3	Q03657	Q03657 bacillus ci
14	1244	46.7	492	16	Q08TU21	Q08TU21 anaabaena sp
15	1233	46.2	484	2	Q07Q49	Q07Q49 streptococc
16	1230.5	46.2	484	2	Q050583	Q050583 streptococc

17	1.228	44.6	1.484	16	Q8BPC8
18	1.197.5	44.9	488	16	Q8E6P6
19	1.126.5	44.9	488	16	Q8E6M2
20	1.195.5	44.8	486	16	Q8BTP08
21	1.182.5	44.4	485	2	Q53786
22	1.156.5	43.4	486	2	Q68875
23	1.108	41.6	491	16	Q9GC59
24	1.091.5	40.9	506	16	Q80916
25	1.053	39.3	494	16	Q8Z555
26	1.048	39.3	495	16	Q8FCL8
27	1.047	39.3	495	16	Q8XBB6
28	1.037	38.9	495	16	Q7UAB0
29	1.035	38.8	495	16	Q8R340
30	1.018.5	38.2	529	3	Q877B1
31	1.018.5	38.2	460	1	Q9P910
32	1.018.5	38.2	460	1	Q08452
33	1.018.5	38.2	473	17	Q8U319
34	1.018.5	38.2	473	17	Q8U319
35	1.018.5	38.2	473	17	Q8U319
36	1.018.5	38.2	473	17	Q8U319
37	1.018.5	38.2	473	17	Q8U319
38	1.018.5	38.2	473	17	Q8U319
39	1.018.5	38.2	473	17	Q8U319
40	1.018.5	38.2	473	17	Q8U319
41	1.018.5	38.2	473	17	Q8U319
42	1.018.5	38.2	473	17	Q8U319
43	1.018.5	38.2	473	17	Q8U319
44	1.018.5	38.2	473	17	Q8U319
45	1.018.5	38.2	473	17	Q8U319

ALIGNMENTS

0Y	4	NTLMOYFEWMPNDGQHMRLNDSDAYLAEHGITVAWIPYAKYGTQADVYGAYDLYD	63
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Db 32 NGTLMQFFENYAPBDGNHNRRLRTDVENLAKEGTSVWLPYAKGTQNDVGYAGAYDLYD 91
Qy 64 LGEEFHOKGTVRYKGTGKGBLOSIAKLSHRSRDINVTGVVJNHKGADATEVTAWEVDPA 122
Db 92 LGEEFNQGTVRTKGTGAOLKSAIDALHKKKINDVGVGVVNNHKGADATEVTVTAWEVDP 150
Qy 124 DRRNVISGEHLIAKWNTHFHFPRGGSYSYDQFKMWNTHFDGTDMDBSRKKNRYKFO--GKA 181
Db 152 NRRNVEASDEIISAMWGFPNPGDGSYSNFKMKWNTHFDGTDMDBSRKKNRYKFRGIGKA 211
Qy 182 WDMVESNENANYUWYADIDYDHPVVAEIKRMGWTANELQLGFEPLDVKHIIKSF 249
Db 212 WDMVESSENANYUWYADIDFDPHPVVAEMKKMGWTANELDLGFEPLDVKHIDHEYL 271
Qy 242 RDWNNHREKGTGKEMFTVAEYWNQNDGALENYLNKTNFNHSYFVDVPLHYOFHASTOGGG 301
Db 272 RDWNNHRRQGTGKEMFTVAEYWNQDQTLNNTIAKVNINQSFDPALPHNHYASTNGN 331
Qy 302 YDRKRLINGVYSKHPILKSYTFPDNHDTPQGSLESTYQTFMFKPLAFAFILTRESGPV 361
Db 332 YDMKNILKGTIVVANHPLAVTLVVENHDSPOGOSLESVSVPWFKPLAFAFIITRAEGVPSV 391
Qy 362 FYGDMYGTGKDSQREIPALKHKLEPIELKARKOYAGAONDVDHHDIDYGMTREDSV 421
Db 392 FYGDIYGTGKNSNYEIPALKDKIDPILTKRKPAFGTQDIFDHPDVGIMTREDSV 451
Qy 422 SGLAALLTDPGGAkakmyyGRONAGETWHDITGNRSBPVINSBEGMFEHTNGSVSIYV 481
Db 452 SGLATLISDPGGAkmmDVgonnAGEvWHDIDGNGTNTVYTIKMOGQFOYSGGSVSIIY 511
Qy 482 QR 483
Db 512 QQ 513

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RESULT 2				
Q9RQ78	PRELIMINARY;	PRT;	519	AA.
ID Q9RQ78				
AC Q9RQ78				
DT 01-MAY-2000	(TREMBLrel. 13, Created)			
DT 01-MAY-2000	(TREMBLrel. 13, Last sequence update)			
DT 01-JUN-2003	(TREMBLrel. 24, Last annotation update)			
DE	Raw starch digesting amylase precursor.			
OS	Cytophaga sp.			
OC	Bacteria; Bacteroidetes; Sphingobacteriales; Sphingobacteriales;			
OC	Flexibacteraceae; Cytophaga.			
OX	NCBI_TaxID=29535;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RL	Jiang C.L., Chen L.S., Chen M.Y.;			
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF067653; AAF00567.1; -.			
DR	HSSP; P06278; IVUS.			
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR006047; Alpha_amy1_cat.			
DR	InterPro; IPR006589; Alp_amy1_cat_sub.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Pfam; PF00128; alpha-amylase; 1.			
DR	PRINTS; PR00110; ALPHAMYLASE.			
DR	SMART; SM00642; Amyy; 1.			
KW	Signal.			
FT	SIGNAL.	1	57	POTENTIAL.
FT	CHAIN	58	519	RAW STARCH DIGESTING AMYLASE.
QO	SEQUENCE	519	AA; 58337	MM; 3E6B88ADD98B163 CRC64;

```
Query Match      75.8%; Score 2021; DB 2; Length 519;  
Best Local Similarity 73.4%; Pred.No. 4.8e-140;  
Matches 356; Conservative 60; Mismatches 2; Gaps 1,  
  
QY    1 ANLNGTLMQVEFWMPNDGCMRRLQNDSATIAEHGIATNWIIPPKYGTSQADVGKAYD 60  
| :||:::||:||||:||||:||||: ||: |::|:|
```

Db	3	AAITNGTMMQJFENYVYVPRDGGQOMRLRTDAPYLSSVIGTIAWTTPRAYKTSQADVCYGPYD	94
Qy	61	LYDGEFHQKJTVRTKYGTKGBLQSAIKSLHSRDINYGDVYVNHKGADATDVTAVEV	120
Db	95	LYDGEFNOQKJTVRTKYGTKGBELKSAMVTLHSNGIQVYGDVVMNHKAGADYTENVTAVEV	154
Qy	121	DPADRNVRVLSGHELIKAMTHFHPHPPGSGSYSDPFKMNWHFPGTMDSESRKLNRYKQKQ--	178
Db	155	NPSRRNDETSGEARNQDMQMGFNPPGGGITYNSPFKQMOMHFQGTMDOSRSJSLRPFKRGCT	214
Qy	179	GKAWDMVSNENGNQYDYLWYADIDYDHPDVAALIRKMGTYANBELDGFELDAVKAIKF	238
Db	215	GKAWDMVSESNENQYDYLWYADIDYDHPDVVNMKKMGWYANEEYGLDGYSRLDAVKIKF	274
Qy	239	SFLRDMNHNHREKTGEMFTVAEYVQNDIGALENTLKTNRNHSYFVLYLQYHAASTQ	298
Db	275	SFLKDMVDNHRATYTGEMFTVABYVQNDIGALNNYLAIVANNQSLFDPALHYNNYAASTQ	334
Qy	299	GGGYDMRKLNGTVSVSKHPLKSVTFVNDHDTQPGQSLSESTVQTQTFKPLAVALITRESGY	358
Db	335	GGYYDMRNLNTLTVASNPTKAVTLVEAHNDTPQGSLESTVQPMFKPLAVALITRESGY	394
Qy	359	POVYFGDMYTKCDQSORETIPALKHTEIPLKARKKYAAGAHYFDDHDIYGVTRBEDSS	418
Db	395	PSVYFGDMYTKCTTTTIREIIPALKSKIEPLKARKKOYAAGTGRDYIDNDPVYGMWTRBEDST	454
Qy	419	VANSGLAALTDPGGGAKARVYGRONAGETWHDITGNRSSEPVVNSBEGCFHHNGGSVS	478
Db	455	KAKSGALATYITTPGPGSKRMVYGTSMAGBIWYDLGNRTDKITLIGSDGYATFPVNGGSVS	514
Qy	479	IYYOR 483	
Db	515	vvvQO 519	

RESULT 3			
ID	Q9A054	PRELIMINARY;	PRT; 533 AA.
AC	Q9A054;		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	Alpha-amyase.		
OS	Bacillus megaterium.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxId=1404;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,		
RA	Park K.-H.;		
RT	"Cloning of maltopentase-producing amyase from <i>Bacillus megaterium</i>		
RT	KSM B-404.";		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF220440; AAK00598.1; -		
DR	HSP; P06278; IVUS.		
DR	GO; GO:0004556; F:alpha-amyase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	InterPro; IPR006047; Alpha_amy1_cat.		
DR	InterPro; IPR006589; Alp_amy1_cat_sub.		
DR	Pfam; PF00128; alpha-amyase; 1.		
DR	SMART; SM00642; Aamy; 1.		
DR	SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;		

Query Match	75.8%	Score 2021:	DB 2:	Length 533;
Local Similarity	74.38%	Pred. No.	4.9e-140;	
Matches	358;	Conservative	49;	Mismatches 73; Indels 2; Gaps 1.

QY	4	NGTLMQFFEWMPMDGOHMRRLONDSAYLAHGHTAAWIPPAKYGTSQADYGCGAYDYLD	63
Db	52	NGTLMQFFEWMPMDGOHMRRLONDSAYLAHGHTAAWIPPAKYGTSQADYGCGAYDYLD	111
QY	64	LGEFHQKGVATYKXGKIGELQSAIKLSHSRDINYGAVINHKSGADATEDVTVAEVDPA	123

Db	11	LGEPNKGVTRTKYGTKAQLKSAIDALHKKONIDVGDVVMHKGGADEVTEFVTAVEVDP	171
Qy	124	DRNRVYSGEHLKAMTHFHFPRGSGTSDPFKKNMTHFPGTMDSRKLNRYKQ--GKA	161
Db	172	NRNVEVSQGYEISAMWGFMFPGRGDSYSNFKMKWTHFPGTMDGARKLNRYKFRFG	231
Qy	182	MDNEVSENGNVDYLMYADIDVHPVAAEIRKMGTVANELODGPFLAVKHIKESFL	241
Db	232	MDNEVSENGNVDYLMYADIDVHPVAAEIRKMGTVANELODGPFLAVKHIDHEYL	231
Qy	242	RDVWNVHREKTGKEMPTVAEYQNDLGALENYLNKTENFNSVFDPVPLHYQFAASTOGG	301
Db	292	RDVWNVHROQTGEMFAVAEYQNDIQTLNNVLAQVNNQSVFAPLPHNHYASKNGN	351
Qy	302	YDMRKLTNGTVSKHPKSVTVVDNHDTPGGSLSTVQTFPKPLANAFLITRESGPV	361
Db	352	YDMRKLTNGTVVANHPLTAVLVLENHDSQPGSLESVSPWPKPLAFAFLITRAEGYPSV	411
Qy	362	FYGDYGTGKDSQREIPLAKHTEPLTKARKOYAGAODVFPDHDIVGWMREBDSVAN	421
Db	412	FYGDYGTGKDSNVEIPLAKDKIDPLTKARKVAAGTQRPYDHDVYGMREBDSVHAN	471
Qy	422	SGLAALITDGGCGAKKMYVGRONAGETWHDITGNRSSEPVVINSBEGEFHNQGSVSIY	481
Db	472	SGLATLTISDGGCAKMMYGVKNNAGELIWDIGNQTNVTYINKOMQGFVYSGGSVSIY	531
Qy	482	QR 483	
Db	532	QR 533	
RESULT 4			
Q81YJ4	PRELIMINARY;	PRT;	513 AA.
O81YJ4			
AC	O81YJ4;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Alpha-amyase.		
GN	AMYS OR BA3551.		
OS	Bacillus anthracis (strain Ames).		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=198094;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22608414; PubMed=12721629;		
RA	Read T.D., Peterson S.N., Tourasse N., Baillye L.W., Paulsen I.T.,		
RA	Neelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,		
RA	Holtzapple E.K., Orsted O.A., Helgason E., Ristone J., Wu M.,		
RA	Kolony J.T., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,		
RA	Deboy R.T., Madpu R., Daugherty S.C., Durkin A.S., Hatt D.H.,		
RA	Neelson W.C., Peterson J.D., Pop M., Khoui H.M., Radue D.,		
RA	Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,		
RA	Berry K.J., Platt R.D., Wolf A.M., Watkins K.L., Niemman W.C.,		
RA	Hezen A., Clime R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,		
RA	Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,		
RA	Fraser C.M.;		
RT	"The genome sequence of Bacillus anthracis Ames and comparison to		
RL	closely related bacteria."		
RL	Nature 423:41-66(2003)		
RL	EMBL; AE017035; MAP27311.1; -.		
DR	TIGR; BA3551; -.		
DR	TIGR; GO:0004556; F:alpha-amyase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	InterPro; IPR006047; Alpha_ami_1_cat.		
DR	InterPro; IPR006589; Alp_ami_1_cat_sub.		
DR	Pfam; PF00128; alpha-amyase; 1.		
DR	SMART; SM00642; Amy; 1.		
DR	Complete proteome.		
QW	SEQUENCE 513 AA; 58445 MW; 55806DEF282FD159B CRC64;		

Query Match	74.7%;	Score 1991;	DB 16;	Length 513;
Best Local Similarity	73.0%;	Pred. No. 7.5e-138;		

	-Matches	352;	Conservative	51;	Mismatches	77;	Indels	2;	Gaps	1
Qy	4	NGTLMQYFEMTPMPDGGHMRRLQNDASVLAHEGITAAMIIPRAYKTSQSADVCYGAYDLVD	63							
Dd	32	NGTLMQYFEWYAAPDRHRMMLRDAENLAAKGITISVMIIPRAYKTQTQNDVGAYGLVD	91							
Qy	64	LGEFHQGVATYTKTGTELGSATIKSLHSRDINIVYGDVVIHNKSGADATEDTVAEVEDPA	123							
Dd	92	LGEFNQGVATYTKGTGAQLKSALIALHKQNIIDVYGDVVNHHKSGADITYETVAEVEDRN	151							
Qy	124	DRNEVISGEHLIKAMTHFPFRGRSTYSDFKMHWTYFDGTDWDESRKLRIYKFQ--GKA	181							
Dd	152	NRYAVESGDYEIISAWTGFNFPRGDDGNVSINFKKMYHFQDGTWDDEGRKLRIYKFRIGRA	211							
Qy	182	WMDEVSNENGNYDYLTMTADIDYHPDVAAELIKRCTWTANELQLDFRLDAYKHILKFTSL	241							
Dd	212	WMDEVSSENGNYDYLTMTADLPDPHDVANEMKNMGWTYANEIMLDGFLDAVKHIDLHEYL	271							
Qy	242	RDMVNHYREKTKGMFPTVAEYWNODLGALEMYLNKTNFNHSFYVDPLVHQFFAASIQGGG	301							
Dd	272	RDMVNHYRQQGKEPFVAEYWQNDIQTLNNYLAKVNTNQSVFDAPLVNFFYASKGNEN	331							
Qy	302	YDMERLLNGTVVSKHPLKSYTFPVNHDPQGQSELESTYQTFWEKPLAYAFILTRBSGPQV	361							
Dd	332	YDMENIINGTMQNHPALAVTLVENHDSQPQGSLESVSVPWFKPILAYAFILTRAEGPSV	391							
Qy	362	FYGMVYGTGDSQREIPALKKIEPILKARQYAYGAOHDIYDHDDIYGMTTEBGSSVAN	421							
Dd	392	FYGYGYGTGNSGSYEIPALKOKIPIPIILARKNFAFGTYORDYDHPDVIYGMTREGSVMAN	451							
Qy	422	SGLAALLTTDGCGGAKRMVYVRGONGETMHDITGNSSEPVVINSDEMGEPHVAGSVSIYV	481							
Dd	452	SGLATLLISDGGSKMMQDVGRKNAGEVMHMDGTQNTVTYINKDGMQGHVSGSVSIYV	511							
Qy	482	QR 483								
Dd	512	QQ 513								
RESULT 5										
O82839		PRELIMINARY; PRT; 516 AA.								
AC	O82839.									
DT	01-NOV-1998 (TREMBLrel. 08, Created)									
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)									
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)									
DE	Amylase.									
OS	Bacillus sp.									
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.									
OX	NCBI_TaxId=1409;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RC	STRAIN=KSM-1378;									
RX	MEDLINE=98342096; PubMed=9675143;									
RA	Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,									
RT	Ozaki K., Ito S.;									
RT	"Improved thermostability of a Bacillus alpha-amylase by deletion of									
RT	an arginine-glycine residue is caused by enhanced calcium binding.";									
RL	Biochem. Biophys. Res. Commun. 248:372-377(1998).									
DR	EMBL; AB008763; BAAJ2431.1; -.									
DR	HSSP; P06278; IVIS.									
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.									
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.									
DR	InterPro; IPRO06047; Alpha_amy1_cat.									
DR	InterPro; IPRO06589; Alp_amy1_cat_sub.									
DR	InterPro; IPRO06046; Glyco_hydro_13.									
DR	Pfam; PF00128; alpha-amylase; 1.									
DR	PRINTS; PR00110; ALPHAMYLAASE.									
DR	SMART; SMO0642; Amy1; 1.									
SQ	SEQUENCE 516 AA; 58841 MW; D90ABCG90ECCLB2F8 CRC64;									

Query Match	71.6%;	Score 1909;	DB 2;	Length 516;
Best Local Similarity	69.1%;	Pred. No. 8e-132;		

	Matches	335; Conservative	68; Mismatches	72; Indels	10; Gaps	4
QY	4	NGTLMQYETWMPDNDQHWRRLONDSAVIAEHGTAWVTPRAYKGTSGADYGYADLYD	63			
Db	37	NGTMMQYETWMLPNDGNHNRRLRDDAANLKSGITAWVTPRAWKGTSGQNDVGYGYADLYD	96			
QY	64	LGEFHQKGTVPRTKYGTKELOGAISLHSRDLNNYGDVYVNHKGGADATEDVTAVEVPA	123			
Db	97	LGEFHQKGTVPRTKYGTSTQLOGAVTSLKNNNGIQVYGDVVMNHKGGADTEMTVAEVAVR	156			
QY	124	DRNRVISEGHLIKAWTFHFPGRGSTYSDFKHWYHFPDGTIDESGRKL-NRIYKFO--GK	180			
Db	157	NRNGTISEBYYTIAWTKFDPRGRGTHSNFKRMKTHFGCTIDQSRQLONKTKYRGTK	216			
QY	181	AMDWEVSNENGYDYLTAMDIDYDHPDYAAETKRWGTAYANELQDGEFLDLAVKHIKFSF	240			
Db	217	AMDWEVDIENGNYDYLTAMDIDMDHPEVYNELRNMGVWYTTNTLNDGRIDAVKHIKSY	276			
QY	241	LRDVNVHREKTKGKMFVYAEYQWDLGALENYLNKTNPNHNSVFPVPLHYQFHAASTOGG	300			
Db	277	TRDMTLHYRNTYTKKMPFAVAFEPWKDLAIEYVLYNKTSWNHSVFEPVPLHYMLYNASNSGG	336			
QY	301	GYDRKRLTNGYSKPLKSVTFVNDHTOPQSHSTVQVMPKFLAAYLITLRESGVPQ	360			
Db	337	YFDNRNLINGSVQKHPILHAVTYFVNDHNSQPEBALESFVQSMFKPLAAYLITLRESGVPS	396			
QY	361	VFYGDWY--TKDSQREIIPALKHIEIPILAKKOYAAGAOHDYEDHHDITVGMTREGPS	418			
Db	397	VFYGYGYIIPHG-----VPSKSKSIDPLQARQYTAGTGQHDHYDDHDDITIGMTREGPS	451			
QY	419	VANSGLAALITDGPAGARMTYVGRONAGEETMHDITGNSEPVVINSBGWGEFHNNGSVS	478			
Db	452	HPNSGLATIMSDGPGCNKMTYVGRKAKAQVWRDITGNSSGTVTINADMGFTYVNGAVS	511			
QY	479	IYYOR 483				
Db	512	VWVKQ 516				

RESULT 6			
ID	031193	PRELIMINARY;	PRT; 549 AA.
AC	031193		
DT	01-JAN-1998	(TREMBLrel. 05, Created)	
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	
DE	Alpha amylase.		
GN	AMT.		
OS	Bacillus stearothermophilus.		
OC	Bacteria, Firmicutes, Bacillales, Bacillaceae, Geobacillus.		
OX	NCBI_TaxID=1422;		
RP	[1]		
RC	SEQUENCE FROM N.A.		
RA	STRAIN=ATCC 31195;		
RL	da Silva A.C.R., Fernandes E., Puyeo M.T.;		
DR	Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AF032864; AAB86961.1; --		
DR	PIR; A54541; A54541.		
DR	HSPB; P06278; IVDS.		
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	InterPro; IPR006047; Alpha_amy1_cat.		
DR	InterPro; IPR006589; Alp_amy1_cat_sub.		
DR	Pfam; PF00128; alpha-amylase; 1.		
DR	PRINTS; PR00110; ALPHAMYLASE.		
DR	SMART; SM00642; Amyy; 1.		
SQ	SEQUENCE 549 AA; 62651 MW; 2CNA699EDACG4D262 CRC64;		
Query Match	67.1%;	Score 1789.5;	DB: 2; Length 549;
Best Local Similarity	64.9%;	Pred. No. 5.2e-123;	
Matches 315; Conservative	67;	Mismatches 99;	Indels 5; Gaps 24;

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QY 1 ANLNTGLTQYFWMYWPBNQOHWRRRLONDSAYIAEHGITAVMJLPPRAYKGSQADVYGAYD 60
Db AFPNQTMQYFEMWYLPDDGTLMTKXANENANNJSSLSIGTALMLBPAPYKGSRSRSDVGYGYD 95
QY 61 LYDLBEPHOKGVVRKYGTGKELQSAIKSLHSRDINVDVYJNHNGGADATBEDVAYVEY 120
Db LYDLBEPHOKGVVRKYGTGKAOYLQAHAAHAGOVYADVDFDHKGADGTBWDVAYVEY 155
QY 121 DPAADRNRVLSGEHLIKAWTHFHRPGRGSTYSDPFKMHVYHFDGTGDMDESKLNRIYKFO-- 178
Db 156 NPSDNGEISGTUQIOWMTKFPDFRGKNTYSSFFKRWYHFDGDVDMDESKLSIYFRRGI 215
QY 179 GKAMDVEVSNENGYDYLMTADIDYDHPVAAEIKRWGTWYANELQDGRFLDAYHIXE 238
Db 216 GKAMWMEVDTEGNGYDYLMTADLDMDHPEVVELKRWGKMYVNTTNIIDGFRDLAVXHXIE 275
QY 239 SFLBPMWNVHREKTKKEMETVAEYQNDLGALENTLNKTNFPHSVYDVLPHQFHAASIQ 298
Db 276 SFEPFMLSYSQTSKPLPTVGEWYSYDNLKLNHTYTKTNGTMSLPEADPLANKFXYASKS 335
QY 299 GGGYMWKRLNGLNGTVVSKHPLKSVTVVDNDHDTPQGSLESTVQWTFEKLAYAFILITRESGY 358
Db 336 GGAFFMRKLTMTNTMLKKQDPTLAVTVVDNHDIPEFGALQGSWDVWPFKFLAYAFILITRQBEY 395
QY 359 PQVFYGMVYGTGKDSQREIPLAKHIEPLKARKOYAYGAOHYDFDNDIVGWTREBGSS 418
Db 396 PCVFPGDYGYD---PQYNIPLSKSIDPLILARRDYAVYGTQDYLDSHDIIGWTRGAYTE 452
QY 419 VANSGLTALLIDGPGGAKRMVYGRONAGETMHDITGNSEFPVYINSSEGEFTHVNGSGYS 478
Db 453 KPGSGTALLITDGPGSKMYVYGGHAKGVFDLTGNRSDITVINSDBGEFKXVNGSGYS 512
QY 479 IYVOR 483
Db 513 VWVPR 517

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	RESULT	7			
ID	P71034		PRELIMINARY;	PRT;	521 AA.
AC	P71034				
DT	01-FEB-1997	(TRENBLrel. 02,	Created)		
DT	01-FEB-1997	(TRENBLrel. 02,	Last sequence update)		
DE	01-JUN-2003	(TRENBLrel. 24,	Last annotation update)		
OS	Alpha-amylase precursor.				
OC	Bacillus sp. MK 716				
OX	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
RN	NCBI_TaxID=54116;				
RP	[1]				
RC	SEQUENCE FROM N.A.				
RA	STRAIN=MK 716;				
RT	Sidhu G.S., Chakrabarti T.;				
RL	"Molecular cloning and expression of the gene encoding for thermostable alpha-amylase of a thermophilic bacterial isolate.";				
DR	Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.				
DR	EMBL; U75445; AAB18785.1; -				
DR	HSSP; P06278; IVUS.				
DR	GO: GO:0004556; F:alpha-amylase activity; IEA.				
DR	GO: GO:0005975; P:carbohydrate metabolism; IEA.				
DR	InterPro; IPR006047; Alpha_amyl_cat.				
DR	InterPro; IPR006589; Alp_amy1_cat_sub.				
DR	InterPro; IPR006046; Glyco_hydro_13.				
DR	Pfam; PF00128; alpha-amylase; 1.				
DR	PRINTS; PR00110; ALPHAMYLASE.				
DR	SMART; SMO0642; Amyy; 1.				
KW	Signal.				
FT	SIGNAL	1	34	POTENTIAL.	
FT	CHAIN	35	521	ALPHA-AMYLAZE.	
SQ	SEQUENCE	521 AA;	59311 MM;	5612A8B596D922E1 CRC64;	
Query Match		66.9%;	Score 1784.5;	DB 2;	Length 521;
Best Local Similarity		64.7%;	Pred. No. 1.1e-122;		
Matches 314;	Conservative	67;	Mismatches 99;	Indels 5;	Gaps 27;

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QY 1 ANINGTLMQFEMWMPNDGQHRRLONDSAYLAHSGITAVWIPRAYKTSQADYGYAYD 60
D 36 APFNGTMMQFEMWLPDGLMTKRVANBANNSLSGITLMLPRAKYKTSRSDYGYAYD 95
QY 61 LYDGEFHQKGVTRTKYGTGKELQSAIKSLHSDINYGVDVINHKGADATEDVYAVEV 120
D 96 LYDGEFHQKGVTRTKYGTGKELQSAIKSLHSDINYGVDVINHKGADATEDVYAVEV 155
QY 121 DPADNRNVIAGEHLIKATWHPHFGSGTYSDFKRWYHFDGTDWDSRKLNRITYKQ-- 178
D 156 NPSRNDNEISGTVOIQAMTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLNRITYKRG 215
QY 179 GKAMDVEVSNENGVYDLMTADIDYDHPDVAELIKRWGTWYANLQDGFRLDVKHIF 238
D 216 GKAMDVEVDTENGVYDLMTADIDYDHPDVAELIKRWGTWYANLQDGFRLDVKHIF 275
QY 239 SFLADWVNHREKTKEMFTVAEYQNDLGALENYLNKTNFNHSDVPDPLHYOFAASTQ 298
D 276 SFPEDMLSYRSQGTGKELFTVGEYWSYDINKLNHYIKTNQTMSLFPAFLNKEFYTAS 335
QY 299 GGGYDMRKLNGTVVSHPLKSVTFVNDHTOPQGSLESTVQTFKPLAYAFILTRBSGY 358
D 336 GGAFDKRTMLMTMLMKOQPTLAVTFVNDHTEPGALQSWDVPFKELAYAFILTRQEGY 395
QY 359 POFYFGMYGTGKDSOREIPALKHIEPILKARKQVAYGAOHYFDHDIWGTRBGDS 418
D 396 PGVFTGYGDI--PQYNISLSKSIDPLIARADYVGTQHDYDLSHDIIGWREBVT 452
QY 419 VANSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGWGFHNGSVS 478
D 453 KPSSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGWGFHNGSVS 512
QY 479 IYVQR 483
D 513 VWVPR 517
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RESULT 8

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Q9KMY6 PRELIMINARY; PRT; 549 AA.
ID Q9KMY6;
AC Q9KMY6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DS1100;
RA Beijar S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17557; CAB93517.1; -.
DR F1R; A54541; A54541.
DR HSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3B6DP9120BCE CRC64;
```

Query Match 66.9%; Score 1784.5; DB 2; Length 549;
Best Local Similarity 64.7%; Pred. No. 1.2e-122;
Matches 314; Conservative 67; Mismatches 99; Indels 5; Gaps 2;

```
QY 1 ANINGTLMQFEMWMPNDGQHRRLONDSAYLAHSGITAVWIPRAYKTSQADYGYAYD 60
D 36 APFNGTMMQFEMWLPDGLMTKRVANBANNSLSGITLMLPRAKYKTSRSDYGYAYD 95
QY 61 LYDGEFHQKGVTRTKYGTGKELQSAIKSLHSDINYGVDVINHKGADATEDVYAVEV 120
D 96 LYDGEFHQKGVTRTKYGTGKELQSAIKSLHSDINYGVDVINHKGADATEDVYAVEV 155
QY 121 DPADNRNVIAGEHLIKATWHPHFGSGTYSDFKRWYHFDGTDWDSRKLNRITYKQ-- 178
D 156 NPSRNDNEISGTVOIQAMTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLNRITYKRG 215
QY 179 GKAMDVEVSNENGVYDLMTADIDYDHPDVAELIKRWGTWYANLQDGFRLDVKHIF 238
D 216 GKAMDVEVDTENGVYDLMTADIDYDHPDVAELIKRWGTWYANLQDGFRLDVKHIF 275
QY 239 SFLADWVNHREKTKEMFTVAEYQNDLGALENYLNKTNFNHSDVPDPLHYOFAASTQ 298
D 276 SFPEDMLSYRSQGTGKELFTVGEYWSYDINKLNHYIKTNQTMSLFPAFLNKEFYTAS 335
QY 299 GGGYDMRKLNGTVVSHPLKSVTFVNDHTOPQGSLESTVQTFKPLAYAFILTRBSGY 358
D 336 GGAFDKRTMLMTMLMKOQPTLAVTFVNDHTEPGALQSWDVPFKELAYAFILTRQEGY 395
QY 359 POFYFGMYGTGKDSOREIPALKHIEPILKARKQVAYGAOHYFDHDIWGTRBGDS 418
D 396 PGVFTGYGDI--PQYNISLSKSIDPLIARADYVGTQHDYDLSHDIIGWREBVT 452
QY 419 VANSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGWGFHNGSVS 478
D 453 KPSSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGWGFHNGSVS 512
QY 479 IYVQR 483
D 513 VWVPR 517
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RESULT 9

```
Q59222 PRELIMINARY; PRT; 613 AA.
ID Q59222;
AC Q59222;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Alpha-amylase (EC 3.2.2.1).
GN Amy.
OS Bacillus sp. TS-23.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=38441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TS-23;
RA Lin L.-L., Chu W.S., Hou W.H.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22045; AAA63900.1; -.
DR HSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0008477; F:purine nucleosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF00686; CBM 20; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR PRODOM; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 613 AA; 69537 MW; 14684A30FC2895E8 CRC64;
```

Query Match 65.8%; Score 1755.5; DB 2; Length 613;

Best Local Similarity 64.1%; Pred. No. 1.9e-120;
Matches 311; Conservative 68; Mismatches 101; Indels 5; Gaps 2;

QY 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDSDAYLAHGIITAVWIPPAKYGTSGADYGVAYD 60
DB 33 APINETMQYFEWMLPNDGTLMTKYNKEANLSSLGITLMLPRAKGTSGSIVSGAYD 92
QY 61 LYDGEFHOKGIVRTKTKGTGELQSAIKSLHSPDINVGDVYVNHKGADATEDYTAVEV 120
DB 93 LYDGEFHOKGIVRTKTKGTGYOYIQAIAKAKAGMOVYADVVENHKAAGDTEFPDAVEV 152
QY 121 DPADRNKVISGEHLIKAMTHFHPGSGTSDYDFKMWYHPDGDMDPESKRLRIYEQ-- 178
DB 153 DPNRNQETSGYQIQAMTKEDFPFGNGNTSSFKMWYHPDGDMDPESKRLRIYKERT 212
QY 179 GKAMDVEVSENNNTYIYLAADIDYHPDVAEIKKMGWYANELQDGFRLDAVKHIF 238
DB 213 GKAMDVEVDTENNNTYIYLAADIDMDHPEVTELEKMGWYVNTNIDGFRDAVKHIF 272
QY 239 SFLADVNHVREKTKEMFTVAEYQNDLGALENTYKTNPMHSPVDPVLAHQFAASTQ 298
DB 273 SFPDMLTYVRNQTGNTLPAVGEFWSYDVNKLHNTYTKNGSMSLPDAPLHNNFYTAKS 332
QY 299 GGGYDMRKILNGTVSVKHPKSVTFVNDHTQPGQSLBSTVQTFWFKPLAAYAFILTRBSGY 358
DB 333 SGYFDMRYLLNNTLMKQDQSLAVTLVDNHDTPGQSLQSWEPWFKPLAAYAFILTRBSGY 392
QY 359 POFVYGDWYGTGDSQREIPALKKHIEPLTKARKQYAGQHDYDPHHDIVGMTREGDSS 418
DB 393 PCVFGDYDT--PKNIPGLSKSIDPLLIARRDYAGTORDYIDHODIIGMTREGIDT 449
QY 419 VANSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVYINSEMGSEFHNQGSVS 478
DB 450 KENSGLAALITDGPAGSKMYVYKKGAKKVPYDLTGNRSDTYTINADMGSEFKNQGSVS 509
QY 479 IYVQR 483
DB 510 IYVAK 514

RESULT 10
Q93148 PRELIMINARY; PRT; 501 AA.
AC O93148.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
GN AMYK38.
OS Bacillus sp. KSM-K38.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=129736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-K38;
RA Hayaishi Y.;
RT "Isolation of a new Bacillus alpha-amylase."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051102; BAB71820.1; -
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR InterPro; IPR006047; P:carbohydrate metabolism; IEA.
DR Pfam; PF00128; alpha-amylase; 1.
SQ SEQUENCE 501 AA; 57485 MW; 1240F46739A5CC11 CRC64;

Query Match 64.6%; Score 1723.5; DB 2; Length 501;
Best Local Similarity 62.8%; Pred. No. 3.2e-118;
Matches 302; Conservative 72; Mismatches 104; Indels 3; Gaps 1;

QY 3 LNTGTMQYFEWYMPNDGQHWRLQNDSDAYLAHGIITAVWIPPAKYGTSGADYGVAYD 62
DB 24 LNTGTMQYFEWYMPNDGQHWRLQNDSDAYLAHGIITAVWIPPAKYGTSGADYGVAYD 83

QY 63 DLGEFHOKGIVRTKTKGTGELQSAIKSLHSPDINVGDVYVNHKGADATEDYTAVEV 122
DB 84 DLGEFHOKGIVRTKTKGTGYOYIQAIAKAKAGMOVYADVVENHKAAGDTEFPDAVEV 143
QY 123 ADNRNRVISGEHLIKAMTHFHPGSGTSDYDFKMWYHPDGDMDPESKRLRIYKFGQKAM 182
DB 144 TNRMODISGAYTIDAMTGFPSSGRNNAYSDFKRMRFHFNVDMDQKIQSHNITREFANTW 203
QY 183 DMEYSNNGNDYLMYADIDYHPDVAEIKKMGWYANELQDGFRLDAVKHIFKSPLR 242
DB 204 NMRVDEENGVNDYLGNSIDPSHPEVDELKMGSEFTDELDDGYRLDAIKHIFPMYIS 263
QY 243 DNVNHRVREKTKEMFTVAEYQNDLGALENTYKTNPMHSPVDPVLAHQFAASTQGGY 302
DB 264 DNVNHRVREKTKEMFTVAEYQNDLGALENTYKTNPMHSPVDPVLAHQFAASTQGGY 323
QY 303 DMRKILNGTVSVKHPKSVTFVNDHTQPGQSLBSTVQTFWFKPLAAYAFILTRBSGY 362
DB 324 DMRKILNGTVSVKHPKSVTFVNDHTQPGQSLBSTVQTFWFKPLAAYAFILTRBSGY 383
QY 363 YGDWYGTGDSQREIPALKKHIEPLTKARKQYAGQHDYDPHHDIVGMTREGDSSVANS 422
DB 384 YGDYTGIPND--ISAKDMIDELDAKQYAGQHDYDPHHDIVGMTREGDSSVANS 440
QY 423 GLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVYINSEMGSEFHNQGSVS 482
DB 441 GLATIMSNGPAGSKMYVGRONAGETWHDITGNRSEPVYINSEMGSEFHNQGSVS 500
QY 483 R 483
DB 501 Q 501

RESULT 11
Q87HG6 PRELIMINARY; PRT; 507 AA.
AC Q87HG6.
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN VPA0999.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
CX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Naito M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae."
RL Lancet 361:743-749(2003).
DR EMBL; AP005087; BAC62342.1; -
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha-amylase; 1.
DR Pfam; PF00128; alpha-amylase; 1.
KW Complete proteome.
SQ SEQUENCE 507 AA; 58428 MW; 91B549E2B80700BD CRC64;

Query Match 56.4%; Score 1502.5; DB 16; Length 507;
Best Local Similarity 55.8%; Pred. No. 5.6e-102;
Matches 271; Conservative 81; Mismatches 125; Indels 9; Gaps 7;

QY 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDSDAYLAHGIITAVWIPPAKYGTSGADYGVAYD 59
DB 23 AGQNGTMQYFEWYMPNDGQHWRLQNDSDAYLAHGIITAVWIPPAKYGTSGADYGVAYD 82
QY 60 DLYDLGEFHOKGIVRTKTKGTGELQSAIKSLHSPDINVGDVYVNHKGADATEDYTAVEV 119

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Db      83 DMYDLGEPDQGSVRYTKYGTGAQYISAINAHNNNIQYGDVVFNRHGADGKSWDTKR 142
Qy      120 VDPDRNRVRVSGEHLIKAWTHFHPGRGSTYSDFKMWHYHFDGTDMPDSRKLRIYKFP-- 177
Db      143 VDMNMRN-IELGDMKIEAWEFNPPGRNDKYSNFHMTWYHFDGVDMDAGKKAIFPKG 201
Qy      178 OGKAMDEVSENNNGNYLYMADIDYDHPDVAAEIKEMGTWYANELQDGFRLDAVAKHIK 237
Db      202 EGKAMDEVSENNNGNYLYMADIDYDHPDVAAEIKEMGTWYANELQDGFRLDAVAKHIK 261
Qy      238 FSLRLDWNHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSEVDPVLAHYQFHAAS 297
Db      262 YQYLQEMIDHLRMTKGELEFVGEYMYNDVQNLNFTKTSGMSLDPALHMFYASK 321
Qy      298 OGGSYDKRLKNGTVSKHPLKSTYFVDNHDTPGQSLSTVQWMPKPLAFLITSSG 357
Db      322 SGGNYDMKQJNNGTLMKNDPVKAVTLVENHDTPLQALSTVDMWFPKPLAFLITREEG 381
Qy      358 YPOVFYGDWYGTG-KGDSQREI PALK-HKIEPILKAROYAGAHDYFDHHDIVGWTREG 415
Db      382 YPSFYADYGAQYSDGKYNINMAKVPYIEELVTLREYAGKONSYLDMWDVIGWTRG 441
Qy      416 DSSVANSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVYINSEGMGEFHYNGG 475
Db      442 DAHPNS-MAYIMSDGCGTGMVTKRST--RYVDKLGITREVTWDMANMAEPVYNGG 498
Qy      476 SVSIVV 481
Db      499 SVSYVW 504

```

RESULT 12

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ID      089YPI      PRELIMINARY;      PRT;      481 AA.
AC      089YPI;
DT      01-JUN-2003 (TREMblrel. 24, Created)
DT      01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT      01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE      Alpha-amylase precursor.
GN      BT4690.
OS      Bacteroides thetaiotaomicron.
OC      Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC      Bacteroidaceae; Bacteroides.
OX      NCBI_TaxID=818;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=VPI-5482 / ATCC 29148;
RX      MEDLINE=2250858; PubMed=12663928;
RA      Xu J., Björnsell M.K., Himrod J., Deng S., Carmichael L.K.,
RA      Chiang H.C., Hooper L.V., Gordon J.I.;
RA      "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL      Science 299:2074-2076(2003).
DR      EMBL; AB016946; AAC079795.1; -.
DR      GO: GO:0004556; F:alpha-amylase activity; IEA.
DR      GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR      InterPro; IPR006047; Alpha_amyl_cat.
DR      InterPro; IPR006589; Alp_amyl_cat_sub.
DR      Pfam; PF00128; alpha-amylase; 1.
DR      SMART; SM00642; Amy; 1.
KW      Complete proteome.
SQ      SEQUENCE 481 AA; 55343 MW; B6BF237011F5EB1A CRC64;

```

Query Match 50.1%; Score 1336; DB 16; Length 481;

Best Local Similarity 49.6%; Pred. No. 8.9e-90;

Matches 239; Conservative 84; Mismatches 153; Indels 6; Gaps 2;

```

Qy      4 NGTLMQFEWYMPNDGQWRRLQNDASVLAHGIITAWIPRAYKGTSGQADVGYGAYLYD 63
Db      3 NGVMQGFEEWHLADPDGKMKQIKEDALHDIQVLAWIIPRAYADEQDGGVATYDLYD 62
Qy      64 LGBFHQKGTVTRTKYGTGELQSAIKSLHSDINYGAVVINHKGADATEDVTAVEVDP 123

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Db      63 LGBFHQKGTVTRTKYGTGELQSAIKSLHSDINYGAVVINHKGADATEDVTAVEVDPK 122
Qy      124 DNRVRVSGEHLIKAWTHFHPGRGSTYSDFKMWHYHFDGTDMPDSRKLRIYKFP--GKA 181
Db      123 ERTALGEPPEIQGWISYHGRKDKSDFKMWHYHSGTGFDQKSGVFOIQSGKA 182
Qy      182 MDWEVSENNNGNYLYMADIDYDHPDVAAEIKEMGTWYANELQDGFRLDAVAKHIKESFL 241
Db      183 MSRGVSENNNGNYFLCNDIDLDHPEVSENNNGKVNSENLNDGRDLAKHMKQFV 242
Qy      242 RDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSEVDPVLAHYQFHAAS 301
Db      243 AQFLDAVSRGNDPFAVGEYMGDLEALDAYIEAVGHKNLFPVPLHYMFPQASQEGKD 302
Qy      302 YDMRKLKNGTVSKHPLKSTYFVDNHDTPGQSLSTVQWMPKPLAFLITSSG 361
Db      303 YDLRLDKDPLVEHHPPLAVITVDNHDTPGQSLSTVQWMPKPLAFLITREEG 362
Qy      362 FYGDMYGTGDSQREI PALK-HKIEPILKAROYAGAHDYFDHHDIVGWTREGDSSVAN 421
Db      363 FYGDIYIKKEKSPH----TRIIDLARKRYAGDQIETFDHPSTIGFRTGDEHNG 418
Qy      422 SGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVYINSEGMGEFHYNGGSAV 481
Db      419 SGVYFLMSNDGASKIMSLGKKGVEWHITGISEITLDEBNGEFSVESHNLAVWV 478
Qy      482 QR 483
Db      479 KK 480

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RESULT 13

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ID      003657      PRELIMINARY;      PRT;      493 AA.
AC      003657;
DT      01-NOV-1996 (TREMblrel. 01, Created)
DT      01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT      01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE      Amylase.
GN      AMYE.
OS      Bacillus circulans.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1397;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Marcel T.;
RL      Nucleic Acids Res. 0:0-0(0).
DR      EMBL; X60779; CAA43194.1; -.
DR      PIR; S15713; S15713.
DR      HSP; P06278; IVUS.
DR      GO: GO:0004556; F:alpha-amylase activity; IEA.
DR      GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR      InterPro; IPR006047; Alpha_amyl_cat.
DR      InterPro; IPR006589; Alp_amyl_cat_sub.
DR      InterPro; IPR006046; Glyco_hydro_13.
DR      Pfam; PF00128; alpha-amylase; 1.
DR      PRINTS; PR00110; ALPHAMYLASE.
DR      SMART; SM00642; Amy; 1.
SQ      SEQUENCE 493 AA; 56537 MW; FECCD2F805BB4694 CRC64;

```

Query Match 47.3%; Score 1262; DB 2; Length 493;

Best Local Similarity 47.6%; Pred. No. 2.5e-84;

Matches 230; Conservative 75; Mismatches 166; Indels 12; Gaps 3;

```

Qy      4 NGTLMQFEWYMPNDGQWRRLQNDASVLAHGIITAWIPRAYKGTSGQADVGYGAYLYD 63
Db      4 NHTMQGFEEWHLADPDGKMKQIKEDALHDIQVLAWIIPRAYADEQDGGVATYDLYD 63
Qy      64 LGBFHQKGTVTRTKYGTGELQSAIKSLHSDINYGAVVINHKGADATEDVTAVEVDP 123
Db      64 LGBFHQKGTVTRTKYGTGELQSAIKSLHSDINYGAVVINHKGADATEDVTAVEVDP 123
Qy      124 DNRVRVSGEHLIKAWTHFHPGRGSTYSDFKMWHYHFDGTDMPDSRKLRIYKFP--KA 181

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Db      124 DTKSEIESEFELEGMTKFTFPGGDDQSSSEKNNSEHFGTDPDABERKGVFRIGENKK 183
      182 WMWVENENGNVDYLMYADIDYDHPVAAEIKRWGWYANELODGFRLDAVKHKFSTL 241
      184 KMNENVDDEBGNVDYLMFANI DYNHVPVREMI DWGMGLIDTLCGGFRLDAIKHINHEI 243
      242 RDMVNHVREKTEGKEMFTVAEYMONDICALENYINKTNFNHVSFVPLHYQFPAASOGGG 301
      244 KEFAEMIKRGODPIYVEEFNNSINDACREFLDTYDIOIDLFDVSLHKHLEASLKGKD 303
      302 YMKRLKNGTVSKHPKLSVTVDNHDTPGSGLESTVQWTKPLAVALFILTRESGYPOV 361
      304 PDLSTKIFDDTLVQTPHTHVAFTVDNHDSPHEALSWIGDMFKPSAVALTLRLRDGYFV 363
      362 FPGDMVGTGK----DSGREIPALKKIEPIILAKRQYAGAHQDYFDHHDVGTREBDS 417
      364 FYGDYTGIGGEPFVVGKKEI-----LDLISARCNKAYGEQEDYFDHANTIGWRRGVE 417
      418 SVANSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSRGWGFPHVNGGSV 477
      418 EIESSGCAVVISNGDGEKRMFIGHRAGEVAVDLTKSCDDQITIEEDGMATFHVCGGCV 477
      478 STY 480
      478 SVW 480

```

RESULT 14

```

ID 08YU21 PRELIMINARY; PRT; 492 AA.
AC 08YU21;

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```

DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Alpha-amyase.
GN ALR2190.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxId=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriyuchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.,
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003588; BAB73889.1; -.
DR PIR; AH2079; AH2079.
DR GO; GO:0004556; P:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
KW Complete proteome.
SQ SEQUENCE 492 AA; 57063 MW; 11B5D6EC2F18288 CRC64;

```

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Query Match 46.7%; Score 1244; DB 16; Length 492;
Best Local Similarity 47.5%; Pred. No. 5,2e-83;
Matches 234; Conservative 84; Mismatches 161; Indels 14; Gaps 6;

```

```

QY 1 ANLNGTLMQYFETWMDGQHWRLQNDASVLAHGTITAVMIPPAYKG-TSQADVGAY 59
      2 AOMNGTMMQYFHWYIPNDGMLMSKVEASAPELADAGFTAWMLPAYKGFAGSPDVGAY 61
      60 DLVDLGEFHKGRTVYGTGKGLQSAIKSLHSRDINVDVYINIKGADAEEDYTA 119
      62 DLVDLGEFDDQGSVRIKYGTRQYTLDAVKSLLQTHGLQVAVDAVLNKHMGDAVETPKAP 121

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QY 120 VDPADRRNRVISEHILITAMTHFHPFGGSGTYSOPKMTWYFDGTDWDESKLAR--LYKF 177
      122 FPQDRLNPKGGLODITTYTHYNEPGRQKYSNEEMWHPDAVDYNEVNSGRSTVYLL 181
      178 QGKAMDEVSNENGNVDYLMYADIDYDHPVAAEIKRWGWYANELODGFRLDAVKHK 237
      182 EGRKFPDYVVALEKKNFAYLNGCGLDPQNEVNRGEVYTWGKRCDDTTYKDFRLDAIKHIS 241
      238 FSPLRDMVNHVREKTEGKEMFTVAEYMONDICALENYINKTNFNHVSFVPLHYQFPAAS 297
      242 TWFPPEWIDALEHRAKGLFMVGEYWNIDINTLLMYDAVRGKGSYFEDVPLHYNFPQASK 301
      298 QGGGYDMRKILNGTVSKHPKLSVTVDNHDTPGSGLESTVQWTKPLAVALFILTRESG 357
      302 SGGNYDMRRLIDTGMQRPHTHVAFTVEENHDSPDLALBESVBEWPKPLAVALTLRLROEG 361
      358 YPOVFYDGMTGK----GDSORE---IPALKKIEPIILAKRQYAGAHQDYFDHHDV 409
      362 YPCVTHADYTGAEYEDMGKDNRYNIFMESHRIIDLTYARKHAYIGPOYNTLDHMTTL 421
      410 GMTREGSSVANSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSRGWGF 469
      422 GMTRELGDAD-HPOGMAYIMSDGSEGIKMEVGKPT--KFDLTHEIKKAVYTNEMGWGE 478
      470 FHNNGGSVSITYQ 482
      479 FRLCGSSVSVMVQ 491

```

RESULT 15

```

ID 097049 PRELIMINARY; PRT; 484 AA.
AC 097049;

```

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DT 01-OCT-2001 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Alpha-amyase.
GN SP1382.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxId=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettein H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Uetereback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RL Science 293:498-506(2001).
DR EMBL; AE007435; NAAT5480.1; -.
DR PIR; G95160; G95160.
DR TIGR; SP1382; -.
DR GO; GO:0004556; P:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 484 AA; 55918 MW; 4B90A450A90EFB8C CRC64;

```

```

Query Match 46.2%; Score 1233; DB 16; Length 484;

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Best Local Similarity 48.6%; Pred. No. 3.3e-82;
Matches 234; Conservative 72; Mismatches 167; Indels 8; Gaps 4;

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QY 4 NGTLMQYHEWMPDQGWRLQNDQSAVLAHGHTAWIPRAYKTSQADVGYGAYDLYD 63
Db 3 NQTLMOYFEWYLPFGQGHMRLAENAPHLAIGISHWMPAPAKATNEKDVGYGYDLFD 62
QY 64 LGEPHOKGTVTKTKGELQSAIKSLHSRDINVGVDVINHGKGAADATEDVTAVEVDP 123
Db 63 LGERNQKGTVTKTKGKEDYLOAIQALKAQGIQPMADVVLNKKAAADHREAFQVIEVDPV 122
QY 124 DRNRVISEHLIKAWTHFHPGSGTYSDFKMWYHEDGTWDSRKLRIYKFG--KA 181
Db 123 DRTVELGEPFTINGWTSTFTPDGQDITYGFMHWYHFTGTDYDAKRSKSGIYLIQGDNKG 182
QY 182 WDMW--VSNENGNTDYLMTADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIFS 239
Db 183 WANBELVDNENGNDYLMYADLDFFGHPEVIONIYDMADMFMETTGVAQFRLDAVKHIDSF 242
QY 240 PLRDMVNHVRREKTKEMFTVAEYQNDLGALENTLNTNFHNSVFDVPLHYQFHAASDQ 299
Db 243 FMRNFIRDMKEKYGDDFYVGFSEFMPDKEANLDYEKTEEHFDLVVRLHONLFEASQAG 302
QY 300 GGYDMRKLLNGTVVSKHPLKSVTFVNDHDTQPGQSLBSTVQTWPKPLAYAFILTRBSGYP 359
Db 303 ANYDLRGIFFTDSLVBLKPKDKAVTFVDNHDITQGCALBSTVEWFKPAAYALILRQDGLP 362
QY 360 QVFYGDMTGYKDSQREIPLAKHIEPILKARKOYANGAHYFDHHDIVGWTREGDSSV 419
Db 363 CVFYGDYVIGISQYAE--DFKEILDRLLAIRKDLAYGEQNDYFDHANCIGWVRSGAEN- 419
QY 420 ANSGIALITDGPAGAKMYGRQAGETWHDITGNRSEPVINSGEHGFHNVGGSYSI 479
Db 420 -QSPILAVLISNDQENSKSMFVGQEWNTQTFVDLIGNHQGVYTIDEEGYGFPPVASRVSIV 478
QY 480 Y 480
Db 479 W 479
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Search completed: October 7, 2004, 00:18:59
Job time : 48.3093 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2004, 00:12:34 ; Search time 14.9658 Seconds
(without alignments)
1666.155 Million cell updates/sec

Title: US-09-925-576C-8

Perfect score: 2666

Sequence: 1 ANLNGTLMQYFEWYMPNDQ.....SEGWGEFHVYGSVSIVYQR 483

Scoring table: BIOSIM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PCtus.COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2666	100.0	483	3	US-09-182-859-2 Sequence 2, Appli
2	2666	100.0	483	3	US-09-170-670-4 Sequence 4, Appli
3	2666	100.0	483	3	US-09-193-068-4 Sequence 4, Appli
4	2666	100.0	483	3	US-09-183-412-4 Sequence 4, Appli
5	2666	100.0	483	3	US-09-264-097-2 Sequence 2, Appli
6	2666	100.0	483	4	US-09-291-023A-21 Sequence 21, Appli
7	2666	100.0	483	4	US-09-290-724-4 Sequence 4, Appli
8	2666	100.0	483	4	US-09-537-168-4 Sequence 4, Appli
9	2666	100.0	483	4	US-09-672-459-2 Sequence 2, Appli
10	2666	100.0	483	4	US-09-545-586-4 Sequence 4, Appli
11	2666	100.0	483	4	US-09-540-715A-21 Sequence 21, Appli
12	2666	100.0	483	4	US-10-186-042-2 Sequence 2, Appli
13	2666	100.0	483	4	US-09-769-864-4 Sequence 4, Appli
14	2666	100.0	512	1	US-08-720-899-2 Sequence 2, Appli
15	2666	100.0	512	1	US-08-459-610-2 Sequence 2, Appli
16	2666	100.0	512	2	US-08-343-804-2 Sequence 2, Appli
17	2666	100.0	512	2	US-08-687-389-2 Sequence 2, Appli
18	2666	100.0	512	2	US-08-600-908A-2 Sequence 2, Appli
19	2666	100.0	512	3	US-08-683-838A-2 Sequence 2, Appli
20	2666	100.0	512	4	US-09-636-252A-2 Sequence 8, Appli
21	2666	100.0	631	3	US-08-814-052-8 Sequence 8, Appli
22	2666	100.0	631	3	US-08-812-829-8 Sequence 8, Appli
23	2663	99.9	483	1	US-08-468-700-34 Sequence 34, Appli
24	2663	99.9	483	2	US-08-468-220-32 Sequence 32, Appli
25	2663	99.9	483	2	US-08-468-698-32 Sequence 32, Appli
26	2663	99.9	483	2	US-08-704-706A-34 Sequence 34, Appli
27	2663	99.9	483	3	US-08-890-383-3 Sequence 3, Appli

28	2663	99.9	483	3	US-08-914-679A-3 Sequence 3, Appli
29	2663	99.9	483	3	US-08-985-659-35 Sequence 35, Appli
30	2663	99.9	483	3	US-08-194-664A-32 Sequence 32, Appli
31	2663	99.9	483	5	PCT-US94-01552A-32 Sequence 32, Appli
32	2663	99.9	483	5	PCT-US95-10426-32 Sequence 32, Appli
33	2663	99.9	487	2	US-08-468-220-37 Sequence 37, Appli
34	2663	99.9	487	2	US-08-468-698-37 Sequence 37, Appli
35	2663	99.9	487	3	US-08-194-664A-37 Sequence 37, Appli
36	2663	99.9	487	5	PCT-US94-01553A-37 Sequence 37, Appli
37	2663	99.9	487	5	PCT-US95-10426-37 Sequence 37, Appli
38	2663	99.9	512	1	US-07-623-953-3 Sequence 3, Appli
39	2663	99.9	512	1	US-07-623-953-5 Sequence 5, Appli
40	2663	99.9	512	3	US-08-985-659-34 Sequence 34, Appli
41	2657	99.7	483	2	US-08-468-220-36 Sequence 36, Appli
42	2657	99.7	483	2	US-08-468-698-36 Sequence 36, Appli
43	2657	99.7	483	3	US-08-194-664A-36 Sequence 36, Appli
44	2657	99.7	483	5	PCT-US94-01553A-36 Sequence 36, Appli
45	2657	99.7	483	5	PCT-US95-10426-36 Sequence 36, Appli

ALIGNMENTS

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RESULT 1
US-09-182-859-2
: Sequence 2, Application US/09182859
: Patent No. 6143708
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: APPLICANT: Borchert, Torben
: APPLICANT: Bisgaard-Frantzen, Henrik
: TITLE OF INVENTION: Alpha-Amylase Mutants
: FILE REFERENCE: 4796.204-US
: CURRENT APPLICATION NUMBER: US/09/182.859
: EARLIER FILING DATE: 1998-10-29
: EARLIER APPLICATION NUMBER: 0515/96
: EARLIER FILING DATE: 1996-04-30
: EARLIER APPLICATION NUMBER: 0712/96
: EARLIER FILING DATE: 1996-06-28
: EARLIER APPLICATION NUMBER: 0775/96
: EARLIER FILING DATE: 1996-07-11
: EARLIER APPLICATION NUMBER: 1263/96
: EARLIER FILING DATE: 1996-11-08
: NUMBER OF SEQ. ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 483
: TYPE: PRT
: ORGANISM: Bacillus licheniformis
US-09-182-859-2
Query Match      100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEWYMPNDQHWRLQNDASVLAHGTITAWIPRAYGTSQADVGYGAYD 60
Db 1 ANLNGTLMQYFEWYMPNDQHWRLQNDASVLAHGTITAWIPRAYGTSQADVGYGAYD 60
QY 1 LYLGEFHQGTWTKYGTGKGLQSAIKSLHSRDINNYGVDVINHKSGADTEBTVAEV 120
Db 1 LYLGEFHQGTWTKYGTGKGLQSAIKSLHSRDINNYGVDVINHKSGADTEBTVAEV 120
QY 61 LYLGEFHQGTWTKYGTGKGLQSAIKSLHSRDINNYGVDVINHKSGADTEBTVAEV 120
Db 61 LYLGEFHQGTWTKYGTGKGLQSAIKSLHSRDINNYGVDVINHKSGADTEBTVAEV 120
QY 121 DPADRNIVISGEHLIKAWTHFHPGRCSTYSDFPMWYHFDGTDWDSRKLNRIYKFGQK 180
Db 121 DPADRNIVISGEHLIKAWTHFHPGRCSTYSDFPMWYHFDGTDWDSRKLNRIYKFGQK 180
QY 181 AMDEVENENGNVYLYADIDVHPVAAEIKKMGWYVNEQLDGRDLAVAHKRSF 240
Db 181 AMDEVENENGNVYLYADIDVHPVAAEIKKMGWYVNEQLDGRDLAVAHKRSF 240
QY 241 LRDVNVIVREKGTGKEMFTVAEYWMQNDGALENYLNKTNFNSVDPVPLHYQFHAASQGG 300
Db 241 LRDVNVIVREKGTGKEMFTVAEYWMQNDGALENYLNKTNFNSVDPVPLHYQFHAASQGG 300
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Db      241 LRDVNVHVEKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASSTGG 300
Qy      301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAAYAFILTRSGYPQ 360
Db      301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAAYAFILTRSGYPQ 360
Qy      361 VFYGDWYGTGDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREDSVA 420
Db      361 VFYGDWYGTGDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREDSVA 420
Qy      421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFFHVGGSYSIY 480
Db      421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFFHVGGSYSIY 480
Qy      481 VOR 483
Db      481 VOR 483

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RESULT 2
US-09-170-670-4
; Sequence 4, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170.670
; EARLIER FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063.306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: B. licheniformis
US-09-170-670-4

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Query Match      100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSAVLAHGIITAVWIPRAYKGSQADVGYAYD 60
Db      1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSAVLAHGIITAVWIPRAYKGSQADVGYAYD 60
Qy      61 LYDLGEFHQKGTIVRTKYGTGKELQSAIKSLHSRDINNVGDVVIINHKGADATEDVTAAYEV 120
Db      61 LYDLGEFHQKGTIVRTKYGTGKELQSAIKSLHSRDINNVGDVVIINHKGADATEDVTAAYEV 120
Qy      121 DPADRNRVVISGEHLIKAWTHFHPFGSGTYSDFKMWYHFDGTDWDSRKLNIYKFOGK 180
Db      121 DPADRNRVVISGEHLIKAWTHFHPFGSGTYSDFKMWYHFDGTDWDSRKLNIYKFOGK 180
Qy      121 DPADRNRVVISGEHLIKAWTHFHPFGSGTYSDFKMWYHFDGTDWDSRKLNIYKFOGK 180
Db      121 DPADRNRVVISGEHLIKAWTHFHPFGSGTYSDFKMWYHFDGTDWDSRKLNIYKFOGK 180
Qy      181 AMWMEVSNENGVYDILMYADIDYDHPVAAEIKRWGTWYANLQDGFRLDAVKHIKFSF 240
Db      181 AMWMEVSNENGVYDILMYADIDYDHPVAAEIKRWGTWYANLQDGFRLDAVKHIKFSF 240
Qy      181 AMWMEVSNENGVYDILMYADIDYDHPVAAEIKRWGTWYANLQDGFRLDAVKHIKFSF 240
Db      181 AMWMEVSNENGVYDILMYADIDYDHPVAAEIKRWGTWYANLQDGFRLDAVKHIKFSF 240
Qy      241 LRDVNVHVEKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASSTGG 300
Db      241 LRDVNVHVEKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASSTGG 300
Qy      301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAAYAFILTRSGYPQ 360
Db      301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAAYAFILTRSGYPQ 360
Qy      361 VFYGDWYGTGDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREDSVA 420

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Db      361 VFYGDWYGTGDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREDSVA 420
Qy      421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFFHVGGSYSIY 480
Db      421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFFHVGGSYSIY 480
Qy      481 VOR 483
Db      481 VOR 483

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RESULT 3
US-09-193-068-4
; Sequence 4, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjulliff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193.068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: B. licheniformis
US-09-193-068-4

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Query Match      100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSAVLAHGIITAVWIPRAYKGSQADVGYAYD 60
Db      1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSAVLAHGIITAVWIPRAYKGSQADVGYAYD 60
Qy      61 LYDLGEFHQKGTIVRTKYGTGKELQSAIKSLHSRDINNVGDVVIINHKGADATEDVTAAYEV 120
Db      61 LYDLGEFHQKGTIVRTKYGTGKELQSAIKSLHSRDINNVGDVVIINHKGADATEDVTAAYEV 120
Qy      121 DPADRNRVVISGEHLIKAWTHFHPFGSGTYSDFKMWYHFDGTDWDSRKLNIYKFOGK 180
Db      121 DPADRNRVVISGEHLIKAWTHFHPFGSGTYSDFKMWYHFDGTDWDSRKLNIYKFOGK 180
Qy      121 DPADRNRVVISGEHLIKAWTHFHPFGSGTYSDFKMWYHFDGTDWDSRKLNIYKFOGK 180
Db      121 DPADRNRVVISGEHLIKAWTHFHPFGSGTYSDFKMWYHFDGTDWDSRKLNIYKFOGK 180
Qy      181 AMWMEVSNENGVYDILMYADIDYDHPVAAEIKRWGTWYANLQDGFRLDAVKHIKFSF 240
Db      181 AMWMEVSNENGVYDILMYADIDYDHPVAAEIKRWGTWYANLQDGFRLDAVKHIKFSF 240
Qy      181 AMWMEVSNENGVYDILMYADIDYDHPVAAEIKRWGTWYANLQDGFRLDAVKHIKFSF 240
Db      181 AMWMEVSNENGVYDILMYADIDYDHPVAAEIKRWGTWYANLQDGFRLDAVKHIKFSF 240
Qy      241 LRDVNVHVEKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASSTGG 300
Db      241 LRDVNVHVEKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASSTGG 300
Qy      301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAAYAFILTRSGYPQ 360
Db      301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAAYAFILTRSGYPQ 360
Qy      361 VFYGDWYGTGDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREDSVA 420
Db      361 VFYGDWYGTGDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREDSVA 420
Qy      421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFFHVGGSYSIY 480
Db      421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFFHVGGSYSIY 480
Qy      481 VOR 483
Db      481 VOR 483

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RESULT 4
US-09-183-412-4
; Sequence 4, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjærulff, Søren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-183-412-4
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Query Match 100.0%; Score 2666; DB 3; Length 483;

Best Local Similarity 100.0%; Pred. No. 2,9e-240; Mismatches 0; Indels 0; Gaps 0;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ANLNGTLMQYFWMYMPDQGHWRRLQNDSAVLAHSGITAWIPRAYKTSQADVGYGAYD 60
QY 61 LYDGEFHQGTVTKTKGTGKELQSAIKLSHSRDINVGDVVNHKGGADTEVTAVEV 120
DB 61 LYDGEFHQGTVTKTKGTGKELQSAIKLSHSRDINVGDVVNHKGGADTEVTAVEV 120
QY 121 DPADRNVISGEHLIKAWTHFHPFGKSTYSDFKMHWYHFDGTWDSRKLNRIYKFOGK 180
DB 121 DPADRNVISGEHLIKAWTHFHPFGKSTYSDFKMHWYHFDGTWDSRKLNRIYKFOGK 180
QY 121 DPADRNVISGEHLIKAWTHFHPFGKSTYSDFKMHWYHFDGTWDSRKLNRIYKFOGK 180
DB 121 DPADRNVISGEHLIKAWTHFHPFGKSTYSDFKMHWYHFDGTWDSRKLNRIYKFOGK 180
QY 181 AMDWESNENGNVYLYMAYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
DB 181 AMDWESNENGNVYLYMAYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
QY 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHNSVDPVPLHYQFHAASVTOGG 300
DB 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHNSVDPVPLHYQFHAASVTOGG 300
QY 301 GYDMRKLINGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAFAFLITRESGYPQ 360
DB 301 GYDMRKLINGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAFAFLITRESGYPQ 360
QY 361 VFYGDWYGTGDSQREIPALHKIEPLIKARKQAYAGQHDYFPHHDI VGTWTRGDSVVA 420
DB 361 VFYGDWYGTGDSQREIPALHKIEPLIKARKQAYAGQHDYFPHHDI VGTWTRGDSVVA 420
QY 421 NSGIALAIIITDGPQAKMYVGRQNAGETWHDITGNRSEPVVINSNGEFPVNGSVSIIY 480
DB 421 NSGIALAIIITDGPQAKMYVGRQNAGETWHDITGNRSEPVVINSNGEFPVNGSVSIIY 480
QY 481 VQR 483
DB 481 VQR 483
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RESULT 5

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US-09-264-097-2
; Sequence 2, Application US/09264097
; Patent No. 6287826
; GENERAL INFORMATION:
; APPLICANT: Hendriksen, Hanne Vang
; APPLICANT: Enzymatic Preparation of Glucose Syrup
; TITLE OF INVENTION: From Starch
; FILE REFERENCE: 5278.200-US
; CURRENT APPLICATION NUMBER: US/09/264,097
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: PA 0321/98
; EARLIER FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: 60/079,209
; EARLIER FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-264-097-2
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Query Match 100.0%; Score 2666; DB 3; Length 483;

Best Local Similarity 100.0%; Pred. No. 2,9e-240; Mismatches 0; Indels 0; Gaps 0;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLMQYFWMYMPDQGHWRRLQNDSAVLAHSGITAWIPRAYKTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFWMYMPDQGHWRRLQNDSAVLAHSGITAWIPRAYKTSQADVGYGAYD 60
QY 61 LYDGEFHQGTVTKTKGTGKELQSAIKLSHSRDINVGDVVNHKGGADTEVTAVEV 120
DB 61 LYDGEFHQGTVTKTKGTGKELQSAIKLSHSRDINVGDVVNHKGGADTEVTAVEV 120
QY 121 DPADRNVISGEHLIKAWTHFHPFGKSTYSDFKMHWYHFDGTWDSRKLNRIYKFOGK 180
DB 121 DPADRNVISGEHLIKAWTHFHPFGKSTYSDFKMHWYHFDGTWDSRKLNRIYKFOGK 180
QY 121 DPADRNVISGEHLIKAWTHFHPFGKSTYSDFKMHWYHFDGTWDSRKLNRIYKFOGK 180
DB 121 DPADRNVISGEHLIKAWTHFHPFGKSTYSDFKMHWYHFDGTWDSRKLNRIYKFOGK 180
QY 181 AMDWESNENGNVYLYMAYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
DB 181 AMDWESNENGNVYLYMAYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
QY 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHNSVDPVPLHYQFHAASVTOGG 300
DB 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHNSVDPVPLHYQFHAASVTOGG 300
QY 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHNSVDPVPLHYQFHAASVTOGG 300
DB 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHNSVDPVPLHYQFHAASVTOGG 300
QY 301 GYDMRKLINGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAFAFLITRESGYPQ 360
DB 301 GYDMRKLINGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAFAFLITRESGYPQ 360
QY 361 VFYGDWYGTGDSQREIPALHKIEPLIKARKQAYAGQHDYFPHHDI VGTWTRGDSVVA 420
DB 361 VFYGDWYGTGDSQREIPALHKIEPLIKARKQAYAGQHDYFPHHDI VGTWTRGDSVVA 420
QY 421 NSGIALAIIITDGPQAKMYVGRQNAGETWHDITGNRSEPVVINSNGEFPVNGSVSIIY 480
DB 421 NSGIALAIIITDGPQAKMYVGRQNAGETWHDITGNRSEPVVINSNGEFPVNGSVSIIY 480
QY 481 VQR 483
DB 481 VQR 483
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RESULT 6

US-09-291-023A-21

; Sequence 21, Application US/09291023A

; Patent No. 6309871

; GENERAL INFORMATION:

; APPLICANT: Outtrup, Helle

; APPLICANT: Borchert, Torben

; APPLICANT: Nielsen, Bjarne

; APPLICANT: Nielsen, Vibeke

```

; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
; FILE OF INVENTION: Encoding Same
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/291,023A
; CURRENT FILING DATE: 1999-04-13
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 21
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus
US-09-291-023A-21
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Query Match      100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 ANLNGTLMQYFEWYMPNDGQHRRLQNDGAYLAHGTITAWIIPAYKGTSGADVGYAYD 60
DB      1 ANLNGTLMQYFEWYMPNDGQHRRLQNDGAYLAHGTITAWIIPAYKGTSGADVGYAYD 60
QY      61 LYDLGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGDVVINHKGADATEDVTAVEV 120
DB      61 LYDLGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGDVVINHKGADATEDVTAVEV 120
QY      121 DPADRNKRVISGEHLIKAWTHFHFPGSGTYSDFKMWYHFGDTWDESRKLNRIYKFGK 180
DB      121 DPADRNKRVISGEHLIKAWTHFHFPGSGTYSDFKMWYHFGDTWDESRKLNRIYKFGK 180
QY      121 DPADRNKRVISGEHLIKAWTHFHFPGSGTYSDFKMWYHFGDTWDESRKLNRIYKFGK 180
DB      121 DPADRNKRVISGEHLIKAWTHFHFPGSGTYSDFKMWYHFGDTWDESRKLNRIYKFGK 180
QY      181 AMDWEVSNENGYDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
DB      181 AMDWEVSNENGYDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
QY      241 LRDWNVHREKTKGKEMFTVAEYQNDLGALENVYLNKTNFNHNSVFDVPLHYQFHAASVTOGG 300
DB      241 LRDWNVHREKTKGKEMFTVAEYQNDLGALENVYLNKTNFNHNSVFDVPLHYQFHAASVTOGG 300
QY      301 GYDMRKLTNGTVSKRPLKSTYTFVNDHDTQPGQSLESTVQTFWFKPLAYAFILTRSGVPO 360
DB      301 GYDMRKLTNGTVSKRPLKSTYTFVNDHDTQPGQSLESTVQTFWFKPLAYAFILTRSGVPO 360
QY      361 VFYGDWYGTGKDSQREIPALKKIEPIPKARKQYAYGAQHDYFDHDIIVGWTREGDSSVA 420
DB      361 VFYGDWYGTGKDSQREIPALKKIEPIPKARKQYAYGAQHDYFDHDIIVGWTREGDSSVA 420
QY      421 NSGLAALITDGGGAKRMVYGRONAGETWHDITGNRSEPVYINSBGWGFHYVNGGSVSIY 480
DB      421 NSGLAALITDGGGAKRMVYGRONAGETWHDITGNRSEPVYINSBGWGFHYVNGGSVSIY 480
QY      481 VQR 483
DB      481 VQR 483
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RESULT 7
US-09-290-734-4
; Sequence 4, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Tordten Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylaae And -Amylaae Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
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; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: B. licheniformis
US-09-290-734-4
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Query Match      100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 ANLNGTLMQYFEWYMPNDGQHRRLQNDGAYLAHGTITAWIIPAYKGTSGADVGYAYD 60
DB      1 ANLNGTLMQYFEWYMPNDGQHRRLQNDGAYLAHGTITAWIIPAYKGTSGADVGYAYD 60
QY      61 LYDLGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGDVVINHKGADATEDVTAVEV 120
DB      61 LYDLGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGDVVINHKGADATEDVTAVEV 120
QY      121 DPADRNKRVISGEHLIKAWTHFHFPGSGTYSDFKMWYHFGDTWDESRKLNRIYKFGK 180
DB      121 DPADRNKRVISGEHLIKAWTHFHFPGSGTYSDFKMWYHFGDTWDESRKLNRIYKFGK 180
QY      181 AMDWEVSNENGYDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
DB      181 AMDWEVSNENGYDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
QY      241 LRDWNVHREKTKGKEMFTVAEYQNDLGALENVYLNKTNFNHNSVFDVPLHYQFHAASVTOGG 300
DB      241 LRDWNVHREKTKGKEMFTVAEYQNDLGALENVYLNKTNFNHNSVFDVPLHYQFHAASVTOGG 300
QY      301 GYDMRKLTNGTVSKRPLKSTYTFVNDHDTQPGQSLESTVQTFWFKPLAYAFILTRSGVPO 360
DB      301 GYDMRKLTNGTVSKRPLKSTYTFVNDHDTQPGQSLESTVQTFWFKPLAYAFILTRSGVPO 360
QY      361 VFYGDWYGTGKDSQREIPALKKIEPIPKARKQYAYGAQHDYFDHDIIVGWTREGDSSVA 420
DB      361 VFYGDWYGTGKDSQREIPALKKIEPIPKARKQYAYGAQHDYFDHDIIVGWTREGDSSVA 420
QY      421 NSGLAALITDGGGAKRMVYGRONAGETWHDITGNRSEPVYINSBGWGFHYVNGGSVSIY 480
DB      421 NSGLAALITDGGGAKRMVYGRONAGETWHDITGNRSEPVYINSBGWGFHYVNGGSVSIY 480
QY      481 VQR 483
DB      481 VQR 483
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RESULT 8
US-09-537-168-4
; Sequence 4, Application US/09537168
; Patent No. 6410295
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amylaae Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/09/537,168
; CURRENT FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: PA 1999 00437
; EARLIER FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: 60/127,427
; EARLIER FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
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US-09-537-168-4

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLMQYFEWMPNDGQHMRLQNDSDAYLAHGTTAVI PPAYKTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFEWMPNDGQHMRLQNDSDAYLAHGTTAVI PPAYKTSQADVGYGAYD 60
QY 61 LYDGEFHQKGTAVTKYGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
DB 61 LYDGEFHQKGTAVTKYGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
QY 121 DPADRNVISGEHLIKAMTHFHPGRGSTYSDFKMHWHPDGTMDSRKLNRIYKFGQK 180
DB 121 DPADRNVISGEHLIKAMTHFHPGRGSTYSDFKMHWHPDGTMDSRKLNRIYKFGQK 180
QY 181 AMDWEVENNGNVDYLYMADIDYDHPVAAEIKKMGTYANELQDGFRLDAVHKIKFSF 240
DB 181 AMDWEVENNGNVDYLYMADIDYDHPVAAEIKKMGTYANELQDGFRLDAVHKIKFSF 240
QY 241 LRDMVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVPDVLHYQFHAASIQGG 300
DB 241 LRDMVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVPDVLHYQFHAASIQGG 300
QY 301 GYDMRKLLNGTVSKHPLKSTYFVDNHDTPQGSLSTVQTFKPLAYAFILITRESGYPO 360
DB 301 GYDMRKLLNGTVSKHPLKSTYFVDNHDTPQGSLSTVQTFKPLAYAFILITRESGYPO 360
QY 361 VFYGDWYGTGKDSQREIIPALGHKIEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 420
DB 361 VFYGDWYGTGKDSQREIIPALGHKIEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSPVYINSEGWGEFFHVGGSYSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSPVYINSEGWGEFFHVGGSYSIY 480
QY 481 VQR 483
DB 481 VQR 483
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RESULT 9

US-09-672-459-2
; Sequence 2, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Biegard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/672.459
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182.859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-2

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLMQYFEWMPNDGQHMRLQNDSDAYLAHGTTAVI PPAYKTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFEWMPNDGQHMRLQNDSDAYLAHGTTAVI PPAYKTSQADVGYGAYD 60
QY 61 LYDGEFHQKGTAVTKYGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
DB 61 LYDGEFHQKGTAVTKYGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
QY 121 DPADRNVISGEHLIKAMTHFHPGRGSTYSDFKMHWHPDGTMDSRKLNRIYKFGQK 180
DB 121 DPADRNVISGEHLIKAMTHFHPGRGSTYSDFKMHWHPDGTMDSRKLNRIYKFGQK 180
QY 181 AMDWEVENNGNVDYLYMADIDYDHPVAAEIKKMGTYANELQDGFRLDAVHKIKFSF 240
DB 181 AMDWEVENNGNVDYLYMADIDYDHPVAAEIKKMGTYANELQDGFRLDAVHKIKFSF 240
QY 241 LRDMVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVPDVLHYQFHAASIQGG 300
DB 241 LRDMVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVPDVLHYQFHAASIQGG 300
QY 301 GYDMRKLLNGTVSKHPLKSTYFVDNHDTPQGSLSTVQTFKPLAYAFILITRESGYPO 360
DB 301 GYDMRKLLNGTVSKHPLKSTYFVDNHDTPQGSLSTVQTFKPLAYAFILITRESGYPO 360
QY 361 VFYGDWYGTGKDSQREIIPALGHKIEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 420
DB 361 VFYGDWYGTGKDSQREIIPALGHKIEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSPVYINSEGWGEFFHVGGSYSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSPVYINSEGWGEFFHVGGSYSIY 480
QY 481 VQR 483
DB 481 VQR 483
```

RESULT 10

US-09-545-586-4
; Sequence 4, Application US/09545586
; Patent No. 6528298
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Biegard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6528298e1 -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/545.586
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US/09/290.734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: B. licheniformis
US-09-545-586-4

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLMQYFEWMPNDGQHMRLQNDSDAYLAHGTTAVI PPAYKTSQADVGYGAYD 60
|||||
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Db 1 ANINGTLMQYFEWYMPNDGQHRRLQNDASAYLAHEGITAAMIPPAKGTSGQADVGYAYD 60
QY 61 LYDGEFHQGTATKTKGTGELQSAIKSLHSRDINVGQVIVNNHGADATEDVTAVEV 120
Db 61 LYDGEFHQGTATKTKGTGELQSAIKSLHSRDINVGQVIVNNHGADATEDVTAVEV 120
QY 121 DPADRNRVVISGEHLIKAMTHFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNRITYFGQK 180
Db 121 DPADRNRVVISGEHLIKAMTHFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNRITYFGQK 180
QY 181 AMDEVSNSNGNNDYIMYADIDYDHPVAAEIKRMGTWYANELQDGFRLDAVGHIKFSF 240
Db 181 AMDEVSNSNGNNDYIMYADIDYDHPVAAEIKRMGTWYANELQDGFRLDAVGHIKFSF 240
QY 241 LRDVNVHREKTEKEMFTVAEYWNQDGLALENTKNTFNHSAFVDPVLAHQFHAASQGG 300
Db 241 LRDVNVHREKTEKEMFTVAEYWNQDGLALENTKNTFNHSAFVDPVLAHQFHAASQGG 300
QY 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTQPGSLESTVQTFKPLAAYAFILTRREGSYPQ 360
Db 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTQPGSLESTVQTFKPLAAYAFILTRREGSYPQ 360
QY 361 VFYGDMTGTGDSOREIPALKKHIEPLIKARKQYAGAQHDYFDHHDIVGWTREGSSVA 420
Db 361 VFYGDMTGTGDSOREIPALKKHIEPLIKARKQYAGAQHDYFDHHDIVGWTREGSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGMEFHVNGSSVSY 480
Db 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGMEFHVNGSSVSY 480
QY 481 VOR 483
Db 481 VOR 483

RESULT 11
US-09-540-715A-21
; Sequence 21, Application US/09540715A
; Patent No. 6623948
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjørne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
; FILE REFERENCE: 5821, 010-US
; CURRENT APPLICATION NUMBER: US/09/540, 715A
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/291, 023
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus
US-09-540-715A-21

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFEWYMPNDGQHRRLQNDASAYLAHEGITAAMIPPAKGTSGQADVGYAYD 60
Db 1 ANINGTLMQYFEWYMPNDGQHRRLQNDASAYLAHEGITAAMIPPAKGTSGQADVGYAYD 60
QY 61 LYDGEFHQGTATKTKGTGELQSAIKSLHSRDINVGQVIVNNHGADATEDVTAVEV 120
Db 61 LYDGEFHQGTATKTKGTGELQSAIKSLHSRDINVGQVIVNNHGADATEDVTAVEV 120
QY 121 DPADRNRVVISGEHLIKAMTHFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNRITYFGQK 180

Db 121 DPADRNRVVISGEHLIKAMTHFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNRITYFGQK 180
QY 181 AMDEVSNSNGNNDYIMYADIDYDHPVAAEIKRMGTWYANELQDGFRLDAVGHIKFSF 240
Db 181 AMDEVSNSNGNNDYIMYADIDYDHPVAAEIKRMGTWYANELQDGFRLDAVGHIKFSF 240
QY 241 LRDVNVHREKTEKEMFTVAEYWNQDGLALENTKNTFNHSAFVDPVLAHQFHAASQGG 300
Db 241 LRDVNVHREKTEKEMFTVAEYWNQDGLALENTKNTFNHSAFVDPVLAHQFHAASQGG 300
QY 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTQPGSLESTVQTFKPLAAYAFILTRREGSYPQ 360
Db 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTQPGSLESTVQTFKPLAAYAFILTRREGSYPQ 360
QY 361 VFYGDMTGTGDSOREIPALKKHIEPLIKARKQYAGAQHDYFDHHDIVGWTREGSSVA 420
Db 361 VFYGDMTGTGDSOREIPALKKHIEPLIKARKQYAGAQHDYFDHHDIVGWTREGSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGMEFHVNGSSVSY 480
Db 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGMEFHVNGSSVSY 480
QY 481 VOR 483
Db 481 VOR 483

RESULT 12
US-10-186-042-2
; Sequence 2, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796, 204-US
; CURRENT APPLICATION NUMBER: US/10/186, 042
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672, 459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182, 859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-2

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFEWYMPNDGQHRRLQNDASAYLAHEGITAAMIPPAKGTSGQADVGYAYD 60
Db 1 ANINGTLMQYFEWYMPNDGQHRRLQNDASAYLAHEGITAAMIPPAKGTSGQADVGYAYD 60
QY 61 LYDGEFHQGTATKTKGTGELQSAIKSLHSRDINVGQVIVNNHGADATEDVTAVEV 120
Db 61 LYDGEFHQGTATKTKGTGELQSAIKSLHSRDINVGQVIVNNHGADATEDVTAVEV 120
QY 121 DPADRNRVVISGEHLIKAMTHFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNRITYFGQK 180

Db 121 DPAORNRVISEGHLIKAMTHHFPGRGSTYSDFKMHYHFGDTWDSRKLNRITYKQOK 180
Qy 181 AMDVEVSENGENYDYLMTADIDYHPDYAAEIKRWGTYANELDQGRDLAVKHIFSF 240
Db 181 AMDVEVSENGENYDYLMTADIDYHPDYAAEIKRWGTYANELDQGRDLAVKHIFSF 240
Qy 241 LRDVNVHVRKTEGKEMFTVAEYWMNDLGALENYLNKTNPNHNSVDFVPLHYQFHAASQGG 300
Db 241 LRDVNVHVRKTEGKEMFTVAEYWMNDLGALENYLNKTNPNHNSVDFVPLHYQFHAASQGG 300
Qy 301 GYDMRKILNGTVVSKHPLKSVTFVNDHDTOPGQSLBSTVQTFKPLAVAFILITRESGPQ 360
Db 301 GYDMRKILNGTVVSKHPLKSVTFVNDHDTOPGQSLBSTVQTFKPLAVAFILITRESGPQ 360
Qy 361 VFYGDWYGTGDSOREIPLAKHKIEPLIKARKQYAYAGQHDYFPHHDI VGMTRGDSVA 420
Db 361 VFYGDWYGTGDSOREIPLAKHKIEPLIKARKQYAYAGQHDYFPHHDI VGMTRGDSVA 420
Qy 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVSIY 480
Db 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVSIY 480
Qy 481 VQR 483
Db 481 VQR 483

RESULT 13
US-09-769-864-4
Sequence 4, Application US/09769864
Patent No. 6673589
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nissen, Torben L.
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCE: 5368.200-US
CURRENT APPLICATION NUMBER: US/09/769,864
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-769-864-4

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ANLNGTLMQYFEWMPNDGQHRRLQNDASVLAHGTAWMI PPAYKSTQADVGAYD 60
Db 1 ANLNGTLMQYFEWMPNDGQHRRLQNDASVLAHGTAWMI PPAYKSTQADVGAYD 60
Qy 61 LYDGEFHQKQVTKYTKGKELQSAIKLSRSDINVGAVINHKGADATEDVTAVEV 120
Db 61 LYDGEFHQKQVTKYTKGKELQSAIKLSRSDINVGAVINHKGADATEDVTAVEV 120
Qy 121 DPADNRNRYTISEGHLIKAMTHHFPGRGSTYSDFKMHYHFGDTWDSRKLNRITYKQOK 180
Db 121 DPADNRNRYTISEGHLIKAMTHHFPGRGSTYSDFKMHYHFGDTWDSRKLNRITYKQOK 180
Qy 181 AMDVEVSENGENYDYLMTADIDYHPDYAAEIKRWGTYANELDQGRDLAVKHIFSF 240
Db 181 AMDVEVSENGENYDYLMTADIDYHPDYAAEIKRWGTYANELDQGRDLAVKHIFSF 240

Qy 241 LRDVNVHVRKTEGKEMFTVAEYWMNDLGALENYLNKTNPNHNSVDFVPLHYQFHAASQGG 300
Db 241 LRDVNVHVRKTEGKEMFTVAEYWMNDLGALENYLNKTNPNHNSVDFVPLHYQFHAASQGG 300
Qy 301 GYDMRKILNGTVVSKHPLKSVTFVNDHDTOPGQSLBSTVQTFKPLAVAFILITRESGPQ 360
Db 301 GYDMRKILNGTVVSKHPLKSVTFVNDHDTOPGQSLBSTVQTFKPLAVAFILITRESGPQ 360
Qy 361 VFYGDWYGTGDSOREIPLAKHKIEPLIKARKQYAYAGQHDYFPHHDI VGMTRGDSVA 420
Db 361 VFYGDWYGTGDSOREIPLAKHKIEPLIKARKQYAYAGQHDYFPHHDI VGMTRGDSVA 420
Qy 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVSIY 480
Db 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVSIY 480
Qy 481 VQR 483
Db 481 VQR 483

RESULT 14
US-08-720-899-2
Sequence 2, Application US/08720899
Patent No. 5753460
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57534600 No. 5753460disk of No. 5753460th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,899
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowmey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-899-2

Query Match 100.0%; Score 2666; DB 1; Length 512;
Best Local Similarity 100.0%; Pred. No. 3.2e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ANLNGTLMQYFEWMPNDGQHRRLQNDASVLAHGTAWMI PPAYKSTQADVGAYD 60

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Db 30 ANLNGTLMQFEMWMPNDGQHRRLQNDLSAYLAEHGITAWMIPPAKYGTSQADVGCAYD 89
QY 61 LYDLGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVYGDVYINHGADATEDVTAVEV 120
Db 90 LYDLGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVYGDVYINHGADATEDVTAVEV 149
QY 121 DPADNRNVIISGEHLIKAMTHFHPGRGSTYSDPKMWHYFDGTWDESRKLNRIYKFGQK 180
Db 150 DPADNRNVIISGEHLIKAMTHFHPGRGSTYSDPKMWHYFDGTWDESRKLNRIYKFGQK 209
QY 181 AMDWEVSNEKNGNDYLMYADIDYDHPDVAAEIKRWGTYANLQDGFRLDAVKHKFSF 240
Db 210 AMDWEVSNEKNGNDYLMYADIDYDHPDVAAEIKRWGTYANLQDGFRLDAVKHKFSF 269
QY 241 LRDVNVHVRKTKGKEMFTVAEYQNDLGALENYLNKTNFNSVFPVPLHYQFHAASSTGG 300
Db 270 LRDVNVHVRKTKGKEMFTVAEYQNDLGALENYLNKTNFNSVFPVPLHYQFHAASSTGG 329
QY 301 GYDMRKLNGTVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAVALITRESGYPQ 360
Db 330 GYDMRKLNGTVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAVALITRESGYPQ 389
QY 361 VFYGMWGTGKDSQREIPALKHKEIPILKARKQYAYGAQHDYFDHHDIVGWTREGSSVA 420
Db 390 VFYGMWGTGKDSQREIPALKHKEIPILKARKQYAYGAQHDYFDHHDIVGWTREGSSVA 449
QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSBPVYINSEGMGEFHNVGSSVSY 480
Db 450 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSBPVYINSEGMGEFHNVGSSVSY 509
QY 481 VQR 483
Db 510 VQR 512

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RESULT 15

US-08-459-610-2

Sequence 2, Application US/08459610

Patent No. 5801043

GENERAL INFORMATION:

APPLICANT: Bisgaard-Frantzen, Henrik

APPLICANT: Borchert, Torben Vedel

APPLICANT: Svendsen, Allan

APPLICANT: Thellersen, Marianne

APPLICANT: Van der Zee, Pia

TITLE OF INVENTION: AMYLASE VARIANTS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESSES:

ADDRESSEE: No. 58010430 No. 5801043disk of No. 5801043th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,610

FILING DATE: 02-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/343,804

FILING DATE: 22-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lowmey Dr., Karen A.

REGISTRATION NUMBER: 31,274

REFERENCE/DOCKET NUMBER: 4054,214-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-610-2

Query Match 100.0%; Score 2666; DB 1; Length 512;
Best Local Similarity 100.0%; Pred. No. 3,2e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
2920.093 Million cell updates/sec

Title: US-09-925-576C-8

Perfect score: 2666
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Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2666	100.0	483	9	US-09-918-543-8
4	2666	100.0	483	9	US-09-918-543-30
5	2666	100.0	483	9	US-09-925-576C-8
6	2666	100.0	483	12	US-10-665-667-4
7	2666	100.0	483	12	US-10-644-187-2
8	2666	100.0	483	12	US-10-327-837-4
9	2666	100.0	483	14	US-10-146-327-4
10	2666	100.0	483	14	US-10-186-042-2
11	2666	100.0	483	16	US-10-359-161-6
12	2666	100.0	483	16	US-10-477-725-8
13	2666	100.0	512	14	US-10-184-771-2
14	2663	99.9	512	14	US-10-199-922-2
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17	2654	99.5	512	15	US-10-081-739A-8	Sequence 8, Appli
18	2654	99.5	512	15	US-10-385-305-114	Sequence 114, App
19	2582	96.8	481	14	US-10-146-327-2	Sequence 2, Appli
20	2338	87.7	483	14	US-10-184-771-13	Sequence 13, Appli
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22	2184	81.9	483	9	US-09-918-543-10	Sequence 10, Appli
23	2184	81.9	483	10	US-09-925-576C-10	Sequence 6, Appli
24	2184	81.9	483	14	US-10-146-327-6	Sequence 10, Appli
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ALIGNMENTS

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RESULT 1
US-09-769-864-4
Sequence 4, Application US/09769864
Patent No. US20010039253A1
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Torben U.
APPLICANT: Kjærulff, Soren
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5368.200-US
CURRENT APPLICATION NUMBER: US/09/769,864
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-769-864-4
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Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 8, Application US/09854346
; Patent No. US20020068352A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020068352A1ozymes A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Jorgensen, Christel Thea
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
; FILE REFERENCE: 6140,200-US
; CURRENT APPLICATION NUMBER: US/09/854,346
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 483
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; ORGANISM: Bacillus licheniformis
US-09-854-346-8
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; Patent No. US2002015574A1
; GENERAL INFORMATION:
; APPLICANT: No. US2002015574A1ozymes A/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kjaerulff, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fuglsang, Claus Cyron
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062,200-US
; CURRENT APPLICATION NUMBER: US/09/918,543
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
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US-09-918-543-8
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; APPLICANT: No. US20020155574A1ozymes A/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kjaerulff, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fuglaang, Claus Crome
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062.200-US
; CURRENT APPLICATION NUMBER: US/09/918,543
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 30
; LENGTH: 483
; TYPE: PR1
; ORGANISM: Bacillus licheniformis
US-09-918-543-30

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Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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; Sequence 8, Application US/09925576C

; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 483
; TYPE: PR1
; ORGANISM: Bacillus licheniformis
US-09-925-576C-8

Query Match 100.0%; Score 2666; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ANINGTMOYFEWYMPNDGQHWRLQNDSAVLAHGTITAWIPRAYKGTSGADVGYAYD 60
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Db 61 LYDGEFHQKGTVTKYGTGGELOSATKSLHSRDINYGVDVINHKGAADTEVTAVEV 120
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Db 481 VOR 483

RESULT 6
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; Sequence 4, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19

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/ PRIOR APPLICATION NUMBER: US/09/769,864
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 09/183,412
/ PRIOR FILING DATE: 1998-10-30
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 483
/ TYPE: PRF
/ ORGANISM: Bacillus licheniformis
US-10-665-667-4
```

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Query Match      100.0%; Score 2666; DB 12; Length 483;
Best Local Similarity 100.0%; Pred. No. 8,2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ANINGTLMQYFEWYMPNDGQHWRLQNDASAYLAHSGITAWIPPAKGTSGADVGAYD 60
DB 1 ANINGTLMQYFEWYMPNDGQHWRLQNDASAYLAHSGITAWIPPAKGTSGADVGAYD 60
QY 61 LYDLGEFHQKGTVRTKTKGTGELQSAIKSLHSDINVGDDVINHKGADATEDVTAVEV 120
DB 61 LYDLGEFHQKGTVRTKTKGTGELQSAIKSLHSDINVGDDVINHKGADATEDVTAVEV 120
QY 121 DPADRRNVISGEHLIKAWTHFFHPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
DB 121 DPADRRNVISGEHLIKAWTHFFHPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
QY 121 DPADRRNVISGEHLIKAWTHFFHPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
DB 121 DPADRRNVISGEHLIKAWTHFFHPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
QY 181 AMDWEVSNENGVYDLYMADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
DB 181 AMDWEVSNENGVYDLYMADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
QY 241 LRDWNVHVEKTKGEMFTVAEYQNDLGALENYLNKTNPNHNVFVPLHYQFHAASGOG 300
DB 241 LRDWNVHVEKTKGEMFTVAEYQNDLGALENYLNKTNPNHNVFVPLHYQFHAASGOG 300
QY 301 GYDMRKLLNGTVVSKPLKSVTFVNDHDTOPGOSLESTVQTFKPLAFAFILTRESGYPO 360
DB 301 GYDMRKLLNGTVVSKPLKSVTFVNDHDTOPGOSLESTVQTFKPLAFAFILTRESGYPO 360
QY 361 VFYGMVGTGKDSQREIPALKKIEPIILKARKOYAYGAQHDYFPHHDIIVGWTREDSVA 420
DB 361 VFYGMVGTGKDSQREIPALKKIEPIILKARKOYAYGAQHDYFPHHDIIVGWTREDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSKGGEFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSKGGEFHVNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483
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RESULT 7
US-10-644-187-2
/ Sequence 2, Application US/10644187
/ Publication No. US20040048351A1
/ GENERAL INFORMATION:
/ APPLICANT: Svendsen, Allan
/ APPLICANT: Borchert, Torben
/ APPLICANT: Bisgard-Frantzen, Henrik
/ TITLE OF INVENTION: Alpha-Amylase Mutants
/ FILE REFERENCE: 4796.204-US
/ CURRENT APPLICATION NUMBER: US/10/644,187
/ PRIOR APPLICATION NUMBER: 09/182,859
/ PRIOR FILING DATE: 1998-10-29
/ PRIOR APPLICATION NUMBER: 0515/96
/ PRIOR FILING DATE: 1996-04-30
/ PRIOR APPLICATION NUMBER: 0712/96
/ PRIOR FILING DATE: 1996-06-28
/ PRIOR APPLICATION NUMBER: 0775/96
/ PRIOR FILING DATE: 1996-07-11
```

```
/ PRIOR APPLICATION NUMBER: 1263/96
/ PRIOR FILING DATE: 1996-11-08
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 483
/ TYPE: PRF
/ ORGANISM: Bacillus licheniformis
US-10-644-187-2
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Query Match      100.0%; Score 2666; DB 12; Length 483;
Best Local Similarity 100.0%; Pred. No. 8,2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ANINGTLMQYFEWYMPNDGQHWRLQNDASAYLAHSGITAWIPPAKGTSGADVGAYD 60
DB 1 ANINGTLMQYFEWYMPNDGQHWRLQNDASAYLAHSGITAWIPPAKGTSGADVGAYD 60
QY 61 LYDLGEFHQKGTVRTKTKGTGELQSAIKSLHSDINVGDDVINHKGADATEDVTAVEV 120
DB 61 LYDLGEFHQKGTVRTKTKGTGELQSAIKSLHSDINVGDDVINHKGADATEDVTAVEV 120
QY 121 DPADRRNVISGEHLIKAWTHFFHPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
DB 121 DPADRRNVISGEHLIKAWTHFFHPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
QY 121 DPADRRNVISGEHLIKAWTHFFHPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
DB 121 DPADRRNVISGEHLIKAWTHFFHPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
QY 181 AMDWEVSNENGVYDLYMADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
DB 181 AMDWEVSNENGVYDLYMADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
QY 241 LRDWNVHVEKTKGEMFTVAEYQNDLGALENYLNKTNPNHNVFVPLHYQFHAASGOG 300
DB 241 LRDWNVHVEKTKGEMFTVAEYQNDLGALENYLNKTNPNHNVFVPLHYQFHAASGOG 300
QY 301 GYDMRKLLNGTVVSKPLKSVTFVNDHDTOPGOSLESTVQTFKPLAFAFILTRESGYPO 360
DB 301 GYDMRKLLNGTVVSKPLKSVTFVNDHDTOPGOSLESTVQTFKPLAFAFILTRESGYPO 360
QY 361 VFYGMVGTGKDSQREIPALKKIEPIILKARKOYAYGAQHDYFPHHDIIVGWTREDSVA 420
DB 361 VFYGMVGTGKDSQREIPALKKIEPIILKARKOYAYGAQHDYFPHHDIIVGWTREDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSKGGEFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSKGGEFHVNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483
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```
RESULT 8
US-10-327-837-4
/ Sequence 4, Application US/10327837
/ Publication No. US20030211958A1
/ GENERAL INFORMATION:
/ APPLICANT: Svendsen, Allan
/ APPLICANT: Borchert, Torben Vedel
/ APPLICANT: Bisgard-Frantzen, Henrik
/ APPLICANT: Oustrup, Helle
/ APPLICANT: Nielsen, Bjarne Ronfeldt
/ APPLICANT: Nielsen, Vibeke Skovgaard
/ TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
/ FILE REFERENCE: 5276.400-US
/ CURRENT APPLICATION NUMBER: US/10/327,837
/ PRIOR APPLICATION NUMBER: 2002-12-23
/ PRIOR APPLICATION NUMBER: US/09/290,734
/ PRIOR FILING DATE: 1999-04-13
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 483
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TYPE: PRT
ORGANISM: B. licheniformis
US-10-327-837-4

Query Match 100.0%; Score 2666; DB 12; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLMQYFEMWMPNDGQHWRLQNDSDAVLAHGIITAWIPPAYKGTQADVGAYD 60
DB 1 ANLNGTLMQYFEMWMPNDGQHWRLQNDSDAVLAHGIITAWIPPAYKGTQADVGAYD 60
QY 61 LYDGEFHQKGTARTKXGTGKELQSAIKSLHSRDINYGDVVINKGADATEVTAVEV 120
DB 61 LYDGEFHQKGTARTKXGTGKELQSAIKSLHSRDINYGDVVINKGADATEVTAVEV 120
QY 121 DPADRNVIISGEHLIKATWHPHFGSGTYSDFKMHVYHFDGTDWDSRKLRIYKFOGK 180
DB 121 DPADRNVIISGEHLIKATWHPHFGSGTYSDFKMHVYHFDGTDWDSRKLRIYKFOGK 180
QY 181 AMDVESENENGYDLYMADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
DB 181 AMDVESENENGYDLYMADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
QY 241 LRDMVNHVREKTKGEMFTVAEYQNDLGALENYLNTKTNFNHSDVDFLHYQFHAASQGG 300
DB 241 LRDMVNHVREKTKGEMFTVAEYQNDLGALENYLNTKTNFNHSDVDFLHYQFHAASQGG 300
QY 301 GYDMRKLNGTVNSKHPKLSVTFYDNHDTOPGQSLBSTVQTFPKPLAFAFLITRESGYPQ 360
DB 301 GYDMRKLNGTVNSKHPKLSVTFYDNHDTOPGQSLBSTVQTFPKPLAFAFLITRESGYPQ 360
QY 361 VFYQDMYGTGKDSQREIIPALKHKIEPIILKARKQYAYGAQHDYFPHDIIVGWTRGDSVA 420
DB 361 VFYQDMYGTGKDSQREIIPALKHKIEPIILKARKQYAYGAQHDYFPHDIIVGWTRGDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483
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RESULT 9

US-10-146-327-4
Sequence 4, Application US/10146327
Publication No. US20030044954A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Jorgensen, Christel T.
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amylase Variants
FILE REFERENCE: 5886.200-US
CURRENT APPLICATION NUMBER: US/10/146.327
PRIOR FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US/09/537.168
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: PA 1999 00437
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 60/127,427
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-146-327-4

Query Match 100.0%; Score 2666; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLMQYFEMWMPNDGQHWRLQNDSDAVLAHGIITAWIPPAYKGTQADVGAYD 60
DB 1 ANLNGTLMQYFEMWMPNDGQHWRLQNDSDAVLAHGIITAWIPPAYKGTQADVGAYD 60
QY 61 LYDGEFHQKGTARTKXGTGKELQSAIKSLHSRDINYGDVVINKGADATEVTAVEV 120
DB 61 LYDGEFHQKGTARTKXGTGKELQSAIKSLHSRDINYGDVVINKGADATEVTAVEV 120
QY 121 DPADRNVIISGEHLIKATWHPHFGSGTYSDFKMHVYHFDGTDWDSRKLRIYKFOGK 180
DB 121 DPADRNVIISGEHLIKATWHPHFGSGTYSDFKMHVYHFDGTDWDSRKLRIYKFOGK 180
QY 181 AMDVESENENGYDLYMADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
DB 181 AMDVESENENGYDLYMADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
QY 241 LRDMVNHVREKTKGEMFTVAEYQNDLGALENYLNTKTNFNHSDVDFLHYQFHAASQGG 300
DB 241 LRDMVNHVREKTKGEMFTVAEYQNDLGALENYLNTKTNFNHSDVDFLHYQFHAASQGG 300
QY 301 GYDMRKLNGTVNSKHPKLSVTFYDNHDTOPGQSLBSTVQTFPKPLAFAFLITRESGYPQ 360
DB 301 GYDMRKLNGTVNSKHPKLSVTFYDNHDTOPGQSLBSTVQTFPKPLAFAFLITRESGYPQ 360
QY 361 VFYQDMYGTGKDSQREIIPALKHKIEPIILKARKQYAYGAQHDYFPHDIIVGWTRGDSVA 420
DB 361 VFYQDMYGTGKDSQREIIPALKHKIEPIILKARKQYAYGAQHDYFPHDIIVGWTRGDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483
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RESULT 10

US-10-186-042-2
Sequence 2, Application US/10186042
Publication No. US20030171236A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Bisgaard-Frantzen, Torben
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186.042
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/672.459
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 05/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-186-042-2

Query Match 100.0%; Score 2666; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQHMRLONDSAYLAHEGTTAWIPPAKYGTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFEMWMPNDGQHMRLONDSAYLAHEGTTAWIPPAKYGTSQADVGYGAYD 60
QY 61 LYDLGEFHQKGTAVTKTKGTGKELQSAIKSLHSRDINVGDUVINNHKGADATEDVTAVEV 120
DB 61 LYDLGEFHQKGTAVTKTKGTGKELQSAIKSLHSRDINVGDUVINNHKGADATEDVTAVEV 120
QY 121 DPADRNRVISEGHELIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
DB 121 DPADRNRVISEGHELIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
QY 181 AMDWEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHKKFSF 240
DB 181 AMDWEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHKKFSF 240
QY 241 LRDVNVHVRKTEKEMFTVAEYQNDLGALENYLNKTNFNHVSFVDPVPLHYOPHAASQGG 300
DB 241 LRDVNVHVRKTEKEMFTVAEYQNDLGALENYLNKTNFNHVSFVDPVPLHYOPHAASQGG 300
QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTMFKPLAYAFILTRREGSYQ 360
DB 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTMFKPLAYAFILTRREGSYQ 360
QY 361 VFYGDWYGTGKDSOREIPALKKHIEPILKARKQYAYGAQHDYFDHDIYGMTRREGSSVA 420
DB 361 VFYGDWYGTGKDSOREIPALKKHIEPILKARKQYAYGAQHDYFDHDIYGMTRREGSSVA 420
QY 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGFHVGSGSVSY 480
DB 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGFHVGSGSVSY 480
QY 481 VOR 483
DB 481 VOR 483

RESULT 11
US-10-399-161-6
; Sequence 6, Application US/10399161
; Publication No. US20040091994A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: Alpha-amylose variant with altered properties
; FILE REFERENCE: 10115.204-WO
; CURRENT APPLICATION NUMBER: US/10/399,161
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-399-161-6

Query Match 100.0%; Score 2666; DB 16; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 121 DPADRNRVISEGHELIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
QY 181 AMDWEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHKKFSF 240
DB 181 AMDWEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHKKFSF 240
QY 241 LRDVNVHVRKTEKEMFTVAEYQNDLGALENYLNKTNFNHVSFVDPVPLHYOPHAASQGG 300
DB 241 LRDVNVHVRKTEKEMFTVAEYQNDLGALENYLNKTNFNHVSFVDPVPLHYOPHAASQGG 300
QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTMFKPLAYAFILTRREGSYQ 360
DB 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTMFKPLAYAFILTRREGSYQ 360
QY 361 VFYGDWYGTGKDSOREIPALKKHIEPILKARKQYAYGAQHDYFDHDIYGMTRREGSSVA 420
DB 361 VFYGDWYGTGKDSOREIPALKKHIEPILKARKQYAYGAQHDYFDHDIYGMTRREGSSVA 420
QY 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGFHVGSGSVSY 480
DB 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGFHVGSGSVSY 480
QY 481 VOR 483
DB 481 VOR 483

RESULT 12
US-10-477-725-8
; Sequence 8, Application US/10477725
; Publication No. US20040096952A1
; GENERAL INFORMATION:
; APPLICANT: NOVOZYMES A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Thisted, Thomas
; TITLE OF INVENTION: Alpha-amylose variant with altered properties
; FILE REFERENCE: 10182.204-US
; CURRENT APPLICATION NUMBER: US/10/477,725
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-477-725-8

Query Match 100.0%; Score 2666; DB 16; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQHMRLONDSAYLAHEGTTAWIPPAKYGTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFEMWMPNDGQHMRLONDSAYLAHEGTTAWIPPAKYGTSQADVGYGAYD 60
QY 61 LYDLGEFHQKGTAVTKTKGTGKELQSAIKSLHSRDINVGDUVINNHKGADATEDVTAVEV 120
DB 61 LYDLGEFHQKGTAVTKTKGTGKELQSAIKSLHSRDINVGDUVINNHKGADATEDVTAVEV 120
QY 121 DPADRNRVISEGHELIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
DB 121 DPADRNRVISEGHELIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
QY 181 AMDWEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHKKFSF 240
DB 181 AMDWEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHKKFSF 240
QY 241 LRDVNVHVRKTEKEMFTVAEYQNDLGALENYLNKTNFNHVSFVDPVPLHYOPHAASQGG 300
DB 241 LRDVNVHVRKTEKEMFTVAEYQNDLGALENYLNKTNFNHVSFVDPVPLHYOPHAASQGG 300


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QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTWFKPLAFAFLITRESGYPQ 360
DB 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTWFKPLAFAFLITRESGYPQ 360
QY 361 VFYDMYGTGDSQREIPALKHKIEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 420
DB 361 VFYDMYGTGDSQREIPALKHKIEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEHGFHNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEHGFHNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483
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```
RESULT 13
US-10-184-771-2
; Sequence 2, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borcherdt, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 512
; TYPE: PRT
; ORGANISM: B. licheniformis
US-10-184-771-2
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```
Query Match 100.0%; Score 2666; DB 14; Length 512;
Best Local Similarity 100.0%; Pred. No. 8.9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQHMRLQNDASVLAHSGITAWIPRAYGTSQADVGAYD 60
DB 30 ANLNGTLMQYFEMWMPNDGQHMRLQNDASVLAHSGITAWIPRAYGTSQADVGAYD 89
QY 61 LYDGEFHQKGTVAATKGTGELQSAIKSLHSRDINYYGADVINHKGADATEVTAVEV 120
DB 90 LYDGEFHQKGTVAATKGTGELQSAIKSLHSRDINYYGADVINHKGADATEVTAVEV 149
QY 121 DPADRNVISGEHLIKAMTHFHPGRGSTYSDPFKMHYHFDGTDWDSRKLRIYKQK 180
DB 150 DPADRNVISGEHLIKAMTHFHPGRGSTYSDPFKMHYHFDGTDWDSRKLRIYKQK 209
QY 181 AMDMEVSENGNDYLYADIIDYHPVAAEIKKMGWYANELQDGFRLDAVGHKFSF 240
DB 210 AMDMEVSENGNDYLYADIIDYHPVAAEIKKMGWYANELQDGFRLDAVGHKFSF 269
QY 241 LRDVNVHREKTKEMFTVAEYMONDGALENYLNKTNFNSVDPVPLHYQFHAASQGG 300
DB 270 LRDVNVHREKTKEMFTVAEYMONDGALENYLNKTNFNSVDPVPLHYQFHAASQGG 329
QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTWFKPLAFAFLITRESGYPQ 360
DB 330 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTWFKPLAFAFLITRESGYPQ 389
QY 361 VFYDMYGTGDSQREIPALKHKIEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 420
DB 390 VFYDMYGTGDSQREIPALKHKIEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 449
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QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEHGFHNGGSVSIY 480
DB 450 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEHGFHNGGSVSIY 509
QY 481 VQR 483
DB 510 VQR 512
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```
RESULT 14
US-10-199-922-2
; Sequence 2, Application US/10199922
; Publication No. US20030022346A1
; GENERAL INFORMATION:
; APPLICANT: Gist-brocades B.V.
; TITLE OF INVENTION: Alpha-amylase mutants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Gist-brocades B.V.
; STREET: Wateringseweg 1
; CITY: Delft
; COUNTRY: The Netherlands
; ZIP: 2611 XT
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/199,922
; FILING DATE: 18-Jul-2002
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-199-922-2
```

```
Query Match 99.9%; Score 2663; DB 14; Length 512;
Best Local Similarity 99.8%; Pred. No. 1.7e-238;
Matches 482; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQHMRLQNDASVLAHSGITAWIPRAYGTSQADVGAYD 60
DB 30 ANLNGTLMQYFEMWMPNDGQHMRLQNDASVLAHSGITAWIPRAYGTSQADVGAYD 89
QY 61 LYDGEFHQKGTVAATKGTGELQSAIKSLHSRDINYYGADVINHKGADATEVTAVEV 120
DB 90 LYDGEFHQKGTVAATKGTGELQSAIKSLHSRDINYYGADVINHKGADATEVTAVEV 149
QY 121 DPADRNVISGEHLIKAMTHFHPGRGSTYSDPFKMHYHFDGTDWDSRKLRIYKQK 180
DB 150 DPADRNVISGEHLIKAMTHFHPGRGSTYSDPFKMHYHFDGTDWDSRKLRIYKQK 209
QY 181 AMDMEVSENGNDYLYADIIDYHPVAAEIKKMGWYANELQDGFRLDAVGHKFSF 240
DB 210 AMDMEVSENGNDYLYADIIDYHPVAAEIKKMGWYANELQDGFRLDAVGHKFSF 269
QY 241 LRDVNVHREKTKEMFTVAEYMONDGALENYLNKTNFNSVDPVPLHYQFHAASQGG 300
DB 270 LRDVNVHREKTKEMFTVAEYMONDGALENYLNKTNFNSVDPVPLHYQFHAASQGG 329
QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTWFKPLAFAFLITRESGYPQ 360
DB 330 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTWFKPLAFAFLITRESGYPQ 389
QY 361 VFYDMYGTGDSQREIPALKHKIEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 420
DB 390 VFYDMYGTGDSQREIPALKHKIEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 449
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEHGFHNGGSVSIY 480
```

```
Db      450 NSGIALITDPGAKRMVGRONAGEIWDITGNRSEPVINSSEGWGEFHVNGGSVSIY 509
QY      481 VOR 483
Db      510 VOR 512
```

```
Db      450 NSGIALITDPGAKRMVGRONAGEIWDITGNRSEPVINSSEGWGEFHVNGGSVSIY 509
QY      481 VOR 483
Db      510 VOR 512
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Search completed: October 7, 2004, 00:57:29
Job time : 55.2274 secs

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RESULT 15
US-10-081-872-114
; Sequence 114, Application US/10081872
; Publication No. US20030125534A1
; GENERAL INFORMATION:
; APPLICANT: Callen, Walter
; APPLICANT: Richardson, Toby
; APPLICANT: Frey, Gerhard
; APPLICANT: Short, Jay M.
; APPLICANT: Mathur, Eric J.
; APPLICANT: Gray, Kevin A.
; APPLICANT: Kerveno, Janne S.
; APPLICANT: Slupeka, Malgorzata
; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 09010-108001
; CURRENT APPLICATION NUMBER: US/10/081, 872
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,495
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/270,496
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/291,122
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Environmental
US-10-081-872-114
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Query Match 99.5%; Score 2654; DB 14; Length 512;
Best Local Similarity 99.4%; Pred. No. 1.2e-237;
Matches 480; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      1 ANINGTLMQYFEMWMPNDGQHWRLONDSAYLAHSGITAWIPRAYKTSQADVGYAYD 60
Db      30 ANINGTLMQYFEMWMPNDGQHWRLONDSAYLAHSGITAWIPRAYKTSQADVGYAYD 89
QY      61 LYDLGEFHQGTVRTKTKYGTGELQSAIKSLHSRDINVGDVINHKGADATEDVTAVEV 120
Db      90 LYDLGEFHQGTVRTKTKYGTGELQSAIKSLHSRDINVGDVINHKGADATEDVTAVEV 149
QY      121 DPADRNKVIIGEHILIKAWTFHHPGRGSTYSDEFKMWTFDGTWDESRKLNRIYKFQOK 180
Db      150 DPADRNKVIIGEHILIKAWTFHHPGRGSTYSDEFKMWTFDGTWDESRKLNRIYKFQOK 209
QY      181 AMDMWVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWVANELQDGFRLDAVKHKEFSF 240
Db      210 AMDMWVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWVANELQDGFRLDAVKHKEFSF 269
QY      241 LRDMVNHREKGTGEMFTVAEYQNDLGALENTLNKTNFNHSDVPLHYQFHAASTOGG 300
Db      270 LRDMVNHREKGTGEMFTVAEYQNDLGALENTLNKTNFNHSDVPLHYQFHAASTOGG 329
QY      301 GYMRKILNKTIVYSKPLKSVTVFVNDHDTOPGQSLBSTVQTFWFKPLAYAFILTRSGYPQ 360
Db      330 GYMRKILNKTIVYSKPLKSVTVFVNDHDTOPGQSLBSTVQTFWFKPLAYAFILTRSGYPQ 389
QY      361 VFYGDWYGTGDSOREIPLAKHKIEPTLKARKOYAGAOHDYFDHHDIVGWTREGDSVA 420
Db      390 VFYGDWYGTGDSOREIPLAKHKIEPTLKARKOYAGAOHDYFDHHDIVGWTREGDSVA 449
QY      421 NSGIALITDPGAKRMVGRONAGEIWDITGNRSEPVINSSEGWGEFHVNGGSVSIY 480
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 58.3101 Seconds
(without alignments)
2340.424 Million cell updates/sec

Title: US-09-925-576C-10
Perfect score: 2638
Sequence: 1 VNGTLAQYFPMYPTNDGQHW.....SDGWEFPHVNDGSYSIVOK 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2638	100.0	483	2 AAR72448	AAR72448 Bacillus
2	2638	100.0	483	2 AAW31405	AAW31405 Bacillus
3	2638	100.0	483	4 AAY97546	AAY97546 B. amy101
4	2638	100.0	483	5 ABB06937	ABB06937 B. amy101
5	2638	100.0	483	5 AAU12153	AAU12153 Bacillus
6	2638	100.0	483	5 AAB47854	AAB47854 Bacillus
7	2638	100.0	483	5 ABB76590	ABB76590 Termany1-
8	2638	100.0	483	6 ABB60488	ABB60488 Bacillus
9	2638	100.0	514	2 AAY29853	AAY29853 Bacillus
10	2638	100.0	514	3 AAB12433	AAB12433 Bacillus
11	2638	100.0	520	6 ABB60497	ABB60497 Bacillus
12	2638	100.0	520	2 AAW39743	AAW39743 B. amy101
13	2638	100.0	520	2 AAY01584	AAY01584 An alpha-
14	2638	100.0	520	4 AAG56878	AAG56878 B. amy101
15	2635	99.9	514	3 AAB12431	AAB12431 Bacillus
16	2633	99.8	514	3 AAB12430	AAB12430 Bacillus
17	2629	99.7	514	3 AAB12432	AAB12432 Bacillus
18	2626	99.5	514	3 AAB12429	AAB12429 Bacillus
19	2625	99.5	514	2 AAR10379	AAR10379 Wild type
20	2624	99.5	480	2 AAR78268	AAR78268 Bacillus
21	2624	99.5	480	2 AAW14499	AAW14499 Bacillus
22	2624	99.5	480	2 AAY15419	AAY15419 Bacillus
23	2624	99.5	480	2 AAY07385	AAY07385 Wild type
24	2624	99.5	480	3 AAY99606	AAY99606 Bacillus
25	2617	99.2	514	2 AAR10378	AAR10378 Mutant al

ALIGNMENTS

26	2600	98.6	480	3 AAY99771	AAY99771 Bacillus
27	2598	98.5	483	6 ABB60493	ABB60493 Bacillus
28	2570	97.4	485	6 ABB60494	ABB60494 Bacillus
29	2438	92.4	483	6 ABB60492	ABB60492 Bacillus
30	2341	88.7	483	6 ABB60495	ABB60495 Bacillus
31	2290	86.8	481	6 ABB60491	ABB60491 Bacillus
32	2255	85.5	481	6 ABB60490	ABB60490 Bacillus
33	2225	84.3	481	6 ABB60489	ABB60489 Bacillus
34	2213	83.9	483	2 AAW57979	AAW57979 Alpha-amy
35	2211	83.9	512	4 AAU07552	AAU07552 Bacillus
36	2211	83.8	483	2 AAW57975	AAW57975 Alpha-amy
37	2211	83.8	512	4 AAU07556	AAU07556 Bacillus
38	2210	83.8	483	2 AAW57976	AAW57976 Alpha-amy
39	2210	83.8	483	2 AAW57978	AAW57978 Alpha-amy
40	2210	83.8	512	4 AAU07554	AAU07554 Bacillus
41	2208	83.7	483	2 AAW08207	AAW08207 B.licheni
42	2208	83.7	483	2 AAW57971	AAW57971 Alpha-amy
43	2208	83.7	483	2 AAW57981	AAW57981 Alpha-amy
44	2208	83.7	483	2 AAW57973	AAW57973 Alpha-amy
45	2208	83.7	512	4 AAU07551	AAU07551 Bacillus

RESULT 1
ID AAR72448 standard; protein; 483 AA.
AC AAR72448;
XX
XX
DT 25-MAR-2003 (revised)
DT 01-DEC-1995 (first entry)
XX
XX
DE Bacillus amy101quefaciens alpha amylase (mature protein).
XX
XX
KW Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
KW washing; Bacillus licheniformis; Bacillus amy101quefaciens;
KW Bacillus stearotheophilus; dyeing; bleaching; scouring; textile;
KW thermostable.
XX
XX
OS Bacillus amy101quefaciens.
PN
XX
XX
PI W09510603-A1.
XX
XX
PD 20-APR-1995.
XX
XX
PF 05-OCT-1994; 94WO-DK00370.
XX
XX
PR 08-OCT-1993; 93DK-00001133.
PR 02-FEB-1994; 94DK-00000140.
XX
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;
PI Van Der Zee P;
XX
XX
DR WPI; 1995-161790/21.
DR N-PSDB; AAQ88067.
XX
XX
PT New Bacillus derived alpha-amylase variants - having amino acid
PT modifications to improve washing and/or dishwashing performance.
XX
XX
PS Claim 34; Page 11-12; 105pp; English.
XX
XX
CC Variant alpha amylase enzymes which have improved washing and/or as
CC detergent additives. The enzymes have one or more amino acid residues
CC added, deleted or substituted. The variants can also be used for textile
CC desizing prior to scouring, bleaching and dyeing. The variants have
CC improved thermostability, acid/alkaline stability, low temperature
CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to
CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR
CC -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 483 AA:
 SQ Query Match 100.0%; Score 2638; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6.1e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPRAYKGLSGSDNGYGPYDLX 60
 DB 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPRAYKGLSGSDNGYGPYDLX 60
 QY 61 DGEFQOKGTVRKTKGTSELDATGSLHSRNQYGVGVNLHKKAGADTEVTVAVEVNP 120
 DB 61 DGEFQOKGTVRKTKGTSELDATGSLHSRNQYGVGVNLHKKAGADTEVTVAVEVNP 120
 QY 121 ANRNOETSEYQIKAWTDPRFPGRGNTYSDFKMHYHFGADWDSRKISRIKFRGSGK 180
 DB 121 ANRNOETSEYQIKAWTDPRFPGRGNTYSDFKMHYHFGADWDSRKISRIKFRGSGK 180
 QY 181 AMDWEVSSNGNYDYLMYADVDYDHPDVAETKKGIWYANELSDGFRIDAARKIKESF 240
 DB 181 AMDWEVSSNGNYDYLMYADVDYDHPDVAETKKGIWYANELSDGFRIDAARKIKESF 240
 QY 241 LRDWVOAVQATGKEMFTVAEYQONNAGKLENYLNKTSFNOSVFPVPLHFNLOAASSOGG 300
 DB 241 LRDWVOAVQATGKEMFTVAEYQONNAGKLENYLNKTSFNOSVFPVPLHFNLOAASSOGG 300
 QY 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTOPGOSLSTVQTMFKPLAVALITRESGYPQ 360
 DB 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTOPGOSLSTVQTMFKPLAVALITRESGYPQ 360
 QY 361 VFYGMVGTGKTSPEIKSLKDNIEPIIKARKEVAYGQHDYIDHPDVIKGTREGDSAA 420
 DB 361 VFYGMVGTGKTSPEIKSLKDNIEPIIKARKEVAYGQHDYIDHPDVIKGTREGDSAA 420
 QY 421 KSGLAALITDGPGSKRYAGIKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGSVSIY 480
 DB 421 KSGLAALITDGPGSKRYAGIKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGSVSIY 480
 QY 481 VOK 483
 DB 481 VOK 483

RESULT 2
 AAM31405
 ID AAM31405 standard; protein; 483 AA.
 AC AAM31405;
 XX 11-MAY-1998 (first entry)
 DE Bacillus amyloliquefaciens Teramyl-like alpha-amylose.
 KW Teramyl-like alpha-amylose; enzyme engineering; protein engineering; starch;
 KW liquefaction; saccharification; sweetener; textile desizing;
 KW detergent additive; ss.
 OS Bacillus amyloliquefaciens.
 PN MO9741213-A1.
 PD 06-NOV-1997.
 PF 30-APR-1997; 97MO-DK000197.
 PR 30-APR-1996; 96DK-00000515.
 PR 28-JUN-1996; 96DK-00000712.
 PR 11-JUL-1996; 96DK-00000775.
 PR 08-NOV-1996; 96DK-00001263.
 PA (NOVO) NOVO-NORDISK AS.
 XX

PI Svendsen A, Borchert TV, Bisgard-Frantzen H;
 DR WPI; 1997-549718/50.
 DR N-PSDB; AAV02472.
 PT Teramyl-like alpha-amylose variants with improved properties - e.g.
 PT increased stability at low pH and low calcium, useful as detergent
 PT additives and in industrial starch processing e.g. liquefaction.
 PS Disclosure; Page 84; 101pp; English.

XX This protein comprises the Teramyl-like alpha-amylose of Bacillus
 CC amyloliquefaciens. The invention relates to novel variants of Teramyl-
 CC like alpha-amyloses that have alpha-amylose activity and exhibit an
 CC alteration in at least one property selected from: substrate specificity;
 CC binding or cleavage pattern; thermal stability; pH/activity or
 CC pH/stability profile; stability towards oxidation; Ca2+ dependency and
 CC specific activity. The variant has one or more mutations from those
 CC listed in the specification in relation to Bacillus licheniformis
 CC Teramyl (see AAM31404). Also claimed are constructs comprising DNA
 CC encoding the variant (see AAV02471-73), and recombinant expression
 CC vectors and transformed cells containing the DNA. The Teramyl-like alpha
 CC -amylose variant is useful as a detergent additive and can also be used
 CC in industrial starch processing e.g. liquefaction (claimed) or
 CC saccharification to produce sweeteners, and in textile desizing (claimed)

XX Sequence 483 AA:
 SQ Query Match 100.0%; Score 2638; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6.1e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPRAYKGLSGSDNGYGPYDLX 60
 DB 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPRAYKGLSGSDNGYGPYDLX 60
 QY 61 DGEFQOKGTVRKTKGTSELDATGSLHSRNQYGVGVNLHKKAGADTEVTVAVEVNP 120
 DB 61 DGEFQOKGTVRKTKGTSELDATGSLHSRNQYGVGVNLHKKAGADTEVTVAVEVNP 120
 QY 121 ANRNOETSEYQIKAWTDPRFPGRGNTYSDFKMHYHFGADWDSRKISRIKFRGSGK 180
 DB 121 ANRNOETSEYQIKAWTDPRFPGRGNTYSDFKMHYHFGADWDSRKISRIKFRGSGK 180
 QY 181 AMDWEVSSNGNYDYLMYADVDYDHPDVAETKKGIWYANELSDGFRIDAARKIKESF 240
 DB 181 AMDWEVSSNGNYDYLMYADVDYDHPDVAETKKGIWYANELSDGFRIDAARKIKESF 240
 QY 241 LRDWVOAVQATGKEMFTVAEYQONNAGKLENYLNKTSFNOSVFPVPLHFNLOAASSOGG 300
 DB 241 LRDWVOAVQATGKEMFTVAEYQONNAGKLENYLNKTSFNOSVFPVPLHFNLOAASSOGG 300
 QY 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTOPGOSLSTVQTMFKPLAVALITRESGYPQ 360
 DB 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTOPGOSLSTVQTMFKPLAVALITRESGYPQ 360
 QY 361 VFYGMVGTGKTSPEIKSLKDNIEPIIKARKEVAYGQHDYIDHPDVIKGTREGDSAA 420
 DB 361 VFYGMVGTGKTSPEIKSLKDNIEPIIKARKEVAYGQHDYIDHPDVIKGTREGDSAA 420
 QY 421 KSGLAALITDGPGSKRYAGIKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGSVSIY 480
 DB 421 KSGLAALITDGPGSKRYAGIKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGSVSIY 480
 QY 481 VOK 483
 DB 481 VOK 483

RESULT 3
 AAY97546
 ID AAY97546 standard; protein; 483 AA.
 XX

AC AAY97546;
 XX
 DT 12-FEB-2001 (first entry)
 XX
 DE B. amyloliquefaciens termamy1-like alpha amylase.
 XX
 KW Termamy1-like alpha-amylase; variant; starch liquefaction; fuel;
 KW detergent composition; laundry cleaning composition; ethanol production;
 KW dish washing cleaning composition; hard surface cleaning composition;
 KW industrial ethanol production; textile desizing.
 XX
 OS Bacillus amyloliquefaciens.
 XX
 PN WO200060059-A2.
 XX
 PD 12-OCT-2000.
 XX
 PF 28-MAR-2000; 2000WO-DK000148.
 XX
 PR 30-MAR-1999; 99DK-00000437.
 XX
 PA (NOVO) NOVO NORDISK AS.
 PI Andersen C, Jorgensen CT, Bisgard-Frantzen H, Svendsen A;
 PI Kjaerulff S;
 XX
 DR WPI; 2001-015656/02.
 DR N-PSDB; AAA37850.
 XX
 XX New variants of parent Termamy1-like alpha-amylase, useful in starch
 PT liquefaction, in detergent compositions and in ethanol production,
 PT exhibit altered cleavage pattern relative to the parent.
 XX
 PS Claim 9; Page 64-67; 78pp; English.
 XX
 XX This sequence represents a termamy1-like alpha amylase. The invention
 CC relates to a variant (I) of parent Termamy1-like alpha-amylase comprising
 CC alteration at one or more of the positions W13, G48, T49, S50, Q51, A52,
 CC D53, V54, G57, G107, G108, A111, S168 and M197. The alterations in (I)
 CC are independently an insertion of an amino acid downstream of the amino
 CC acid which occupies the position of deletion or substitution of the amino
 CC acid which occupies the position with a different amino acid. The variant
 CC has alpha-amylase activity. (I) or compositions containing it are useful
 CC in starch liquefaction, in detergent composition such as laundry, dish
 CC washing and hard surface cleaning compositions, ethanol production such
 CC as fuel, drinking and industrial ethanol production, desizing of
 CC textiles, fabrics or garments. (I) exhibits a reduced capability of
 CC cleaving a substrate close to the branching point, and further exhibits
 CC improved substrate specificity and/or improved specific activity relative
 CC to the parent alpha-amylase
 CC
 XX Sequence 483 AA;
 XX
 Query Match 100.0%; Score 2638; DB 4; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6.1e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VNGTLMQYFWEYTPNDGQHWKRLQNDAEHLSDIGTAWIPAYKGLSOSDNGYGPYDLY 60
 DB 1 VNGTLMQYFWEYTPNDGQHWKRLQNDAEHLSDIGTAWIPAYKGLSOSDNGYGPYDLY 60
 QY 61 DLGFGQOKGTRTKYTKGTSSELODAIGSHSNVYGVNINRQAGDATEDVYANVNP 120
 DB 61 DLGFGQOKGTRTKYTKGTSSELODAIGSHSNVYGVNINRQAGDATEDVYANVNP 120
 QY 121 ANRQETSESEYQIAWTDFFRPGKNTYSDPKMWHYHFDGADWDSRKISIFFRSGGK 180
 DB 121 ANRQETSESEYQIAWTDFFRPGKNTYSDPKMWHYHFDGADWDSRKISIFFRSGGK 180
 QY 181 AMDWEVSSENGNYDLYADVDYDHPDVAAETKKGWIYANELSLDGRIDAANKIKFSF 240
 DB 181 AMDWEVSSENGNYDLYADVDYDHPDVAAETKKGWIYANELSLDGRIDAANKIKFSF 240

QY 241 LRDWQAVROATGKEMETVAEYWNQNAKLENYLNTKTSFNQSVFVDEVLHFNLOQAASSQGG 300
 DB 241 LRDWQAVROATGKEMETVAEYWNQNAKLENYLNTKTSFNQSVFVDEVLHFNLOQAASSQGG 300
 QY 301 GYDMRRLDGTVVSRHDEKAVTFVENHDTPQGSLESTVOTWFKPLAVALITRESGPQ 360
 DB 301 GYDMRRLDGTVVSRHDEKAVTFVENHDTPQGSLESTVOTWFKPLAVALITRESGPQ 360
 QY 361 VFYGDWYGTGTSPKEIPSLKDNIEPLTKARKEVAYGPOHDYIDHPVIGMTREGDSAA 420
 DB 361 VFYGDWYGTGTSPKEIPSLKDNIEPLTKARKEVAYGPOHDYIDHPVIGMTREGDSAA 420
 QY 421 KSGIALALITDGPQSGSKRMVAGLKNAGETWYDITGNRSPTYKISDGMGEFHVNDGSYSIY 480
 DB 421 KSGIALALITDGPQSGSKRMVAGLKNAGETWYDITGNRSPTYKISDGMGEFHVNDGSYSIY 480
 QY 481 VQK 483
 DB 481 VQK 483
 RESULT 4
 ABB06937
 ID ABB06937 standard; protein; 483 AA.
 AC ABB06937;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE B. amyloliquefaciens termamy1-like alpha-amylase protein SEQ ID NO:10.
 XX
 KW Bacillus; termamy1-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 KW washing; sweetener; ethanol; starch.
 XX
 OS Bacillus amyloliquefaciens.
 XX
 PN WO200166712-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-DK000144.
 XX
 PR 08-MAR-2000; 2000DK-00000376.
 PR 15-MAR-2000; 2000US-0189857P.
 PR 23-FEB-2001; 2001DK-00000303.
 PR 26-FEB-2001; 2001US-0271382P.
 XX
 PA (NOVO) NOVOTYMS AS.
 XX
 PI Andersen C, Borchert TV, Nielsen BR;
 XX
 DR WPI; 2002-239612/29.
 DR N-PSDB; ABL50568.
 XX
 PT Novel variant of parent termamy1-like alpha-amylase useful as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 8; Page 145-146; 153pp; English.
 XX
 XX The present invention describes a variant of a parent termamy1-like alpha
 CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 CC positions of a group of 31 possible amino acid positions. The alteration
 CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
 CC Gly186, Trp189, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
 CC Arg310, Asn314, Arg320, His324, Gly325, Tyr396, Arg400, Trp439, Arg444,
 CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
 CC washing and/or dishwashing, textile desizing, and starch liquefaction.
 CC (I) is useful as a component in hard surface cleaning detergent
 CC composition, and for producing sweeteners and ethanol from starch. (I)
 CC has altered solubility, preferably increased solubility, in particular
 CC under washing, dish washing or hard surface cleaning conditions. The

CC present sequence represents a *Bacillus amyloliquefaciens* termamyl-1-like
 CC alpha-amylase which is used in the exemplification of the present
 CC invention
 CC
 SO Sequence 483 AA;

Query Match 100.0%; Score 2638; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6.1e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 VNGTLNQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSDNGYGPYLY 60
DB 1 VNGTLNQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSDNGYGPYLY 60
QY 61 DLGEFOOKGTVRTKIGTSELDQALGSLHSRNQYGVVNLNKKAGADATEDVTAVERN 120
DB 61 DLGEFOOKGTVRTKIGTSELDQALGSLHSRNQYGVVNLNKKAGADATEDVTAVERN 120
QY 121 ANRNOETSEERYQIKAWTDFRFGKNTYSDPKMHWHPDGADWDESRKISRIFKRGEGK 180
DB 121 ANRNOETSEERYQIKAWTDFRFGKNTYSDPKMHWHPDGADWDESRKISRIFKRGEGK 180
QY 181 AMDWEVSSSENGNDYLMADVDYDHPDVAETKKGWYANBELSDGFRIDAAGHIXFSF 240
DB 181 AMDWEVSSSENGNDYLMADVDYDHPDVAETKKGWYANBELSDGFRIDAAGHIXFSF 240
QY 241 LRDWVOAVROATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDPVPLHFNLOAASOGG 300
DB 241 LRDWVOAVROATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDPVPLHFNLOAASOGG 300
QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLSESTVQWFKPLAFAFILTRESGPQ 360
DB 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLSESTVQWFKPLAFAFILTRESGPQ 360
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPIIKARKEAYGPQHDYIDHPVIGWTRGDSGSA 420
DB 361 VFYGDWYGTGTSPEKIPSLKDNIEPIIKARKEAYGPQHDYIDHPVIGWTRGDSGSA 420
QY 421 KSGLAALITDGPQSGKRWYAGLKNAGETWYDITGNRSPTVKIGSDGGEFHVNDGSYSIY 480
DB 421 KSGLAALITDGPQSGKRWYAGLKNAGETWYDITGNRSPTVKIGSDGGEFHVNDGSYSIY 480
QY 481 VOK 483
DB 481 VOK 483

```

RESULT 5
 AAU12153
 ID AAU12153 standard; protein; 483 AA.

```

XX AAU12153;
XX AC
XX DT 09-APR-2002 (first entry)
XX DE Bacillus TERMAMYL-like alpha-amylase BAN.
XX KW TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;
XX KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
XX KW amylopectin; limit dextrin; NOVAMYL; BAN.
XX OS Bacillus amyloliquefaciens.
XX PN MO20018107-A2.
XX PD 22-NOV-2001.
XX PE 10-MAY-2001; 2001WO-DK00323.
XX PR 12-MAY-2000; 2000DK-00000779.
XX PA (NOVO) NOVOZYMES AS.
XX

```

PI Svendsen A, Jorgensen CT, Nielsen BR;
 XX WPI; 2002-106123/14.
 DR N-PSDB; AAS20026.
 XX

PT New variant of parent Termamyl-like alpha-amylase for use as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 5; Fig 1; 84pp; English.

The invention relates to a variant of parent TERMAMYL-like alpha-amylase comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339, or at position 234, where the variant has alpha-amylase activity and each position corresponds to a position of a parent Termamyl-like alpha-amylase sequence having a *Bacillus licheniformis* alpha-amylase sequence of 483 amino acids, given in specification. The variant alpha-amylase, a detergent additive comprising the variant or a detergent composition comprising the variant, is useful for washing and/or dishwashing or textile desizing. The alpha-amylase is useful for starch liquefaction or ethanol production and as a component in a hard surface cleaning or detergent composition, and for producing sweeteners from starch. The variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic branch linkage cleavage activity of amylopectin or a limit dextrin prepared by TERMAMYL (RIM) or NOVAMYL (RTM). The present sequence is a natural variant of the TERMAMYL alpha-amylase, BAN

Sequence 483 AA;

Query Match 100.0%; Score 2638; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6.1e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 VNGTLNQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSDNGYGPYLY 60
DB 1 VNGTLNQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSDNGYGPYLY 60
QY 61 DLGEFOOKGTVRTKIGTSELDQALGSLHSRNQYGVVNLNKKAGADATEDVTAVERN 120
DB 61 DLGEFOOKGTVRTKIGTSELDQALGSLHSRNQYGVVNLNKKAGADATEDVTAVERN 120
QY 121 ANRNOETSEERYQIKAWTDFRFGKNTYSDPKMHWHPDGADWDESRKISRIFKRGEGK 180
DB 121 ANRNOETSEERYQIKAWTDFRFGKNTYSDPKMHWHPDGADWDESRKISRIFKRGEGK 180
QY 181 AMDWEVSSSENGNDYLMADVDYDHPDVAETKKGWYANBELSDGFRIDAAGHIXFSF 240
DB 181 AMDWEVSSSENGNDYLMADVDYDHPDVAETKKGWYANBELSDGFRIDAAGHIXFSF 240
QY 241 LRDWVOAVROATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDPVPLHFNLOAASOGG 300
DB 241 LRDWVOAVROATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDPVPLHFNLOAASOGG 300
QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLSESTVQWFKPLAFAFILTRESGPQ 360
DB 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLSESTVQWFKPLAFAFILTRESGPQ 360
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPIIKARKEAYGPQHDYIDHPVIGWTRGDSGSA 420
DB 361 VFYGDWYGTGTSPEKIPSLKDNIEPIIKARKEAYGPQHDYIDHPVIGWTRGDSGSA 420
QY 421 KSGLAALITDGPQSGKRWYAGLKNAGETWYDITGNRSPTVKIGSDGGEFHVNDGSYSIY 480
DB 421 KSGLAALITDGPQSGKRWYAGLKNAGETWYDITGNRSPTVKIGSDGGEFHVNDGSYSIY 480
QY 481 VOK 483
DB 481 VOK 483

```

RESULT 6
 AAB47854

ID AAB47854 standard; protein; 483 AA.
 XX AAB47854;
 AC
 XX 02-APR-2002 (first entry)
 DT
 XX
 XX Bacillus alpha amylase BAW.
 DE
 XX Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;
 KM starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
 KM bakery; cereal bar; ice cream; coffee whitener; salad dressing;
 KM cured meat; fermented meat; spice.
 XX
 OS Bacillus amyloliquefaciens.
 PN W0200196537-A2.
 PD 20-DEC-2001.
 XX
 XX 13-JUN-2001; 2001WO-DK000404.
 PF
 XX 14-JUN-2000; 2000DK-00000917.
 PR 20-JUN-2000; 2000US-0212852P.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PT Nielsen BR, Weibye M,
 DR WPI; 2002-098064/13.
 DR N-PSDB; AA172215.
 XX
 PT New modified alpha-amylase derived from the genus Bacillus and/or is a
 PT Termamyl-like alpha-amylase, which has been pre-oxidized for producing
 PT maltodextrin or glucose syrup.
 XX
 PS Claim 5; Page 39-41; 47pp; English.
 XX
 XX The sequences given in AAB47850-56 show modified alpha-amylases derived
 CC from the genus Bacillus. These alpha amylases are Termamyl-like alpha-
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30
 CC kDa has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours
 XX
 SQ Sequence 483 AA;
 Query Match 100.0%; Score 2638; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6.1e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 AMDWEVSENGNYDYLMTYADVDYDHPDVVAETKKMGIVANELSLDGRIDAAKHIFSF 240
 QY 241 LRDWVQAVRQATGKEMPTVAEYQWNNAGKLENTLNTKTSFNQSVFVDFLHNLQAASSQGG 300
 DB 241 LRDWVQAVRQATGKEMPTVAEYQWNNAGKLENTLNTKTSFNQSVFVDFLHNLQAASSQGG 300
 QY 301 GYDMRRLDGTAVSRHPEKAVTFVENHDTPQGSLESTVQTPWPKLVAFLTFRESGYPQ 360
 DB 301 GYDMRRLDGTAVSRHPEKAVTFVENHDTPQGSLESTVQTPWPKLVAFLTFRESGYPQ 360
 QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPLKARKEVAYGPQHDYIDHPDVIGMTREGDSSAA 420
 DB 361 VFYGDWYGTGTSPEKIPSLKDNIEPLKARKEVAYGPQHDYIDHPDVIGMTREGDSSAA 420
 QY 421 KSGLAALITDGPQSGSKRMVAGLKRAGETWYDITGNRSDTYKIGSDGGEFHVNDGSYSIY 480
 DB 421 KSGLAALITDGPQSGSKRMVAGLKRAGETWYDITGNRSDTYKIGSDGGEFHVNDGSYSIY 480
 QY 481 VQK 483
 DB 481 VQK 483
 RESULT 7
 ID ABB76590 standard; protein; 483 AA.
 XX ABB76590;
 AC
 XX 19-AUG-2002 (first entry)
 DT
 XX
 DE Termamyl-like-alpha-amylase #5.
 XX
 KM Termamyl-like alpha amylase; starch liquefaction; ethanol production;
 KM textile desizing; detergent; enzyme.
 XX
 OS Bacillus amyloliquefaciens.
 XX
 XX W0200210355-A2.
 PN
 XX 07-FEB-2002.
 PD
 XX
 PF 12-JUL-2001; 2001WO-DK000488.
 XX
 XX 01-AUG-2000; 2000DK-00001160.
 PR 12-SEP-2000; 2000DK-00001354.
 PR 10-NOV-2000; 2000DK-00001687.
 PR 26-APR-2001; 2001DK-00000655.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PT Thisted T, Kjaerulff S, Andersen C, Fugisang CC;
 DR WPI; 2002-280633/32.
 DR N-PSDB; ABL96211.
 XX
 PT Variant of parent Termamyl-like alpha amylase, useful in detergent
 PT compositions, for starch liquefaction, ethanol production, washing and/or
 PT dish washing, and textile desizing.
 XX
 PS Claim 4; Fig 3; 90pp; English.
 XX
 XX This invention relates to variants of a parent Termamyl-like alpha-
 CC amylases. These are used for starch liquefaction, ethanol production,
 CC detergent, and textile desizing. The amylases have altered stability,
 CC particularly at high temperatures from 70-120pH and low pH in the
 CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
 CC amylase
 XX
 SQ Sequence 483 AA;
 Query Match 100.0%; Score 2638; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6.1e-219;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNPGQHKRLQNDAEHLSDIGITAWIPRAYKGLSOSDNGYGYDLY 60
 DB 1 VNGTLMQYFEMWTPNPGQHKRLQNDAEHLSDIGITAWIPRAYKGLSOSDNGYGYDLY 60
 QY 61 DLGFPQKGTVRTKYGTSKSELQDAISLHSRNQYGVGVVLAHKKAGADATEVTAVENP 120
 DB 61 DLGFPQKGTVRTKYGTSKSELQDAISLHSRNQYGVGVVLAHKKAGADATEVTAVENP 120
 QY 121 ANRNOETSEBYQIKAWTDRFFPGRGNTYSDFKMHWHPGADWDSRKISRIFKRGEGK 180
 DB 121 ANRNOETSEBYQIKAWTDRFFPGRGNTYSDFKMHWHPGADWDSRKISRIFKRGEGK 180
 QY 181 AMDMEVSSNGNDYLMYADVVDYDHPDVAEYKKGIMWANELSLDGFRIDAAKIKTSF 240
 DB 181 AMDMEVSSNGNDYLMYADVVDYDHPDVAEYKKGIMWANELSLDGFRIDAAKIKTSF 240
 QY 241 LRDWQAVRQATGKEMFTVAEYWQNNAGLENYLNTKTSFNQSVFDPVPLHFNLOAASQGG 300
 DB 241 LRDWQAVRQATGKEMFTVAEYWQNNAGLENYLNTKTSFNQSVFDPVPLHFNLOAASQGG 300
 QY 301 GYDMRRLDGTIVSSRPEKAVTFVENHDTQPGQSLESTVQTFKPLAAYAFILITRESGYPQ 360
 DB 301 GYDMRRLDGTIVSSRPEKAVTFVENHDTQPGQSLESTVQTFKPLAAYAFILITRESGYPQ 360
 QY 361 VFYGDWYGTGKTSPEKIEPSLKDNIIEPILKARKEVAYGPHDITDHPDVIIGWTRGDSAA 420
 DB 361 VFYGDWYGTGKTSPEKIEPSLKDNIIEPILKARKEVAYGPHDITDHPDVIIGWTRGDSAA 420
 QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFHNDGSYSIY 480
 DB 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFHNDGSYSIY 480
 QY 481 VOK 483
 DB 481 VOK 483

RESULT 8
 ID ABP60488 standard; protein; 483 AA.
 AC ABP60488;
 XX 10-MAY-2003 (first entry)
 DT
 XX
 DE Bacillus amyloliquefaciens alpha-amylase SEQ ID NO 4.
 DB
 XX Bacillus amyloliquefaciens; alpha-amylase; washing; cleaning; textile;
 KM dishwashing machine; starch-based capsule; EC 3.2.1.1; enzyme.
 XX
 OS Bacillus amyloliquefaciens.
 XX
 PN WO2003014358-A2.
 XX
 PD 20-FEB-2003.
 XX
 PF 27-JUL-2002; 2002WO-EP008391.
 XX
 PR 07-AUG-2001; 2001DE-01038753.
 XX
 PA (HENKEL) HENKEL KGAA.
 XX
 PI Kottwitz B, Breves R, Maurer K.
 XX
 DR WPI: 2003-278480/27.
 DR N-PSDB; ABZ59264.
 XX
 PT Washing and cleaning composition, useful for laundry and hard surface
 XX cleaning, contains hybrid amylase derived from two Bacillus enzymes.
 PS Claim 4; Fig 2; 118pp; German.

XX The invention relates to a washing and cleaning composition (A)
 CC containing an amylolytic hybrid protein (I) containing sequences from the
 CC alpha-amylases (EC 3.2.1.1) of Bacillus amyloliquefaciens and B.
 CC licheniformis. (A) are used for cleaning textiles (by hand or machine) or
 CC hard surfaces (metal, glass, plastics etc.), especially in dishwashing
 CC machines. (I) can also be used to release other components of the
 CC compositions from starch-based capsules. The present sequence is that of
 CC the Bacillus amyloliquefaciens alpha-amylase of the invention
 XX

Sequence 483 AA:

Query Match 100.0%; Score 2638; DB 6; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6; 1e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNPGQHKRLQNDAEHLSDIGITAWIPRAYKGLSOSDNGYGYDLY 60
 DB 1 VNGTLMQYFEMWTPNPGQHKRLQNDAEHLSDIGITAWIPRAYKGLSOSDNGYGYDLY 60
 QY 61 DLGFPQKGTVRTKYGTSKSELQDAISLHSRNQYGVGVVLAHKKAGADATEVTAVENP 120
 DB 61 DLGFPQKGTVRTKYGTSKSELQDAISLHSRNQYGVGVVLAHKKAGADATEVTAVENP 120
 QY 121 ANRNOETSEBYQIKAWTDRFFPGRGNTYSDFKMHWHPGADWDSRKISRIFKRGEGK 180
 DB 121 ANRNOETSEBYQIKAWTDRFFPGRGNTYSDFKMHWHPGADWDSRKISRIFKRGEGK 180
 QY 181 AMDMEVSSNGNDYLMYADVVDYDHPDVAEYKKGIMWANELSLDGFRIDAAKIKTSF 240
 DB 181 AMDMEVSSNGNDYLMYADVVDYDHPDVAEYKKGIMWANELSLDGFRIDAAKIKTSF 240
 QY 241 LRDWQAVRQATGKEMFTVAEYWQNNAGLENYLNTKTSFNQSVFDPVPLHFNLOAASQGG 300
 DB 241 LRDWQAVRQATGKEMFTVAEYWQNNAGLENYLNTKTSFNQSVFDPVPLHFNLOAASQGG 300
 QY 301 GYDMRRLDGTIVSSRPEKAVTFVENHDTQPGQSLESTVQTFKPLAAYAFILITRESGYPQ 360
 DB 301 GYDMRRLDGTIVSSRPEKAVTFVENHDTQPGQSLESTVQTFKPLAAYAFILITRESGYPQ 360
 QY 361 VFYGDWYGTGKTSPEKIEPSLKDNIIEPILKARKEVAYGPHDITDHPDVIIGWTRGDSAA 420
 DB 361 VFYGDWYGTGKTSPEKIEPSLKDNIIEPILKARKEVAYGPHDITDHPDVIIGWTRGDSAA 420
 QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFHNDGSYSIY 480
 DB 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFHNDGSYSIY 480
 QY 481 VOK 483
 DB 481 VOK 483

RESULT 9
 ID AAY29853
 XX AAY29853 standard; protein; 514 AA.
 AC AAY29853;
 XX
 DT 18-NOV-1999 (first entry)
 XX
 DE Bacillus amyloliquefaciens Termamyl-like alpha-amylase.
 XX
 KM Alpha-amylase; Termamyl-like alpha-amylase; glucose syrup; starch.
 XX
 OS Bacillus amyloliquefaciens.
 XX
 FH Key
 FH Peptide 1..31
 FT /label= signal
 FT Protein 32..514
 FT /label= Termamyl-like_alpha-amylase
 XX

PN WO9946399-A1.
 XX 16-SEP-1999.
 PD
 XX 08-MAR-1999; 99WO-DK000114.
 XX
 XX 09-MAR-1998; 98DK-00000321.
 PR
 XX (NOVO) NOVO-NORDISK AS.
 PA
 XX Norman BE, Hendriksen HV;
 PI
 XX WPI; 1999-551422/46.
 DR
 DR N-PSDB; AAZ21079.
 XX
 PT Preparation of a glucose syrup, using a Termamyl-like alpha-amylase.
 PS
 XX Disclosure; Page 32-34; 36pp; English.
 CC
 CC A method has been developed for the preparation of a glucose syrup using
 CC a Termamyl-like alpha-amylase containing a substitution at Val(54). The
 CC glucose syrup obtained by the process is useful as an ingredient in food
 CC products. The Termamyl-like alpha-amylase facilitates the preparation of
 CC glucose syrups suitable for the food industry, previously only possible
 CC using acid hydrolysis. The present sequence represents *Bacillus*
 CC *amyloliquefaciens* Termamyl-like alpha-amylase
 CC
 XX
 SQ Sequence 514 AA;

Query Match 100.0%; Score 2638; DB 2; Length 514;
 Best Local Similarity 100.0%; Pred. No. 6,7e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLQYFEMYTPNDGQHWKRLONDAEHLSDIGITAWIPRAYKLSQSDNGYGPYDLY 60
 DB 32 VNGTLQYFEMYTPNDGQHWKRLONDAEHLSDIGITAWIPRAYKLSQSDNGYGPYDLY 91
 QY 61 DLGFEQKGTGRTYKTKSELODAIGSLHSRNVOYGDVVLNHRKAGADATEDVTAVEVNP 120
 DB 92 DLGFEQKGTGRTYKTKSELODAIGSLHSRNVOYGDVVLNHRKAGADATEDVTAVEVNP 151
 QY 121 ANRQETSEEVQIKAWTDFRPPRGNTYSDPKMWHYFDGADWDESKISRIFFRGEK 180
 DB 152 ANRQETSEEVQIKAWTDFRPPRGNTYSDPKMWHYFDGADWDESKISRIFFRGEK 211
 QY 181 AMDWEVSENGNYLYMAYDVYDHPVVAETKKMGWYANELSLDGRIDAAGHIKFSF 240
 DB 212 AMDWEVSENGNYLYMAYDVYDHPVVAETKKMGWYANELSLDGRIDAAGHIKFSF 271
 QY 241 LRDVQAVRQATGKEMFTVAEYMONNAGKLENTYLNKTSFNOSVDPVPLHFNLOAASSQGG 300
 DB 272 LRDVQAVRQATGKEMFTVAEYMONNAGKLENTYLNKTSFNOSVDPVPLHFNLOAASSQGG 331
 QY 301 GYDMRRLDGTVVSRRHEKAVTFVFNHDTOPGQSLSTVQTFPKPLAFAFLITRESGYPQ 360
 DB 332 GYDMRRLDGTVVSRRHEKAVTFVFNHDTOPGQSLSTVQTFPKPLAFAFLITRESGYPQ 391
 QY 361 VFYGDWGTGKTSPEKIEPLSKONTIEPLIKARKEYAYGPHDYIDHPVYIGTREGDSSAA 420
 DB 392 VFYGDWGTGKTSPEKIEPLSKONTIEPLIKARKEYAYGPHDYIDHPVYIGTREGDSSAA 451
 QY 421 KSGIAALITOPGSKWYAGLKNAGETWYDITGNRSTVYIGSDGCEFFHVNQGSYIY 480
 DB 452 KSGIAALITOPGSKWYAGLKNAGETWYDITGNRSTVYIGSDGCEFFHVNQGSYIY 511
 QY 481 VQK 483
 DB 512 VQK 514

RESULT 10
 AAB12433
 ID AAB12433 standard; protein; 514 AA.

XX AAB12433;
 AC 19-OCT-2000 (first entry)
 DT
 XX
 XX *Bacillus amyloliquefaciens* amylase protein SEQ ID NO:9.
 DE
 XX *Bacillus amyloliquefaciens*; alpha-amylase; thermostable; bread.
 KM
 XX *Bacillus amyloliquefaciens*.
 OS
 XX
 XX JP2000135093-A.
 PN
 XX 16-MAY-2000.
 PD
 XX 20-AUG-1999; 99JP-00234813.
 PF
 XX 24-AUG-1998; 98JP-00237839.
 PR
 XX (DAIW) DAIWA KASEI KK.
 PA
 XX WPI; 2000-403584/35.
 DR
 XX Novel thermostable alpha-amylase, useful for improving the preparation of
 PT bread, comprises alpha-amylase activity with less than 80% activity after
 PT treatment at 65degreesC for 30 min.
 CC
 CC Claim 1; Page 18-19; 22pp; Japanese.
 PS
 XX
 XX The present invention describes a thermostable alpha-amylase (1)
 CC comprising the sequence given in AAB12433 (A) or deletions, replacements
 CC or insertions of one or more amino acids) in the sequence and alpha-
 CC amylase activity with less than 80% activity after treatment at 65 plus
 CC degrees Celsius for 30 minutes. Also described are: (1) DNA encoding (1)
 CC ; (2) DNAs containing one of 4 nucleotide sequences comprising 1545 base
 CC pairs (see AAB60576 to AAB60579); (3) expression vectors containing the
 CC above mentioned DNAs; (4) host cells containing the above mentioned
 CC expression vectors; (5) preparation of a polypeptide having alpha-amylase
 CC activity by culture of the recombinant host cells; and (6) preparation of
 CC bread including a process to add (1) to the dough. (1) is useful in the
 CC preparation of bread. (1) improves the soft volume of the bread and
 CC prevents it aging
 CC
 XX
 SQ Sequence 514 AA;

Query Match 100.0%; Score 2638; DB 3; Length 514;
 Best Local Similarity 100.0%; Pred. No. 6,7e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLQYFEMYTPNDGQHWKRLONDAEHLSDIGITAWIPRAYKLSQSDNGYGPYDLY 60
 DB 32 VNGTLQYFEMYTPNDGQHWKRLONDAEHLSDIGITAWIPRAYKLSQSDNGYGPYDLY 91
 QY 61 DLGFEQKGTGRTYKTKSELODAIGSLHSRNVOYGDVVLNHRKAGADATEDVTAVEVNP 120
 DB 92 DLGFEQKGTGRTYKTKSELODAIGSLHSRNVOYGDVVLNHRKAGADATEDVTAVEVNP 151
 QY 121 ANRQETSEEVQIKAWTDFRPPRGNTYSDPKMWHYFDGADWDESKISRIFFRGEK 180
 DB 152 ANRQETSEEVQIKAWTDFRPPRGNTYSDPKMWHYFDGADWDESKISRIFFRGEK 211
 QY 181 AMDWEVSENGNYLYMAYDVYDHPVVAETKKMGWYANELSLDGRIDAAGHIKFSF 240
 DB 212 AMDWEVSENGNYLYMAYDVYDHPVVAETKKMGWYANELSLDGRIDAAGHIKFSF 271
 QY 241 LRDVQAVRQATGKEMFTVAEYMONNAGKLENTYLNKTSFNOSVDPVPLHFNLOAASSQGG 300
 DB 272 LRDVQAVRQATGKEMFTVAEYMONNAGKLENTYLNKTSFNOSVDPVPLHFNLOAASSQGG 331
 QY 301 GYDMRRLDGTVVSRRHEKAVTFVFNHDTOPGQSLSTVQTFPKPLAFAFLITRESGYPQ 360
 DB 332 GYDMRRLDGTVVSRRHEKAVTFVFNHDTOPGQSLSTVQTFPKPLAFAFLITRESGYPQ 391

QY 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKKEYAYGPOHDYIDHPDVIQWTRBGSSAA 420
| | | | |
Db 392 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKKEYAYGPOHDYIDHPDVIQWTRBGSSAA 451
| | | | |
QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKISGDDGGEFHVNDGSVSIY 480
| | | | |
Db 452 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKISGDDGGEFHVNDGSVSIY 511
| | | | |
QY 481 VQK 483
| | | | |
Db 512 VQK 514
| | | | |
RESULT 11
ABP60497
ID ABP60497 standard; protein; 514 AA.
XX
AC ABP60497;
XX
DT 10-MAY-2003 (first entry)
XX
DE Bacillus amyloliquefaciens alpha-amylase.
XX
KW Bacillus amyloliquefaciens; alpha-amylase; washing; cleaning; textile;
XX dishwashing machine; starch-based capsule; EC 3.2.1.1; enzyme.
XX
OS Bacillus amyloliquefaciens.
XX
FH Key Location/Qualifiers
FT Peptide 1..31
FT /label= signal_peptide
FT Protein 32..514
FT /label= mature_protein
XX
PN WO2003014358-A2.
XX
PD 20-FEB-2003.
XX
PF 27-JUL-2002; 2002WO-EP008391.
XX
PR 07-AUG-2001; 2001DE-01038753.
XX
PA (HENKEL) HENKEL KGAA.
XX
PI Kottwitz B, Breves R, Maurer K;
XX
DR WPI; 2003-278480/27.
XX
PT Washing and cleaning composition, useful for laundry and hard surface
PT cleaning, contains hybrid amylase derived from two Bacillus enzymes.
XX
PS Disclosure; Fig 2; 11pp; German.
XX
CC The invention relates to a washing and cleaning composition (A)
CC containing an amylolytic hybrid protein (I) containing sequences from the
CC alpha-amylases (EC 3.2.1.1) of Bacillus amyloliquefaciens and B.
CC licheniformis. (A) are used for cleaning textiles (by hand or machine) or
CC hard surfaces (metal, glass, plastics etc.), especially in dishwashing
CC machines. (I) can also be used to release other components of the
CC compositions from starch-based capsules. The present sequence is that of
CC the full length Bacillus amyloliquefaciens alpha-amylase protein
XX
SQ Sequence 514 AA;
| | | | |
Query Match 100.0%; Score 2638; DB 6; Length 514;
Best Local Similarity 100.0%; Pred. No. 6,7e-219.
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
| | | | |
QY 1 VNGTLMQYFFMYTPNDQHWKRLONDAEHLSDIGITAWIPAYKGLSGSDNGYGPYDLY 60
| | | | |
Db 32 VNGTLMQYFFMYTPNDQHWKRLONDAEHLSDIGITAWIPAYKGLSGSDNGYGPYDLY 91
| | | | |
QY 61 DLGEFOQKGTIVRTKYGKSELQDAISLHSRNQYGVAVLNKAGADATEVTAVERN 120
| | | | |

Db 92 DLGEFOQKGTIVRTKYGKSELQDAISLHSRNQYGVAVLNKAGADATEVTAVERN 151
| | | | |
QY 121 ANRQETSEEVQIAWTDFFRPGGNTYSDPKMHWYHFDGADWDESKISRIKFRGEGK 180
| | | | |
Db 152 ANRQETSEEVQIAWTDFFRPGGNTYSDPKMHWYHFDGADWDESKISRIKFRGEGK 211
| | | | |
QY 181 AMDWEVSENGNYDLYWADVDYDHPDVAETKKWGIWYANELSLGCFRIDAKKHKEF 240
| | | | |
Db 212 AMDWEVSENGNYDLYWADVDYDHPDVAETKKWGIWYANELSLGCFRIDAKKHKEF 271
| | | | |
QY 241 LRDWQAVRQATGKEMFTVAEYQWONNAGKLENTYKNTSPQSVFDPVLFHFNQAASSQGG 300
| | | | |
Db 272 LRDWQAVRQATGKEMFTVAEYQWONNAGKLENTYKNTSPQSVFDPVLFHFNQAASSQGG 331
| | | | |
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDPQPGSLSTYQTWKPLAYAPILTRSGYRQ 360
| | | | |
Db 332 GYDMRRLDGTIVSRHPEKAVTFVENHDPQPGSLSTYQTWKPLAYAPILTRSGYRQ 391
| | | | |
QY 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKKEYAYGPOHDYIDHPDVIQWTRBGSSAA 420
| | | | |
Db 392 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKKEYAYGPOHDYIDHPDVIQWTRBGSSAA 451
| | | | |
QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKISGDDGGEFHVNDGSVSIY 480
| | | | |
Db 452 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKISGDDGGEFHVNDGSVSIY 511
| | | | |
QY 481 VQK 483
| | | | |
Db 512 VQK 514
| | | | |

RESULT 12
AAM39743
ID AAM39743 standard; protein; 520 AA.
XX
AC AAM39743;
XX
DT 20-MAY-1998 (first entry)
XX
DE B. amyloliquefaciens alpha amylase protein.
XX
KW Alpha-amylase; calcium binding; starch liquefaction; detergent;
XX baking aid; textile industry.
XX
OS Bacillus amyloliquefaciens.
XX
PN WO9743424-A1.
XX
PD 20-NOV-1997.
XX
PF 06-MAY-1997; 97WO-US007609.
XX
PR 14-MAY-1996; 96US-00645971.
XX
PA (GENEV) GENENCOR INT INC.
XX
PI Bott R, Shaw A;
XX
DR WPI; 1998-008893/01.
XX
PT New modified alpha-amylase enzymes - having altered calcium binding
PT properties to alter e.g. high or low pH activity, thermostability or
PT oxidative stability.
XX
PS Disclosure; Fig 5A; 31pp; English.
XX
CC This sequence represents an alpha-amylase isolated from Bacillus
CC amyloliquefaciens. This sequence is used in the analysis of novel alpha-
CC amylases comprising of an A domain, a C domain and a calcium binding site
CC associated with the A domain and the C domain. Ligand residues in the A
CC and/or C domain allow the modification of the alpha-amylase which alter
CC the characteristics of the calcium binding site and thereby alter

CC performance. This modified enzyme can be used for e.g. starch
CC liquefaction, in laundry or dishwashing detergent compositions, as baking
CC aids or in textile desizing. The alpha-amylase variants can have
CC increased activity at low pH and high temperatures, increased high pH and
CC oxidative stability and improved stability in the absence or low
CC concentrations of calcium ion

XX Sequence 520 AA;

Query Match 100.0%; Score 2638; DB 2; Length 520;
Best Local Similarity 100.0%; Pred. No. 6,8e-219;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 VNGTLMQYFEMWTPNDGQHWKRLONDAEHLSDIGITAVWIPPAKGLSOSDNGGYPDLY 60
DB 38 VNGTLMQYFEMWTPNDGQHWKRLONDAEHLSDIGITAVWIPPAKGLSOSDNGGYPDLY 97
QY 61 DLGFFQCKGTVRTKYGKSELDALIGSLHSRNVOYGVVNLHAKAGADATEDVAVEVNP 120
DB 98 DLGFFQCKGTVRTKYGKSELDALIGSLHSRNVOYGVVNLHAKAGADATEDVAVEVNP 157
QY 121 ANRNOETSEERYQIKAMTDFRPPGKNTYSDPKMWHFPGADWDSEKRSIRIFKRGEGK 180
DB 158 ANRNOETSEERYQIKAMTDFRPPGKNTYSDPKMWHFPGADWDSEKRSIRIFKRGEGK 217
QY 181 AMDWVSSSENGNYDLYMAYADVVDHPVVAETKKMGIMYANELSLDGFRIIDAAGHKIRSF 240
DB 218 AMDWVSSSENGNYDLYMAYADVVDHPVVAETKKMGIMYANELSLDGFRIIDAAGHKIRSF 277
QY 241 LRDVQAVRQATGKEMFTVAEYMONNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSQGG 300
DB 278 LRDVQAVRQATGKEMFTVAEYMONNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSQGG 337
QY 301 GYDMRRLDGTVVSRRHPEKAVTFVENHDTOPGQSLSESTVQTFKPLAYAFILITRESGYPQ 360
DB 338 GYDMRRLDGTVVSRRHPEKAVTFVENHDTOPGQSLSESTVQTFKPLAYAFILITRESGYPQ 397
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPQHDYIDHPVIGMTRGDSAA 420
DB 398 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPQHDYIDHPVIGMTRGDSAA 457
QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSPTVYKISDGEFFHNDGSYSIY 480
DB 458 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSPTVYKISDGEFFHNDGSYSIY 517
QY 481 VQK 483
DB 518 VQK 520
```

RESULT 13
ID AAY01584 standard; protein; 520 AA.

AC AAY01584;

XX 17-JUN-1999 (first entry)

DE An alpha-amylase (Am-Amylo) protein sequence.

XX Alpha-amylase; mutant; liquefaction; starch processing;

KW alcohol production; cleaning agent; detergent matrix; starch desizing.

XX Bacillus amyloliquefaciens.

XX WO9909183-A1.

XX 25-FEB-1999.

XX 14-AUG-1998; 98WO-US016906.

XX 19-AUG-1997; 97US-00914679.

XX

PA (GENV) GENENCOR INT INC.

XX Day A.; Swanson B;

XX WPI; 1999-190168/16.

XX New mutant Bacillus licheniformis -a-amylase - useful in starch

PT liquefaction processes and detergents.

XX Disclosure; Fig 3; 35pp; English.

XX The present sequence represents an alpha-amylase from Bacillus
CC amyloliquefaciens. The specification describes a mutant alpha-amylase
CC derived from a precursor alpha-amylase by the deletion, substitution, or
CC addition of a residue corresponding to A210, H405, and/or T412 in B.
CC licheniformis alpha-amylase. The mutant alpha-amylase is used in the
CC initial stages (liquefaction) of starch processing, in alcohol
CC production, as a cleaning agent in detergent matrices, and in the textile
CC industry for starch desizing. The enzyme can be used in a detergent for
CC cleaning soiled laundry and/or dishes, and to liquefy starch

XX Sequence 520 AA;

Query Match 100.0%; Score 2638; DB 2; Length 520;
Best Local Similarity 100.0%; Pred. No. 6,8e-219;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 VNGTLMQYFEMWTPNDGQHWKRLONDAEHLSDIGITAVWIPPAKGLSOSDNGGYPDLY 60
DB 38 VNGTLMQYFEMWTPNDGQHWKRLONDAEHLSDIGITAVWIPPAKGLSOSDNGGYPDLY 97
QY 61 DLGFFQCKGTVRTKYGKSELDALIGSLHSRNVOYGVVNLHAKAGADATEDVAVEVNP 120
DB 98 DLGFFQCKGTVRTKYGKSELDALIGSLHSRNVOYGVVNLHAKAGADATEDVAVEVNP 157
QY 121 ANRNOETSEERYQIKAMTDFRPPGKNTYSDPKMWHFPGADWDSEKRSIRIFKRGEGK 180
DB 158 ANRNOETSEERYQIKAMTDFRPPGKNTYSDPKMWHFPGADWDSEKRSIRIFKRGEGK 217
QY 181 AMDWVSSSENGNYDLYMAYADVVDHPVVAETKKMGIMYANELSLDGFRIIDAAGHKIRSF 240
DB 218 AMDWVSSSENGNYDLYMAYADVVDHPVVAETKKMGIMYANELSLDGFRIIDAAGHKIRSF 277
QY 241 LRDVQAVRQATGKEMFTVAEYMONNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSQGG 300
DB 278 LRDVQAVRQATGKEMFTVAEYMONNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSQGG 337
QY 301 GYDMRRLDGTVVSRRHPEKAVTFVENHDTOPGQSLSESTVQTFKPLAYAFILITRESGYPQ 360
DB 338 GYDMRRLDGTVVSRRHPEKAVTFVENHDTOPGQSLSESTVQTFKPLAYAFILITRESGYPQ 397
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPQHDYIDHPVIGMTRGDSAA 420
DB 398 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPQHDYIDHPVIGMTRGDSAA 457
QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSPTVYKISDGEFFHNDGSYSIY 480
DB 458 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSPTVYKISDGEFFHNDGSYSIY 517
QY 481 VQK 483
DB 518 VQK 520
```

RESULT 14
ID AAG65878 standard; protein; 520 AA.

AC AAG65878;

XX 11-FEB-2002 (first entry)

DE B. amyloliquefaciens alpha-amylase.

```
XX Bacillus; mutant; alpha-amylase; oxidative stability; thermal stability;
KM detergent; starch.
XX
XX Bacillus amyloliquefaciens.
OS
PN US6297037-B1.
XX
PD 02-OCT-2001.
XX
PF 10-FEB-1994; 94US-00194664.
XX
PR 11-FEB-1993; 93US-00016395.
XX
XX (BARN/) BARNETT C. C.
PA (MITC/) MITCHINSON C.
PA (POWE/) POWER S. D.
PA (REGU/) REGUADR C. A.
XX
PI Barnett CC, Mitchinson C, Power SD, Reguadr CA;
XX WPI; 2001-638043/73.
XX
XX Mutant alpha amylase, derived from Bacillus, for use in detergents and
PT starch liquefaction compositions, comprising substituted amino acids.
XX
XX Example; Fig 3A-B; 57pp; English.
XX
XX The invention relates to a mutant alpha-amylase, derived from Bacillus.
CC The mutant has a substitution or a deletion of a methionine residue in
CC Bacillus licheniformis alpha amylase. The mutant alpha-amylases have
CC altered oxidative stability and/or altered thermal stability and altered
CC pH performance profiles. They are useful in detergents or starch
CC liquefaction compounds. The present sequence represents the B.
CC amyloliquefaciens alpha-amylase
XX
SQ Sequence 520 AA;
Query Match 100.0%; Score 2638; DB 4; Length 520;
Best Local Similarity 100.0%; Pred. No. 6.8e-219;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNGTLMQYFEWYTPNDGQHMRLQNDAEHLSDIGITAWMIPPAKGLSOSDNGGYPDLY 60
DB 38 VNGTLMQYFEWYTPNDGQHMRLQNDAEHLSDIGITAWMIPPAKGLSOSDNGGYPDLY 97
QY 61 DLGEFOQKGTVRTKYGKSELQDAIGSLHSRNVOYGVVNLNKAAGADATEDVTAVERN 120
DB 98 DLGEFOQKGTVRTKYGKSELQDAIGSLHSRNVOYGVVNLNKAAGADATEDVTAVERN 157
QY 121 ANRNOETSEEVQIKAWTDFRPPRGNTYSDPKMWHYHFDGADWDESKRSIRIFRGEK 180
DB 158 ANRNOETSEEVQIKAWTDFRPPRGNTYSDPKMWHYHFDGADWDESKRSIRIFRGEK 217
QY 181 AMDREVSEENNYIYAWADVDYDHPVNAETKMGITVANEISLDGFRIDAANKHIFSF 240
DB 218 AMDREVSEENNYIYAWADVDYDHPVNAETKMGITVANEISLDGFRIDAANKHIFSF 277
QY 241 LRDWVOAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFPOSYEDVYLHFNLAASSQGG 300
DB 278 LRDWVOAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFPOSYEDVYLHFNLAASSQGG 337
QY 301 GYDNRRLIDGTVVRNHEPKAVTVENHDTPQGSLESTVQTWKPLAFAFILTRBSGYRQ 360
DB 338 GYDNRRLIDGTVVRNHEPKAVTVENHDTPQGSLESTVQTWKPLAFAFILTRBSGYRQ 397
QY 361 VFYGDMTGKTGTSKPELPSLKDNTEPILKARKXAYAGPOHDYLDHNDVIGMTREGSSAA 420
DB 398 VFYGDMTGKTGTSKPELPSLKDNTEPILKARKXAYAGPOHDYLDHNDVIGMTREGSSAA 457
QY 421 KSGIALAALITDGPQGSKRMVAGLNAGETWYDITGNRSDTVKIGSDMGFEFHVNDGSVSIY 480
DB 458 KSGIALAALITDGPQGSKRMVAGLNAGETWYDITGNRSDTVKIGSDMGFEFHVNDGSVSIY 517
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```
QY 481 VQK 483
DB 518 VQK 520
RESULT 15
AAB12431
ID AAB12431 standard; protein; 514 AA.
XX
XX AAB12431;
AC
XX
DT 19-OCT-2000 (first entry)
XX
XX Bacillus amyloliquefaciens clone number 24 protein SEQ ID NO:5.
DE Bacillus amyloliquefaciens; alpha-amylase; thermostable; bread.
XX
XX Bacillus amyloliquefaciens.
OS
XX JP2000135093-A.
XX
XX 16-MAY-2000.
PD
XX
XX 20-AUG-1999; 99UP-00234813.
PF
XX
XX 24-AUG-1998; 98UP-00237839.
PR
XX
XX (DAIW ) DAIWA KASEI KK.
PA
XX
XX WPI; 2000-403584/35.
DR
XX N-PSDB; AAA60578.
XX
XX Novel thermostable alpha-amylase, useful for improving the preparation of
PT bread, comprises alpha-amylase activity with less than 80% activity after
PT treatment at 65degreesC for 30 min.
XX
XX
XX Example 6; Page 15-16; 22pp; Japanese.
XX
XX The present invention describes a thermostable alpha-amylase (1)
CC comprising the sequence given in AAB12431 (A) or deletions, replacements
CC or insertions of one or more amino acid(s) in the sequence and alpha-
CC amylase activity with less than 80% activity after treatment at 65 plus
CC degrees Celsius for 30 minutes. Also described are: (1) DNAs encoding (1)
CC : (2) DNAs containing one of 4 nucleotide sequences comprising 1545 base
CC pairs (see AAA60576 to AAA60579); (3) expression vectors containing the
CC above mentioned DNAs; (4) host cells containing the above mentioned
CC expression vectors; (5) preparation of a polypeptide having alpha-amylase
CC activity by culture of the recombinant host cells; and (6) preparation of
CC bread including a process to add (1) to the dough. (1) is useful in the
CC preparation of bread. (1) improves the soft volume of the bread and
CC prevents it aging. The present sequence represents a Bacillus
CC amyloliquefaciens clone number 24 protein, which is used in the
CC exemplification of the present invention
XX
SQ Sequence 514 AA;
Query Match 99.9%; Score 2635; DB 3; Length 514;
Best Local Similarity 99.8%; Pred. No. 1.2e-218;
Matches 482; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNGTLMQYFEWYTPNDGQHMRLQNDAEHLSDIGITAWMIPPAKGLSOSDNGGYPDLY 60
DB 32 VNGTLMQYFEWYTPNDGQHMRLQNDAEHLSDIGITAWMIPPAKGLSOSDNGGYPDLY 91
QY 61 DLGEFOQKGTVRTKYGKSELQDAIGSLHSRNVOYGVVNLNKAAGADATEDVTAVERN 120
DB 92 DLGEFOQKGTVRTKYGKSELQDAIGSLHSRNVOYGVVNLNKAAGADATEDVTAVERN 151
QY 121 ANRNOETSEEVQIKAWTDFRPPRGNTYSDPKMWHYHFDGADWDESKRSIRIFRGEK 180
DB 152 ANRNOETSEEVQIKAWTDFRPPRGNTYSDPKMWHYHFDGADWDESKRSIRIFRGEK 211
```

Qy	181	AMDEVSSENGNYDYLNAVADVDPVVAETKKMGIMYANELSLDGFRIIDAKHIESF	240
Db	212	AMDEVSSENGNYDYLNAVADVDPVVAETKKMGIMYANELSLDGFRIIDAKHIESF	271
Qy	241	LRDWVQAVROATGKEMFTVAEYWMONNAGKLENYLNKTSFNOSVDPVPLHFNLOAASSQGG	300
Db	272	LRDWVQAVROATGKEMFTVAEYWMONNAGKLENYLNKTSFNOSVDPVPLHFNLOAASSQGG	331
Qy	301	GYPDRLLDGTVVSRHPEKAVTFVENHDTOPGQSLSESTVQTFWFKPLAYAFILITRESGYPO	360
Db	332	GYPDRLLDGTVVSRHPEKAVTFVENHDTOPGQSLSESTVQTFWFKPLAYAFILITRESGYPO	391
Qy	361	VFYGDMYGTGKTSPEKEIPSLKONIEPILKARKEAYAGPOHDYIDHPDVIIGWTRGDSAA	420
Db	392	VFYGDMYGTGKTSPEKEIPSLKONIEPILKARKEAYAGPOHDYIDHPDVIIGWTRGDSAA	451
Qy	421	KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSPTYKIGSDGMBEFHNDGSYSIY	480
Db	452	KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSPTYKIGSDGMBEFHNDGSYSIY	511
Qy	481	VOK 483	
Db	512	VOK 514	

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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 ; Search time 14.8246 Seconds
(without alignments)
3134.012 Million cell updates/sec

Title: US-09-925-576C-10

Perfect score: 2638
Sequence: 1 VNGTLMQYFEMVYTPNDGQHW.....SDGMGEFHVNDGSVSIYVK 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR 78:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2638	100.0	514	1	ALBSN
2	2184	82.8	512	1	ALBSL
3	1835	69.6	518	1	A27705
4	1773.5	67.2	549	1	A54541
5	1759.5	66.8	549	1	A24436
6	1759.5	66.7	549	1	A24549
7	1700	64.4	548	1	ALBSF
8	1253	47.5	493	2	S15713
9	1217	46.1	484	2	G95160
10	1212	45.9	484	2	P98026
11	1206	45.7	492	2	AH2079
12	1136	43.1	492	2	C86781
13	1054	40.0	495	2	AD3038
14	1054	40.0	506	2	G98247
15	1019	38.6	494	1	B45738
16	1010	38.3	494	2	AD0751
17	1003	38.0	495	2	B90962
18	1002	38.0	495	1	A45738
19	984	37.3	495	1	B85810
20	620	23.5	217	2	A19506
21	351.5	13.3	826	2	B36750
22	346	13.1	826	2	S14958
23	333.5	12.6	421	2	S10514
24	324	12.3	437	2	S14956
25	323	12.2	1196	2	A29130
26	319	12.1	438	2	S14957
27	318	12.1	435	2	S12625
28	317	12.0	435	2	UC7137
29	315.5	12.0	437	2	UT0946

ALIGNMENTS

RESULT 1

ALBSN
alpha-amylase (EC 3.2.1.1) precursor - *Bacillus amyloliquefaciens*

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C/Species: *Bacillus amyloliquefaciens*

C/Date: 30-Nov-1980 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999

C/Accession: A92389, A90307, I39756, I39763, A00843

J/Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L

U. Biol. Chem. 258, 1007-1013, 1983

A/Title: Amino acid sequence of alpha-amylase from *Bacillus amyloliquefaciens* deduced fr

A/Reference number: A92389, MUID:63108608, PMID:6185474

A/Contents: PUB110

A/Accession: A92389

A/Molecule type: DNA

A/Residues: 1-514 <TAK>

A/Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:G142428; PIDN:AAA221

Biochem. U. 185, 387-393, 1980

A/Title: Sequence of the N-terminal half of *Bacillus amyloliquefaciens* alpha-amylase.

A/Reference number: A90307, MUID:80241725, PMID:6156671

A/Accession: A90307

A/Molecule type: protein

A/Residues: 32-53, 'I', 55-63, 'L', 65-78, 'D', 80-83, 'S', 85-222 <CHU>

R/Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtoavaara, P.; Sarvas, M.; Soderlund, H.;

Gene 15, 43-51, 1981

A/Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t

A/Reference number: I39756, MUID:82051296, PMID:6170539

A/Accession: I39756

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-96 <RES>

A/Cross-references: EMBL:V00092; NID:G39297; PIDN:CAA23430.1; PID:G39298

R/Ruohonen, L.; Hackman, P.; Lehtoavaara, P.; Knowles, J.K.C.; Karanen, S.

Gene 59, 161-170, 1987

A/Title: Efficient secretion of *Bacillus amyloliquefaciens* alpha-amylase cells by its ow

A/Reference number: I39763, MUID:86137952, PMID:2830166

A/Accession: I39763

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-39 <RE2>

A/Cross-references: GB:M18424; NID:G142430; PIDN:AAA22192.1; PID:G142431

C/Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A/Pathway: glycogen/starch degradation

C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F/32-514/Product: alpha-amylase #status predicted <SIG>

F/229-362/Domin: alpha-amylase core homology <AMY>

F/133,221,266/Binding site: calcium (Asn, Asp, Asp) #status predicted

F/262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 2638; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 4, 7e-182;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKYGLSQSDNGYGPYDLY 60
 DB 32 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKYGLSQSDNGYGPYDLY 91

QY 61 DLGEFOOKGTVPKRYGKSKSLQDAIGLSIRNVOYGVVLMHKAQADTEVTAVEVNP 120
 DB 92 DLGEFOOKGTVPKRYGKSKSLQDAIGLSIRNVOYGVVLMHKAQADTEVTAVEVNP 151

QY 121 ANNNGETSEBYQIKAWTDFRPFGRGNTYSDPKWHYFPDQADWDSRKISRIFKRGEEK 180
 DB 152 ANNNGETSEBYQIKAWTDFRPFGRGNTYSDPKWHYFPDQADWDSRKISRIFKRGEEK 211

QY 181 AMDWEVSSNGNYDYLMYADVDDYDHPDVVAETKKGCIWYANELSLDGEPRIDAAKHKPSF 240
 DB 212 AMDWEVSSNGNYDYLMYADVDDYDHPDVVAETKKGCIWYANELSLDGEPRIDAAKHKPSF 271

QY 241 LRDWQVAVRQATGKEMFTVAEYVONNAGKLENYLNTKTSNOSVDPVPLHFNLOAASQCG 300
 DB 272 LRDWQVAVRQATGKEMFTVAEYVONNAGKLENYLNTKTSNOSVDPVPLHFNLOAASQCG 331

QY 301 GTDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLESTVQTFKFLAVAFILTRBSGPQ 360
 DB 332 GTDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLESTVQTFKFLAVAFILTRBSGPQ 391

QY 361 VYGYMGYKGTSPKEIPBLKNIPILKARKEYAVGQHDYIDHPDYIGMTREGDSGA 420
 DB 392 VYGYMGYKGTSPKEIPBLKNIPILKARKEYAVGQHDYIDHPDYIGMTREGDSGA 451

QY 421 KSGLAALITDGPGRKMYAGKNAGETMYDITGRSPVTKIGSDGMEFPYHNGSVSY 480
 DB 452 KSGLAALITDGPGRKMYAGKNAGETMYDITGRSPVTKIGSDGMEFPYHNGSVSY 511

QY 481 VOK 483
 DB 512 VOK 514

RESULT 2
 ALBTL
 alpha-amyase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
 N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C/Species: Bacillus licheniformis
 C/Date: 30-Jun-1987 #sequence revision 24-Apr-1998 #text change 15-Sep-2000
 C/Accession: A91997; B24549; A91796; A21663; I39772; A26151; S53788; A00844
 R/Yunki, T.; Nomura, T.; Teruka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uda, S.
 J. Biochem. 98, 1147-1156, 1985
 A/Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amyases deduced from the DNA sequences.
 A/Reference number: A91997; PMID:8611694; PMID:2418011
 A/Accession: A91997
 A/Molecule type: DNA
 A/Residues: 1-162, 'R', 164-512 <YUN>
 A/Cross-references: GB:X03236, NID:g39551, PIDN:CAA26981.1; PID:g39552
 A/Experimental source: ATCC 27811
 R/Gray, G.L.; Maltzer, S.E.; Rey, M.W.; Lamea, M.H.; Kindle, K.L.; Carmona, C.; Requiad, J. Bacteriol. 166, 635-643, 1986
 A/Title: Structural genes encoding the thermophilic alpha-amyases of Bacillus stearothermophilus
 A/Reference number: A91817; PMID:86195857; PMID:3009417
 A/Accession: B24549
 A/Molecule type: DNA
 A/Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>
 A/Cross-references: GB:M13256; NID:g142510; PIDN:AAA22240.1; PID:g142511
 A/Experimental source: NCIB 8061
 R/Stephens, M.A.; Orlepp, S.A.; Ollington, J.F.; McConnell, D.J.
 J. Bacteriol. 158, 369-372, 1984
 A/Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amyase
 A/Reference number: A91796; PMID:84185455; PMID:6609154
 A/Accession: A91796
 A/Molecule type: DNA

A/Residues: 1-104 <STE>
 A/Cross-references: GB:X01984; NID:g142432; PIDN:AAA22193.1; PID:g142433
 R/Sibakov, M.; Palva, I.
 Eur. J. Biochem. 145, 567-572, 1984
 A/Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amyase
 A/Reference number: A21663; PMID:65076654; PMID:6334606
 A/Accession: A21663
 A/Molecule type: DNA
 A/Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 8;
 A/Experimental source: chromosomal DNA of ATCC 14580
 A/Note: the authors translated the codon CGT for residue 48 as Gly and GAC for residue 64
 R/laide, B.M.; Chambliss, G.H.; McConnell, D.J.
 J. Bacteriol. 171, 2435-2442, 1989
 A/Title: Bacillus licheniformis alpha-amyase gene, amyL, is subject to promoter-independent
 A/Reference number: I39773; PMID:89213924; PMID:2540150
 A/Accession: I39774
 A/Molecule type: DNA
 A/Status: translated from GB/EMBL/DBJ
 A/Residues: 1-29 <LAC>
 A/Cross-references: GB:M26412; NID:g341477; PIDN:AAA22237.1; PID:g516590
 R/Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Didrichsen, B.
 Gene 96, 37-41, 1990
 A/Title: In vivo genetic engineering: homologous recombination as a tool for plasmid construction
 A/Reference number: I39772; PMID:91092499; PMID:2265757
 A/Accession: I39772
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-32, 'T' <DOR>
 A/Cross-references: GB:M62637; NID:g142498; PIDN:AAA22232.1; PID:g142499
 R/Kuhn, H.; Fietzek, P.P.; Lampen, J.O.
 J. Bacteriol. 149, 372-373, 1982
 A/Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amyase: comparison
 A/Reference number: A26151; PMID:82098050; PMID:6172418
 A/Accession: A26151
 A/Molecule type: protein
 A/Residues: 30-37, 'E', 39-41, 'X', 43-47 <KUH>
 R/Machius, M.; Wiegand, G.; Huber, R.
 J. Mol. Biol. 246, 545-559, 1995
 A/Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amyase at 2.2 Å
 A/Reference number: S53788; PMID:95182462; PMID:787175
 A/Accession: S53788
 A/Molecule type: protein
 A/Residues: 'D', 220-227 <MAC>
 A/Note: sequence represents amino end of an internal fragment created by a single enzymatic
 R/Machius, M.; Wiegand, G.; Huber, R.
 submitted to the Brookhaven Protein Data Bank, July 1995
 A/Reference number: A65206; PDB:1BPL
 A/Contents: annotation; X-ray crystallography; 2.2 angstroms, residues 32-210; 222-511
 A/Note: these structural studies suggest 163 is Leu rather than Arg
 R/Song, H.K.; Huang, K.Y.; Chang, C.; Suh, S.W.
 submitted to the Brookhaven Protein Data Bank, October 1996
 A/Reference number: A66860; PDB:1VDS
 A/Contents: annotation; X-ray crystallography; 1.7 angstroms, residues 32-210; 222-511
 C/genetics:
 A/Gene: amyL
 C/Function:
 A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 C/Pathway: glycogen/starch degradation
 C/Superfamily: alpha-amyase, amyloidogenic type; alpha-amyase core homology
 C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/30-512/Product: alpha-amyase #status experimental <MAT>
 F/227-360/Domain: alpha-amyase core homology <AMY>
 F/133, 229, 264/Binding site: calcium (ben, Asp, His) #status experimental
 F/260, 290, 357/Active site: Asp, Glu, Asp #status experimental

Query Match 82.8%; Score 2184; DB 1; Length 512;
 Best Local Similarity 80.5%; Pred. No. 2, 2e-149;
 Matches 389; Conservative 42; Mismatches 50; Indels 2; Gaps 1;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKYGLSQSDNGYGPYDLY 60
 DB 32 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKYGLSQSDNGYGPYDLY 91


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Qy 61 DLGFOOKGTARTKTYGKSELQDAIGSLHSRNVQYGVVNLHKAADATEDVTAVERNPN 120
Db 92 DLGFOOKGTARTKTYGKSELQDAIGSLHSRNVQYGVVNLHKAADATEDVTAVERNPN 151
Qy 121 ANRQETSEEYOIKAMTDFRPPRGNTYSDFKMHYHFDGADMDERKRI-SRIFFRGEK 180
Db 152 ANRQETSEEYOIKAMTDFRPPRGNTYSDFKMHYHFDGADMDERKRI-SRIFFRGEK 209
Qy 181 AMDMEVSENGNDYLYMAYADVDYDHPVVAETKMGKIWANELSLDGERIDAHAHIXFSF 240
Db 210 AMDMEVSENGNDYLYMAYADVDYDHPVVAETKMGKIWANELSLDGERIDAHAHIXFSF 269
Qy 241 LRDVQAVRQATGKEMFTVAEYVONNAGKLENTYKTSFNQSVFVPLHFNLOAASSQGG 300
Db 270 LRDVQAVRQATGKEMFTVAEYVONNAGKLENTYKTSFNQSVFVPLHFNLOAASSQGG 329
Qy 301 GYDMRLLDGTIVSRHEKAVTFVENHDTOPGQSLSESTVQTFKPLAVAFILITRESGYPO 360
Db 330 GYDMRLLDGTIVSRHEKAVTFVENHDTOPGQSLSESTVQTFKPLAVAFILITRESGYPO 389
Qy 361 VFYGDYGYGTFKSPKIPSLKONIEPIILKARKEVAYGPQHDYIDHPVIGMTREGSSAA 420
Db 390 VFYGDYGYGTFKSPKIPSLKONIEPIILKARKEVAYGPQHDYIDHPVIGMTREGSSAA 449
Qy 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGMEFHVNDGSVS 480
Db 450 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGMEFHVNDGSVS 509
Qy 481 YVOK 483
Db 510 YVOK 512

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RESULT 3

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alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase; 6G-amylase
C/Species: Bacillus sp.
C/Date: 31-Mar-1999 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
R/Accession: A27705
R/Author: A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A/Title: Nucleotide sequence of the maltotriase-producing amylase gene from an alkalophilic
A/Reference number: A27705; MUID:86162814; PMID:3258152
A/Accession: A27705
A/Molecule type: DNA
A/Residues: 1-518 <TSU>
A/Cross-references: GB:M18862; NID:g142496; PID:AAA2231.1; PID:g142497
A/Experimental source: Chromosomal DNA of strain 707
C/Note: amino end of mature protein also determined
C/Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
A/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F/1-33/Domain: signal sequence #status predicted <SIG>
F/34-518/Product: alpha-amylase #status experimental <MAT>
F/236-369/Domain: alpha-amylase core homology <AMY>
F/236-369/Binding site: calcium (Asn, Asp, His) #status predicted
F/269,299,366/Active site: Asp, Glu, Asp #status predicted

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Query Match 69.6%; Score 1835; DB 1; Length 518;
Best Local Similarity 66.6%; Pred. No. 2.8e-124;
Matches 323; Conservative 63; Mismatches 91; Indels 8; Gaps 3;
Qy 2 NGTLMQFEWYTPNDGQHWKRLQNDABHLSIDGTTAWIPRAYKGLSQSDNGYGPYDLYD 61
Db 39 NGTLMQFEWYTPNDGQHWKRLQNDABHLSIDGTTAWIPRAYKGLSQSDNGYGPYDLYD 98
Qy 62 LGFEQOKGTARTKTYGKSELQDAIGSLHSRNVQYGVVNLHKAADATEDVTAVERNPN 121
Db 92 LGFEQOKGTARTKTYGKSELQDAIGSLHSRNVQYGVVNLHKAADATEDVTAVERNPN 151

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Db 99 LGFEQOKGTARTKTYGKSELQDAIGSLHSRNVQYGVVNLHKAADATEDVTAVERNPN 158
Qy 122 ANRQETSEEYOIKAMTDFRPPRGNTYSDFKMHYHFDGADMDERKRI-SRIFFRGEK 180
Db 159 ANRQETSEEYOIKAMTDFRPPRGNTYSDFKMHYHFDGADMDERKRI-SRIFFRGEK 218
Qy 181 AMDMEVSENGNDYLYMAYADVDYDHPVVAETKMGKIWANELSLDGERIDAHAHIXFSF 240
Db 210 AMDMEVSENGNDYLYMAYADVDYDHPVVAETKMGKIWANELSLDGERIDAHAHIXFSF 278
Qy 241 LRDVQAVRQATGKEMFTVAEYVONNAGKLENTYKTSFNQSVFVPLHFNLOAASSQGG 300
Db 270 LRDVQAVRQATGKEMFTVAEYVONNAGKLENTYKTSFNQSVFVPLHFNLOAASSQGG 338
Qy 301 GYDMRLLDGTIVSRHEKAVTFVENHDTOPGQSLSESTVQTFKPLAVAFILITRESGYPO 360
Db 330 GYDMRLLDGTIVSRHEKAVTFVENHDTOPGQSLSESTVQTFKPLAVAFILITRESGYPO 398
Qy 361 VFYGDYGYGTFKSPKIPSLKONIEPIILKARKEVAYGPQHDYIDHPVIGMTREGSSAA 420
Db 390 VFYGDYGYGTFKSPKIPSLKONIEPIILKARKEVAYGPQHDYIDHPVIGMTREGSSAA 453
Qy 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGMEFHVNDGSVS 480
Db 450 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGMEFHVNDGSVS 513
Qy 481 YVOK 483
Db 510 YVOK 512

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RESULT 4

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alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DN1792)
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus stearothermophilus
C/Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
R/Accession: A54541
R/Author: R.; Poulsen, G.B.; Diderichsen, B.
FEMS Microbiol. Lett. 77, 271-276, 1991
A/Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A/Reference number: A54541
A/Accession: A54541
A/Molecule type: DNA
A/Residues: 1-549 <DOR>
A/Cross-references: GB:X59476
A/Experimental source: Chromosomal DNA of strain DN1792
C/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C/Genetics:
A/Start codon: GTG
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
F/1-34/Domain: signal sequence #status predicted <SIG>
F/35-549/Product: alpha-amylase #status predicted <MAT>
F/235-368/Domain: alpha-amylase core homology <AMY>
F/235-368/Binding site: calcium (Asp, Asp, His) #status predicted
F/268,298,365/Active site: Asp, Glu, Asp #status predicted

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Query Match 67.2%; Score 1773.5; DB 1; Length 549;
Best Local Similarity 65.4%; Pred. No. 8.2e-120;
Matches 316; Conservative 57; Mismatches 105; Indels 5; Gaps 2;
Qy 2 NGTLMQFEWYTPNDGQHWKRLQNDABHLSIDGTTAWIPRAYKGLSQSDNGYGPYDLYD 61
Db 39 NGTLMQFEWYTPNDGQHWKRLQNDABHLSIDGTTAWIPRAYKGLSQSDNGYGPYDLYD 98
Qy 62 LGFEQOKGTARTKTYGKSELQDAIGSLHSRNVQYGVVNLHKAADATEDVTAVERNPN 121
Db 99 LGFEQOKGTARTKTYGKSELQDAIGSLHSRNVQYGVVNLHKAADATEDVTAVERNPN 158

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QY 122 NNNQETSEBYOIKAWTDFRPGRGNTYSDPKMHWTFDGADWDSRKSISRTFKRGEGKA 181
D 159 DRNGEISGTYOIQAMTKFDPGSGNTYSSFKRWYHFDGVDWDSRKLSTRTFKRGEGKA 218
QY 182 WDEVSSENGYDYLYMADVDYDHPVVAETKKMGWYANELSLDGFRIIDAAKHIFSL 241
D 219 WDEVDTENGYDYLYMADVDYDHPVVAETKKMGWYANELSLDGFRIIDAAKHIFSL 278
QY 242 RDWVQAVRQATGEMFTVAEYQNNAGKLENTYNTKSTFNOGVFVDFLHFNLOAASQGG 301
D 279 PDMLSTVRSQTKGFLFTVGEIWSYDINKLHNTITDGTMSLFDAPLHKKFYTAASKSGA 338
QY 302 YMRRLDGTIVSRPEKAVTFVFNHDTOPGQSLSTQVTKFKPLAFAFILTRESGYPOV 361
D 339 FMRRLMTNTLTKDQPTLAVTFVNDHDTPEGQALQSWDPWFKPLAFAFILTRESGYPOV 398
QY 362 FYGDMVGTGKTSRK-ETPSLKDNIETPLKARKEVAGPQHDYIDHPVIGMTREGDSAA 420
D 399 FYGDIYGI---PQYNIPLSKSIDPLIARRDYVAGTQHDYIDHSDIIGMTREGTEPK 454
QY 421 KSGIALALITDGPGRKMYAGLKNAGETWYDITGNRSDTYKIGSGDGEFHVNDGVSIV 480
D 455 GSGIALALITDGPGRKMYVKGQAHAKVFDLTGNRSDTYVINSDDGEFHVNDGVSIV 514
QY 481 VQK 483
D 515 VPR 517

RESULT 5

A24436
alpha-amylase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* plasmid PAT5
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: *Bacillus stearothermophilus*
C>Date: 05-Jun-1997 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C:Accession: A24436; I39777
R:Nakajima, R.; Imanaka, T.; Aiba, S.
J. Bacteriol. 163, 401-406, 1985
A:Reference number: A24436; UID:85234394; PMID:3924897
A:Accession: A24436
A:Molecule type: DNA
A:Residues: 1-549 <NAK>
A:Cross-references: GB:M11450
A:Experimental source: plasmid PAT5
A:Note: amino end of the mature protein also determined
R:Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A:Title: In vivo genetic engineering: homologous recombination as a tool for plasmid cor
A:Reference number: I39772; UID:91092499; PMID:2265757
A:Accession: I39777
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-45 <RES>
A:Cross-references: GB:M62638; NID:G142514; PID:AAA22242.1; PID:G142515
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
A:Gene: amyS
A:Genome: plasmid
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefactiens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-54/Product: signal sequence #status predicted <SIG>
F:235-368/Domain: alpha-amylase #status experimental <AMT>
F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F:268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 66.8%; Score 1763.5; DB 1; Length 549;
Best Local Similarity 65.2%; Pred. No. 4.3e-119;
Matches 315; Conservative 58; Mismatches 105; Indels 5; Gaps 2;

QY 2 NGTLQYFEMYPNDQOHKRLONDAEHLSDIGITAVWIPRAYKLSQSDNGYPPDYLD 61
D 39 NGTLQYFEMYPNDQOHKRLONDAEHLSDIGITAVWIPRAYKLSQSDNGYPPDYLD 98
QY 62 LGEFQOQKTRTKYTKSELDODAGSLHSRNQYGVVNLHKAQADATEDYTAVEVPA 121
D 99 LGEFQOQKTRTKYTKSELDODAGSLHSRNQYGVVNLHKAQADATEDYTAVEVPA 158
QY 122 NNNQETSEBYOIKAWTDFRPGRGNTYSDPKMHWTFDGADWDSRKSISRTFKRGEGKA 181
D 159 DRNGEISGTYOIQAMTKFDPGSGNTYSSFKRWYHFDGVDWDSRKLSTRTFKRGEGKA 218
QY 182 WDEVSSENGYDYLYMADVDYDHPVVAETKKMGWYANELSLDGFRIIDAAKHIFSL 241
D 219 WDEVDTENGYDYLYMADVDYDHPVVAETKKMGWYANELSLDGFRIIDAAKHIFSL 278
QY 242 RDWVQAVRQATGEMFTVAEYQNNAGKLENTYNTKSTFNOGVFVDFLHFNLOAASQGG 301
D 279 PDMLSTVRSQTKGFLFTVGEIWSYDINKLHNTITDGTMSLFDAPLHKKFYTAASKSGA 338
QY 302 YMRRLDGTIVSRPEKAVTFVFNHDTOPGQSLSTQVTKFKPLAFAFILTRESGYPOV 361
D 339 FMRRLMTNTLTKDQPTLAVTFVNDHDTPEGQALQSWDPWFKPLAFAFILTRESGYPOV 398
QY 362 FYGDMVGTGKTSRK-ETPSLKDNIETPLKARKEVAGPQHDYIDHPVIGMTREGDSAA 420
D 399 FYGDIYGI---PQYNIPLSKSIDPLIARRDYVAGTQHDYIDHSDIIGMTREGTEPK 454
QY 421 KSGIALALITDGPGRKMYAGLKNAGETWYDITGNRSDTYKIGSGDGEFHVNDGVSIV 480
D 455 GSGIALALITDGPGRKMYVKGQAHAKVFDLTGNRSDTYVINSDDGEFHVNDGVSIV 514
QY 481 VQK 483
D 515 VPR 517

RESULT 6

A24549
alpha-amylase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* (strain NZ-3)
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: *Bacillus stearothermophilus*
C>Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C:Accession: A24549; I39501; I39770
R:Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamea, M.H.; Kindle, K.L.; Reguadt,
J. Bacteriol. 166, 635-643, 1986
A:Title: Structural genes encoding the thermophilic alpha-amylases of *Bacillus stearothe*
A:Reference number: A91817; UID:86195857; PMID:3009417
A:Accession: A24549
A:Molecule type: DNA
A:Residues: 1-549 <GRA>
A:Cross-references: GB:M3255; NID:G142512; PID:AAA22241.1; PID:G142513
A:Experimental source: genomic DNA of strain NZ-3
R:Sach, H.; Nishida, H.; Isono, K.
J. Bacteriol. 170, 1034-1040, 1988
A:Title: Evidence for movement of the alpha-amylase gene into two phylogenetically dista
A:Reference number: I39501; UID:88139156; PMID:3257753
A:Accession: I39501
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 536-549 <RES>
A:Cross-references: GB:M29577; NID:G142476; PID:AAA22225.1; PID:G142478
A:Experimental source: strain DY-5
A:Accession: I39770
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 536-549 <RES>
A:Cross-references: GB:M29578; NID:G142484; PID:AAA22228.1; PID:G142486
A:Experimental source: strain 799
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
A:Gene: amyS
A:Genetics:
A:Start codon: GTG

C;Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status predicted <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 66.7%; Score 1759.5; DB 1; Length 549;
Best Local Similarity 65.0%; Pred. No. 8.3e-119;
Matches 314; Conservative 59; Mismatches 105; Indels 5; Gaps 2;

```
QY 2 NGTLMQFEMWYTPNDGQHWKRLQNDAEHLSDGTTAVWPAYKGLSOSNGVGYLYD 61
DB 39 NGTLMQFEMWYTPNDGQHWKRLQNDAEHLSDGTTAVWPAYKGLSOSNGVGYLYD 98
QY 62 LGSEFOQKGVTRTKYKTSKSELDALISLHSHRNQVYGVVNLHKGADATEDVTAVERNPA 121
DB 99 LGSEFOQKGVTRTKYKTSKSELDALISLHSHRNQVYGVVNLHKGADATEDVTAVERNPA 158
QY 122 NNRQETSEERYQIAWTFDFRPGRGNTYSDFRKWHYHFDGADWDSESKISRIFFKRGSKA 181
DB 159 DRNOEISGTYQIOAWTFDFRPGRGNTYSDFRKWHYHFDGADWDSESKISRIFFKRGSKA 218
QY 182 WDMEVSENGNYYLYMADVDYDHPVVAETKKMGVYANLELSDGRIIDAAHKIKSF 241
DB 219 WDMEVSENGNYYLYMADVDYDHPVVAETKKMGVYANLELSDGRIIDAAHKIKSF 278
QY 242 RDWVOAVRQATGKEMFVAEYWMQNNAGKLENYLNTKTSFNOSVDFVPLHFMLOAASOGG 301
DB 279 PDLSTVRSQTKGRLFTVGSYMSYDINKLNYITKNGTMSLDAPLHNFYTAASKGGA 338
QY 302 YDMRRLDGTVSRHPEKAVTVEENHDTPQGSLSTVQTFKPLAYAFILITRESGYPOV 361
DB 339 PDLSTVRSQTKGRLFTVGSYMSYDINKLNYITKNGTMSLDAPLHNFYTAASKGGA 398
QY 362 FYGDWYTGKTSRK-ELPSLKDNIEPLTKARKKAYAPQHDYIDHPVITGWTREGSSAA 420
DB 399 FYGDWYTGKTSRK-ELPSLKDNIEPLTKARKKAYAPQHDYIDHPVITGWTREGSSAA 454
QY 421 KSGIALITDGPGRSKMYAGLKNAGETWYDITGNRSDYTKISGDDGEPHNDGSSVSIY 480
DB 455 GSGIALITDGPGRSKMYAGLKNAGETWYDITGNRSDYTKISGDDGEPHNDGSSVSIY 514
QY 481 VOK 483
DB 515 VPR 517
```

RESULT 7

ALBSP
alpha-amylase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* (strain DY-5) plasmid
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: *Bacillus stearothermophilus*
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Feb-1997
C;Accession: A91999; B91999; A91804; A00845
J;Ihara, H.; Sasaki, T.; Teubol, A.; Yamagata, H.; Teukagoshi, N.; Uda, S.
J. Biochem. 98, 95-103, 1985
A;Title: Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology bet
A;Reference number: A91999; MUID:86008166; PMID:3876333
A;Accession: A91999
A;Molecule type: DNA
A;Residues: 1-548 <1H1>
A;Cross-references: GB:X02769
A;Experimental source: plasmid pHI300 from strain DY-5
A;Accession: B91999
A;Molecule type: protein
A;Residues: 35-48 <1H2>
A;Experimental source: strain DY-5
R;Teukagoshi, N.; Iritani, S.; Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata,

J. Bacteriol. 164, 1182-1187, 1985
A;Title: Efficient synthesis and secretion of a thermophilic alpha-amylase by protein-pr
A;Reference number: A91804; MUID:86059211; PMID:2999073
A;Contents: PBAM101
A;Accession: A91804

A;Molecule type: DNA
A;Residues: 1-29, 'Q', 31-75, 'W', 77-122 <TSU>
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Genome: Plasmid
A;Start codon: GTG

C;Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-548/Product: alpha-amylase #status experimental <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 64.4%; Score 1700; DB 1; Length 548;
Best Local Similarity 63.8%; Pred. No. 1.6e-114;
Matches 308; Conservative 57; Mismatches 112; Indels 6; Gaps 3;

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QY 2 NGTLMQFEMWYTPNDGQHWKRLQNDAEHLSDGTTAVWPAYKGLSOSNGVGYLYD 61
DB 39 NGTLMQFEMWYTPNDGQHWKRLQNDAEHLSDGTTAVWPAYKGLSOSNGVGYLYD 98
QY 62 LGSEFOQKGVTRTKYKTSKSELDALISLHSHRNQVYGVVNLHKGADATEDVTAVERNPA 121
DB 99 LGSEFOQKGVTRTKYKTSKSELDALISLHSHRNQVYGVVNLHKGADATEDVTAVERNPA 158
QY 122 NNRQETSEERYQIAWTFDFRPGRGNTYSDFRKWHYHFDGADWDSESKISRIFFKRGSKA 181
DB 159 DRNOEISGTYQIOAWTFDFRPGRGNTYSDFRKWHYHFDGADWDSESKISRIFFKRGSKA 218
QY 182 WDMEVSENGNYYLYMADVDYDHPVVAETKKMGVYANLELSDGRIIDAAHKIKSF 241
DB 219 WDMEVSENGNYYLYMADVDYDHPVVAETKKMGVYANLELSDGRIIDAAHKIKSF 278
QY 242 RDWVOAVRQATGKEMFVAEYWMQNNAGKLENYLNTKTSFNOSVDFVPLHFMLOAASOGG 301
DB 279 PDLSTVRSQTKGRLFTVGSYMSYDINKLNYITKNGTMSLDAPLHNFYTAASKGGA 338
QY 302 YDMRRLDGTVSRHPEKAVTVEENHDTPQGSLSTVQTFKPLAYAFILITRESGYPOV 361
DB 339 PDLSTVRSQTKGRLFTVGSYMSYDINKLNYITKNGTMSLDAPLHNFYTAASKGGA 397
QY 362 FYGDWYTGKTSRK-ELPSLKDNIEPLTKARKKAYAPQHDYIDHPVITGWTREGSSAA 420
DB 398 FYGDWYTGKTSRK-ELPSLKDNIEPLTKARKKAYAPQHDYIDHPVITGWTREGSSAA 453
QY 421 KSGIALITDGPGRSKMYAGLKNAGETWYDITGNRSDYTKISGDDGEPHNDGSSVSIY 480
DB 454 GSGIALITDGPGRSKMYAGLKNAGETWYDITGNRSDYTKISGDDGEPHNDGSSVSIY 513
QY 481 VOK 483
DB 514 VPR 516
```

RESULT 8

alpha-amylase (EC 3.2.1.1) - *Bacillus circulans*
C;Species: *Bacillus circulans*
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: S15713
R;Marcel, T.
submitted to the EMBL Data Library, May 1991
A;Reference number: S15713
A;Accession: S15713

A:Molecule type: DNA
A:Residues: 1-493 <MR>
A:Cross-references: EMBL:X60779; NID:g39411; PIDN:CAA43194.1; PID:g39412
C:Genetics:
A:Gene: amyE
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amyLase, amyLoliquefaciens type; alpha-amyLase core homology
C:Keywords: glycosidase; hydrolase; polyaccharide degradation
P;200-333/Domain: alpha-amyLase core homology <AMT>

Query Match 47.5%; Score 1253; DB 2; Length 493;

Best Local Similarity 47.2%; Pred. No. 2e-82;

Matches 226; Conservative 74; Mismatches 177; Indels 2; Gaps 1;

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QY      2 NGTLMQFEWYTPNDGQHWKRLQNDAEHLSDIGTITAWIPPAYGLSQSDNGYGPYDLYD 61
      4 NHTMQFEWYTPNDGQHWKRLQNDAEHLSDIGTITAWIPPAYGLSQSDNGYGPYDLYD 63
QY      62 LGFEQKGTVRTKTKGTSKSELQDAIGSLHSRNVOYGVGVNLNKGADATEDVTAVERNPA 121
      64 LGFEQKGTVRTKTKGTSKSELQDAIGSLHSRNVOYGVGVNLNKGADATEDVTAVERNPA 123
QY      122 NRNOETSEEVQIKATWDFRPPRGNTYSDFKMWYHFDGADWDSRKISRIIFKFRGSGKA 181
      124 DRTKEISEPFEIEGWTKEFTFPGRDQYSSFKMSEHFGTDFDAREERTGVFRJAGENKK 183
QY      182 WDMWVSSSENGYDILMADVDYDHPDVAETKKMGIVANELSLDGRIDAAKIKTSFL 241
      184 WNEVWDEFGNYDYLMFANIDYNNHPRREMIIDWGMKILDTLQCGGRLDAIKIHNEFI 243
QY      242 RDWVQAVROATGKEMFTVAEYMONNAGLENYLNTKTSFNOSVFDVPLHFNLOAASQGG 301
      244 KEFAEMIRKKGQDFYVGEFWMNSNLACREFLDYDYLDFVSLHYKLHEASLGRD 303
Db      302 YDKRRLLDGTGVSSHPEKAVTFVENHDTQPGQSLSTVQTFKPLAAYAFILTRBSGYPV 361
      304 FDLKIFDDTLVQHHPHATVFDVNDHDSQPHALLESWIGDWFKPSAVALTLRRDGYPVV 363
QY      362 FYGDMGTGTSPEKISLKNIEPILKARKEVAYGPHDYIDHPDYIGWTRREDSAAK 421
      364 FYGDIYIGG--PFPVQKKEIIDLILSARCNKAYGDEDFDHANTIGWRRGVEIEG 421
QY      422 SGLAALLTDGPGSKRYAGLKNAGETWYDITGNRSDTVKIGSDGMBEFHYNDGSVST 480
      422 SGCAVVISNGDDGKKMFIGHHRAGEVWDLTSCDDQITIEEDGMATFHVCGGGSVW 480
Db
```

RESULT 9

G95160
alpha-amyLase [imported] - Streptococcus pneumoniae (strain TIGR4)

C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001

C/Accession: G95160
R/Retelin: H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

A:Authors: Lotiutis, B.-J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A./Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A/Reference number: A95000; MUID:21357209; PMID:11463916

A/Accession: G95160
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-484 <KUR>

A/Cross-references: GB:AE00672; PIDN:AAK75480.1; PID:g14972868; GSPDB:GN00164; TIGR:SP4
A/Experimental source: strain TIGR4
C/Genetics:
A:Gene: SP1382

C:Superfamily: alpha-amyLase, amyLoliquefaciens type; alpha-amyLase core homology

Query Match 46.1%; Score 1217; DB 2; Length 484;

Best Local Similarity 47.0%; Pred. No. 7.5e-80;

Matches 226; Conservative 81; Mismatches 168; Indels 6; Gaps 3;

```
QY      2 NGTLMQFEWYTPNDGQHWKRLQNDAEHLSDIGTITAWIPPAYGLSQSDNGYGPYDLYD 61
      3 NHTMQFEWYTPNDGQHWKRLQNDAEHLSDIGTITAWIPPAYGLSQSDNGYGPYDLYD 62
Db      62 LGFEQKGTVRTKTKGTSKSELQDAIGSLHSRNVOYGVGVNLNKGADATEDVTAVERNPA 121
      63 LGFEQKGTVRTKTKGTSKSELQDAIGSLHSRNVOYGVGVNLNKGADATEDVTAVERNPA 122
QY      122 NRNOETSEEVQIKATWDFRPPRGNTYSDFKMWYHFDGADWDSRKISRIIFKFRGSGKA 181
      123 DRTKEISEPFEIEGWTKEFTFPGRDQYSSFKMSEHFGTDFDAREERTGVFRJAGENKK 182
QY      182 WDMWVSSSENGYDILMADVDYDHPDVAETKKMGIVANELSLDGRIDAAKIKTSFL 241
      183 WNEVWDEFGNYDYLMFANIDYNNHPRREMIIDWGMKILDTLQCGGRLDAIKIHNEFI 243
QY      240 FLDWVQAVROATGKEMFTVAEYMONNAGLENYLNTKTSFNOSVFDVPLHFNLOAASQGG 299
      243 FMRNFIIDMKKKGDDPYVGEFWMNSNLACREFLDYDYLDFVSLHYKLHEASLGRD 302
QY      300 GGYDMRLLDGTGVSSHPEKAVTFVENHDTQPGQSLSTVQTFKPLAAYAFILTRBSGYPV 359
      303 ANYDLRGIFLDSVLEKPDRAVTFVNDHDTQPGQSLSTVQTFKPLAAYAFILTRBSGYPV 362
QY      360 QVFYDMGTGTSPEKISLKNIEPILKARKEVAYGPHDYIDHPDYIGWTRREDSAAK 419
      363 CVRYGDIYIGGQYQAE--DFKEILDRILAIRKDLAYGENDYFDHANCIGWRRGVEIEG 419
Db      420 -QSPVAVLISNDGNSKSMVVGQEMWTQTFVDLLGNHGGQVTLIDEBGYGQFPVASRSVW 478
QY      480 Y 480
      479 W 479
Db
```

RESULT 10

F98026
alpha-amyLase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)

C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001

C/Accession: F98026
R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgelt, S.; Dehoff, B.S.; Es
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.O.; Lu, J.; Matsushima, P.; McAhren, S.; Mc
J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Balcz, R.H.; Jaskunas, S.R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234

A/Accession: F98026
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-484 <KUR>

A/Cross-references: GB:AE007317; PIDN:AAL00043.1; PID:g15458876; GSPDB:GN00174
C/Genetics:
A:Gene: amy

C:Superfamily: alpha-amyLase, amyLoliquefaciens type; alpha-amyLase core homology
C/Keywords: glycosidase; hydrolase

Query Match 45.9%; Score 1212; DB 2; Length 484;

Best Local Similarity 46.6%; Pred. No. 1.7e-79;

Matches 224; Conservative 84; Mismatches 167; Indels 6; Gaps 3;

```
QY      2 NGTLMQFEWYTPNDGQHWKRLQNDAEHLSDIGTITAWIPPAYGLSQSDNGYGPYDLYD 61
      3 NHTMQFEWYTPNDGQHWKRLQNDAEHLSDIGTITAWIPPAYGLSQSDNGYGPYDLYD 62
Db      62 LGFEQKGTVRTKTKGTSKSELQDAIGSLHSRNVOYGVGVNLNKGADATEDVTAVERNPA 121
      63 LGFEQKGTVRTKTKGTSKSELQDAIGSLHSRNVOYGVGVNLNKGADATEDVTAVERNPA 122
QY      122 NRNOETSEEVQIKATWDFRPPRGNTYSDFKMWYHFDGADWDSRKISRIIFKFRGSGKA 181
      123 DRTKEISEPFEIEGWTKEFTFPGRDQYSSFKMSEHFGTDFDAREERTGVFRJAGENKK 182
QY      182 WDMWVSSSENGYDILMADVDYDHPDVAETKKMGIVANELSLDGRIDAAKIKTSFL 241
      183 WNEVWDEFGNYDYLMFANIDYNNHPRREMIIDWGMKILDTLQCGGRLDAIKIHNEFI 243
QY      240 FLDWVQAVROATGKEMFTVAEYMONNAGLENYLNTKTSFNOSVFDVPLHFNLOAASQGG 299
      243 FMRNFIIDMKKKGDDPYVGEFWMNSNLACREFLDYDYLDFVSLHYKLHEASLGRD 302
QY      300 GGYDMRLLDGTGVSSHPEKAVTFVENHDTQPGQSLSTVQTFKPLAAYAFILTRBSGYPV 359
      303 ANYDLRGIFLDSVLEKPDRAVTFVNDHDTQPGQSLSTVQTFKPLAAYAFILTRBSGYPV 362
QY      360 QVFYDMGTGTSPEKISLKNIEPILKARKEVAYGPHDYIDHPDYIGWTRREDSAAK 419
      363 CVRYGDIYIGGQYQAE--DFKEILDRILAIRKDLAYGENDYFDHANCIGWRRGVEIEG 419
Db      420 -QSPVAVLISNDGNSKSMVVGQEMWTQTFVDLLGNHGGQVTLIDEBGYGQFPVASRSVW 478
QY      480 Y 480
      479 W 479
Db
```


QY 418 SAAKSLAALITDGPCKSKMYAGLNAGETWYDITGNRSDDTVKIGSDGWFHNDGVS 477
 Db 413 DNKEYGLSCLTNTKNGSKTMIIDKAYAGKVYIDLFGRHEIPITILDQNGAEFYNDGVS 472
 QY 478 SIYVQK 483
 Db 473 SVMVDK 478

RESULT 13
 AD3038
 alpha-amylase amYA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AD3038
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCllell
 Science 294, 2317-2323, 2001
 A:Title: Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AD3038
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-495 <KUR>
 A:Cross-references: GB:AE008689; PIDN:AAL44722.1; PID:g17742354; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: amYA
 A:Map position: linear chromosome
 C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 40.0%; Score 1054; DB 2; Length 495;
 Best Local Similarity 43.7%; Pred. No. 4.2e-68;
 Matches 214; Conservative 77; Mismatches 183; Indels 16; Gaps 6;

QY 4 TLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIWPAYKGLSQSDN-GYGFYDLYL 62
 Db 5 TLLQFFHYYPDGKLMSEVAEAKSLAKMGITDVLWLPAYKGAAGGYSVGYDTYDL 64
 QY 63 GEFQKQGVTRTKYKTKSELODAIGSLHSRNQVGVVNLNKHAGADATEDVAVENPAN 122
 Db 65 GEFQKQGVTRTKYKTKSELODAIGSLHSRNQVGVVNLNKHAGADATEDVAVENPAN 124
 QY 123 RNQETSEYQIKAWTDFFRPGRGNTYDFKWHYHFDGADWDSRKRISRIKFP---RGE 179
 Db 125 RTDIDDEDFPALAYTRFTFPGRGNGKSKFIWDLKCFSGVDHIEPTEDGIFRLVNEYG 184
 QY 180 KAMDWEVSSENGNYDLYMADVDYDHPVVAETKKGWYANLSLDGFRIDAANKHIFS 239
 Db 185 E-WNEEVQENGFYDLMGADVEFRNRAVYELKYWRMLSEQVQVDFGLDAAKHIPAW 243
 QY 240 FLRDWQAVRQATGKEMFTVAEYQNNAGKLENLYNKTSPNQSVDVPLHFNLOAASSOG 299
 Db 244 FFRDVGVMHRETVPDLFVVAEYHWPDLKALSYLELVKQMLFDVALHHSFHDASKQ 303
 QY 300 GGYDMRLLDGTVSRHPEKAVTFVENHDTQPGQSLSTVQTFWPKPLAYAFILTRREG 359
 Db 304 GDFMRSIFDGLSVSAVPDHAIVLVDNHTDTPQLQSLSEAPVEPWFKPLAYAIIILLRE 363
 QY 360 QVFYDMYGTGKTSKPK-----EIPSLKDNIEPIILKARKEYAVGPOHDIYDHPDVG 411
 Db 364 CVFYPDLPFGTSYTDGNGNEIKIDIPAI-ECUPKLEARSFANGPQTDFDASCIAF 422
 QY 412 TREGSSAAKSLAALITDGPCKSKMYAGLNAGETWYDITGNRSDDTVKIGSDGWFH 471
 Db 423 IRHGTADA--PGCVVVMNSGEPGEKQADLGPERRAGSVWRDFLGHRHEIITLDES 480
 QY 472 VNDGVSIVY 481
 Db 481 TNGGVSVMV 490

RESULT 15
 B45738
 alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium
 N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: Salmonella typhimurium
 C:Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
 C:Accession: B45738
 R:Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
 J. Bacteriol. 174, 6644-6652, 1992

RESULT 14
 G98247
 cytoplasmic alpha-amylase (1,4-alpha-d-glucan glucanohydrolase) [imported] - Agrobacterium
 C:Species: Agrobacterium tumefaciens
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
 C:Accession: G98247
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman, B.;
 A.; Liu, F.; Woliam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.,
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 C:Accession: G98247
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-506 <KUR>
 A:Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:g15159379; GSPDB:GN00170
 C:Genetics:
 A:Gene: AGR L 1863
 A:Map position: linear chromosome
 C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 40.0%; Score 1054; DB 2; Length 506;
 Best Local Similarity 43.7%; Pred. No. 4.3e-68;
 Matches 214; Conservative 77; Mismatches 183; Indels 16; Gaps 6;

QY 4 TLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIWPAYKGLSQSDN-GYGFYDLYL 62
 Db 16 TLLQFFHYYPDGKLMSEVAEAKSLAKMGITDVLWLPAYKGAAGGYSVGYDTYDL 75
 QY 63 GEFQKQGVTRTKYKTKSELODAIGSLHSRNQVGVVNLNKHAGADATEDVAVENPAN 122
 Db 76 GEFQKQGVTRTKYKTKSELODAIGSLHSRNQVGVVNLNKHAGADATEDVAVENPAN 135
 QY 123 RNQETSEYQIKAWTDFFRPGRGNTYDFKWHYHFDGADWDSRKRISRIKFP---RGE 179
 Db 136 RTDIDDEDFPALAYTRFTFPGRGNGKSKFIWDLKCFSGVDHIEPTEDGIFRLVNEYG 195
 QY 180 KAMDWEVSSENGNYDLYMADVDYDHPVVAETKKGWYANLSLDGFRIDAANKHIFS 239
 Db 196 E-WNEEVQENGFYDLMGADVEFRNRAVYELKYWRMLSEQVQVDFGLDAAKHIPAW 254
 QY 240 FLRDWQAVRQATGKEMFTVAEYQNNAGKLENLYNKTSPNQSVDVPLHFNLOAASSOG 299
 Db 255 FFRDVGVMHRETVPDLFVVAEYHWPDLKALSYLELVKQMLFDVALHHSFHDASKQ 314
 QY 300 GGYDMRLLDGTVSRHPEKAVTFVENHDTQPGQSLSTVQTFWPKPLAYAFILTRREG 359
 Db 315 GDFMRSIFDGLSVSAVPDHAIVLVDNHTDTPQLQSLSEAPVEPWFKPLAYAIIILLRE 374
 QY 360 QVFYDMYGTGKTSKPK-----EIPSLKDNIEPIILKARKEYAVGPOHDIYDHPDVG 411
 Db 375 CVFYPDLPFGTSYTDGNGNEIKIDIPAI-ECUPKLEARSFANGPQTDFDASCIAF 433
 QY 412 TREGSSAAKSLAALITDGPCKSKMYAGLNAGETWYDITGNRSDDTVKIGSDGWFH 471
 Db 434 IRHGTADA--PGCVVVMNSGEPGEKQADLGPERRAGSVWRDFLGHRHEIITLDES 491
 QY 472 VNDGVSIVY 481
 Db 492 TNGGVSVMV 501

RESULT 15
 B45738
 alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium
 N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: Salmonella typhimurium
 C:Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
 C:Accession: B45738
 R:Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
 J. Bacteriol. 174, 6644-6652, 1992

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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:46:32 ; Search time 8.47121 Seconds
(without alignments)
2968.867 Million cell updates/sec

Title: US-09-925-576C-10
Perfect score: 2638
Sequence: 1 VNTLMQYFEWYTPDQGH.....SDGWGEFHVNDGSVIVQK 483

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2638	100.0	514	1 AMY_BACAM	P06692 bacillus li
2	2187	82.9	512	1 AMY_BACLI	P06278 bacillus li
3	1835	69.6	518	1 AMY2_BACS7	P19571 bacillus sp
4	1763.5	66.8	549	1 AMY_BACST	P06279 bacillus st
5	1017	38.6	494	1 AMY2_SALTY	P26613 salmonella
6	1002	38.0	495	1 AMY2_ECOLI	P26612 escherichia
7	346	13.1	440	1 AM3A_ORYSA	P27932 oryza sativ
8	333.5	12.6	421	1 AMYA_VIGMU	P17859 vigna mungo
9	324	12.3	437	1 AM3C_ORYSA	P27939 oryza sativ
10	323	12.2	1196	1 AMYB_PAEPO	P21543 paenibacill
11	319	12.1	438	1 AM3B_ORYSA	P27937 oryza sativ
12	318	12.1	435	1 AM3D_ORYSA	P27933 oryza sativ
13	315.5	12.0	437	1 AM3E_ORYSA	P27934 oryza sativ
14	315	11.9	413	1 AMY3_WHEAT	P08117 triticum ae
15	307.5	11.7	438	1 AMY1_HORVU	P00693 hordeum vul
16	289	11.0	429	1 AMY6_HORVU	P04750 hordeum vul
17	285.5	10.8	713	1 CDGT_BACS8	P17692 bacillus sp
18	284.5	10.8	443	1 AM2A_ORYSA	P27935 oryza sativ
19	284.5	10.8	445	1 AMC2_ORYSA	P27941 oryza sativ
20	283	10.7	427	1 AMY2_HORVU	P04063 hordeum vul
21	282	10.7	368	1 AMY3_HORVU	P04747 hordeum vul
22	277.5	10.5	713	1 CDGU_BACCI	P43379 bacillus ci
23	272	10.3	713	1 CDGT_BACSP	P30921 bacillus sp
24	270	10.2	428	1 AMY1_ORYSA	P17654 oryza sativ
25	267.5	10.1	919	1 AMY_STRLL	Q05884 streptomyce
26	255	9.7	712	1 CDGT_BACS3	P09121 bacillus sp
27	253	9.6	718	1 CDGT_BACCI	P30920 bacillus ci
28	253	9.6	718	1 CDGT_BACSS	P31747 bacillus st
29	251	9.5	713	1 CDGT_BACS0	P05618 bacillus sp
30	246.5	9.3	581	1 AMY1_SCHPO	Q09840 schizosacch
31	245	9.3	719	1 AMYM_BACST	P19531 bacillus st
32	244.5	9.3	478	1 YQ29_SCHPO	P10429 schizosacch
33	244.5	9.3	528	1 AMY_BACCI	P08137 bacillus ci

ALIGNMENTS

RESULT 1

AMY_BACAM	AMY_BACAM	STANDARD;	PRT;	514 AA.
ID	AMY_BACAM			
AC	P00692;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan			
DE	Glucanohydrolase).			
OS	Bacillus amyloliquefaciens.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1390;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=IH;			
RX	MEDLINE=83108808; PubMed=6185474;			
RA	Takkinen K., Pettersson R.F., Kalkkinen N., Palva I., Soederlund H.,			
RA	Kaeerlaeinen L.;			
RT	"Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens			
RT	deduced from the nucleotide sequence of the cloned gene.";			
RL	J. Biol. Chem. 258:1007-1013(1983).			
RN	[2]			
RP	SEQUENCE OF 32-222.			
RX	MEDLINE=80241725; PubMed=6156671;			
RA	Chung H.S., Friedberg F.;			
RT	"Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-			
RT	amylase.";			
RL	Biochem. J. 185:387-395(1980).			
RN	[3]			
RP	SEQUENCE OF 1-96 FROM N.A.			
RX	MEDLINE=82051296; PubMed=6170539;			
RA	Palva I., Pettersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M.,			
RA	Soederlund H., Takkinen K., Kaeerlaeinen L.;			
RT	"Nucleotide sequence of the promoter and NH2-terminal signal peptide			
RT	region of the alpha-amylase gene from Bacillus amyloliquefaciens.";			
RL	Gene 15:43-51(1981).			
RN	[4]			
RP	SEQUENCE OF 1-39 FROM N.A.			
RX	MEDLINE=88137952; PubMed=2830166;			
RA	Ruchonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karaenen S.;			
RT	"Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by			
RT	its own signal peptide from Saccharomyces cerevisiae host cells.";			
RL	Gene 59:161-170(1987).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.			
RX	MEDLINE=20384196; PubMed=10924103;			
RA	Brzowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,			
RA	Stendesen A., Borchart T.V., Dauter Z., Wilson K.S., Davies G.J.;			
RT	"Structural analysis of a chimeric bacterial alpha-amylase.			
RT	High-resolution analysis of native and ligand complexes.";			
RL	Biochemistry 39:9099-9107(2000).			
CC	-I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic			
CC	linkages in oligosaccharides and polysaccharides.			
CC	-I- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.			
CC	-I- SUBUNIT: Monomer.			
CC	-I- SUBCELLULAR LOCATION: Secreted.			

P14014 bacillus li
Q9Y789 schizosacch
P26827 thermoanaer
P21567 saccharomyc
P14899 bacillus st
P14899 dictyoglomu
P80039 thermotoga
P10529 aspergillus
P25718 escherichia
O86956 thermotoga
P30292 aspergillus
Q02905 aspergillus


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FT METAL 233 233 CALCULUM 2.
Query Match 82.9%; Score 2187; DB 1; Length 512;
Best Local Similarity 80.5%; Pred. No. 2.5e-147;
Matches 389; Conservative 43; Mismatches 49; Indels 2; Gaps 1;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
DB 32 LNTGLMQYFEWYTPNDGQHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 91

QY 61 DLGEFQKGTVRTKYTKSELQDAIGLSHNSVGVYDVLNKHAGADATEDVTAVERN 120
DB 92 DLGEFQKGTVRTKYTKSELQDAIGLSHNSVGVYDVLNKHAGADATEDVTAVERN 151

QY 121 ANRQETSEBYQIKAWTDPRFPGRGNTYSDFKWHYHFDGADMDSESKIRIKFRGEGK 180
DB 152 ADNRNVISGEHRIKAWTHFPGRGNTYSDFKWHYHFDGADMDSESKIRIKFRGEGK 209

QY 181 AWDWEVSSENGYDILMYADVDPDHPDVAAETKKGWIYANELSLDGRIDAACHIKFSF 240
DB 210 AWDWEVSSENGYDILMYADVDPDHPDVAAETKKGWIYANELSLDGRIDAACHIKFSF 269

QY 241 LRDWVQAVROATGKEMFTVAEYMNAGKLENLYNKTSSNQSVDPDPLHFNLOAASQGG 300
DB 270 LRDWVHREKTKGEMFTVAEYMNAGKLENLYNKTSSNQSVDPDPLHFNLOAASQGG 329

QY 301 GYDMRLLDGTVVSRRHPEKAVTFVENHDTQPGSLESTVQTFKPLAYAFILTRSGYPQ 360
DB 330 GYDMRLLDGTVVSRRHPEKAVTFVENHDTQPGSLESTVQTFKPLAYAFILTRSGYPQ 389

QY 361 VFYGDYGTGTSKPEIPSLKDNIEPIKARKEYAYGQHDYIDHPDVIGTWREGSSAA 420
DB 390 VFYGDYGTGTSKPEIPSLKDNIEPIKARKEYAYGQHDYIDHPDVIGTWREGSSAA 449

QY 421 KSLGALALITDGPSSKMYAGLKNAGETWYDITGNRSDTVKIGDGCWGEFHNDSVSIY 480
DB 450 NSGLAALITDGPSSKMYAGLKNAGETWYDITGNRSDTVKIGDGCWGEFHNDSVSIY 509

QY 481 VQK 483
DB 510 VQR 512

RESULT 3
AMT6_BACS7 STANDARD; PRT; 518 AA.
AC P19571;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (G6-amyase)
OS Bacillus sp. (strain 707).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1416;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.
RX MEDLINE=88162814; PubMed=3258152;
RA Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
RT "Nucleotide sequence of the maltohexaoside-producing amyase gene from
RT an alkalophilic Bacillus sp. #707 and structural similarity to
RT liquefying type alpha-amyases."
RL Biochem. Biophys. Res. Commun. 151:25-31(1988).
CC -I- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
CC in amylaceous polysaccharides so as to remove successive
CC maltohexaoside residues from the non-reducing chain ends.
CC -I- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By
CC similarity).
CC -I- PATHWAY: Starch degradation.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC -----
CC EMBL; M18862; AAA22231.1; -.
CC PIR; A27705; A27705.
CC HSPP; P06278; LVJS.
CC InterPro; IPR006589; Alp_aml_cat_sub.
CC InterPro; IPR006047; Alpha_aml_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; alpha-amyLase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SM00642; Amy; 1.
CC Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.
CC SIGNAL 1 33
CC CHAIN 34 518 GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE.
CC ACT_SITE 269 269 BY SIMILARITY.
CC ACT_SITE 273 273 BY SIMILARITY.
CC ACT_SITE 366 366 BY SIMILARITY.
CC METAL 139 139 CALCIUM 1 (BY SIMILARITY).
CC METAL 196 196 CALCIUM 2 AND SODIUM (BY SIMILARITY).
CC METAL 219 219 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
CC SIMILARITY).
CC METAL 221 221 CALCIUM 2 AND SODIUM (BY SIMILARITY).
CC METAL 232 232 CALCIUM 1 AND SODIUM (BY SIMILARITY).
CC METAL 238 238 CALCIUM 1 AND SODIUM (BY SIMILARITY).
CC METAL 240 240 CALCIUM 2 (BY SIMILARITY).
CC METAL 242 242 CALCIUM 2 (BY SIMILARITY).
CC METAL 273 273 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
CC SIMILARITY).
CC SEQUENCE 518 AA; 59009 MW; 3A961E21612682C4 CRC64;

Query Match 69.6%; Score 1835; DB 1; Length 518;
Best Local Similarity 66.6%; Pred. No. 2e-122;
Matches 323; Conservative 63; Mismatches 91; Indels 8; Gaps 3;

QY 2 NGTLMQYFEWYTPNDGQHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 61
DB 39 NGTMMQYFEWYTPNDGQHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 98

QY 62 LGEFQKGTVRTKYTKSELQDAIGLSHNSVGVYDVLNKHAGADATEDVTAVERNPA 121
DB 99 LGEFQKGTVRTKYTKSELQDAIGLSHNSVGVYDVLNKHAGADATEDVTAVERNPA 158

QY 122 NRNQTSEBYQIKAWTDPRFPGRGNTYSDFKWHYHFDGADMDSESKIRIKFRGEGK 180
DB 159 NRNQTSEBYQIKAWTDPRFPGRGNTYSDFKWHYHFDGADMDSESKIRIKFRGEGK 218

QY 181 AWDWEVSSENGYDILMYADVDPDHPDVAAETKKGWIYANELSLDGRIDAACHIKFSF 240
DB 219 AWDWEVSSENGYDILMYADVDPDHPDVAAETKKGWIYANELSLDGRIDAACHIKFSF 278

QY 241 LRDWVQAVROATGKEMFTVAEYMNAGKLENLYNKTSSNQSVDPDPLHFNLOAASQGG 300
DB 279 LRDWVHREKTKGEMFTVAEYMNAGKLENLYNKTSSNQSVDPDPLHFNLOAASQGG 338

QY 301 GYDMRLLDGTVVSRRHPEKAVTFVENHDTQPGSLESTVQTFKPLAYAFILTRSGYPQ 360
DB 339 GYDMRLLDGTVVSRRHPEKAVTFVENHDTQPGSLESTVQTFKPLAYAFILTRSGYPQ 398

QY 361 VFYGDYGTGTSKPEIPSLKDNIEPIKARKEYAYGQHDYIDHPDVIGTWREGSSAA 420
DB 399 VFYGDYGTGTSKPEIPSLKDNIEPIKARKEYAYGQHDYIDHPDVIGTWREGSSAA 453

QY 419 AAKSGLAALITDGPSSKMYAGLKNAGETWYDITGNRSDTVKIGDGCWGEFHNDSVSIY 478
DB 454 AAKSGLAALITDGPSSKMYAGLKNAGETWYDITGNRSDTVKIGDGCWGEFHNDSVSIY 513

QY 479 IYVOK 483
DB 510 IYVQR 512

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Db 514 IWNK 518
RESULT 4
AMY_BACST STANDARD; PRT; 549 AA.
AC P06279; Q45519;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYS.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.
RX MEDLINE=85234394; PubMed=3924897;
RA Nakajima R., Imanaka T., Aiba S.;
RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase
RT gene."
RL J. Bacteriol. 163:401-406 (1985).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX STRAIN=DY5/PHI300;
RC MEDLINE=86008166; PubMed=3876333;
RA Ihara H., Sasaki T., Teuboi A., Yamagata H., Teukagoshi N., Uda S.;
RT "Complete nucleotide sequence of a thermophilic alpha-amylase gene:
RT homology between prokaryotic and eukaryotic alpha-amylases at the
RT active sites."
RL J. Biochem. 98:95-103 (1985).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NZ-3.
RX MEDLINE=86195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Requaet C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearothermophilus and Bacillus licheniformis."
RL J. Bacteriol. 166:635-643 (1986).
RN [4]
RP SEQUENCE FROM N.A.
RA Suominen I., Karp M., Lautamo J., Knowles J., Mantsaelae P.;
RT "Thermostable alpha amylase of Bacillus stearothermophilus: cloning,
RT expression, and secretion by Escherichia coli."
RL (In) Chaloupka J., Krumphanz V. (eds.);
RL Extracellular enzymes of microorganisms, pp.129-137, Plenum Press,
RL New York (1987).
RN [5]
RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.
RC STRAIN=DY-5;
RX MEDLINE=86059211; PubMed=2999073;
RA Teukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H.,
RA Idota Y., Yamagata H., Uda S.;
RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by
RT protein-producing Bacillus brevis 47 carrying the Bacillus
RT stearothermophilus amylase gene."
RL J. Bacteriol. 164:1182-1187 (1985).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=21125602; PubMed=11226887;
RA Svud D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;
RT "Crystal structure of Bacillus stearothermophilus alpha-amylase:
RT possible factors determining the thermostability."
RL J. Biochem. 129:461-468 (2001).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC -----
CC EMBL; M11450; AAA22235.2; -
CC EMBL; X02769; CAA26547.1; -
CC EMBL; M57457; AAA22227.1; -
CC EMBL; M13255; AAA22241.1; -
CC PIR; A24436; A24436.
CC PIR; A91999; ALBSF.
CC PDB; 1HVX; 05-AUG-03.
CC InterPro; IPR006589; Alp_aml cat sub.
CC InterPro; IPR006047; Alpha_aml cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; alpha-amylase; 1.
CC PRINTS; SM00110; ALPHAAMYLASE.
CC SMART; SM00642; Amy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 34
FT CHAIN 35 549
FT ACT_SITE 268 268
FT ACT_SITE 272 272
FT ACT_SITE 365 365
FT METAL 139 139
FT METAL 196 196
FT METAL 218 218
FT METAL 220 220
FT METAL 231 231
FT METAL 237 237
FT METAL 238 238
FT METAL 239 239
FT METAL 272 272
FT METAL 337 337
FT METAL 339 339
FT METAL 440 440
FT METAL 441 441
FT METAL 464 464
FT CONFLICT 13 13
FT CONFLICT 19 19
FT CONFLICT 23 23
FT CONFLICT 31 31
FT CONFLICT 107 107
FT CONFLICT 167 167
FT CONFLICT 179 179
FT CONFLICT 251 251
FT CONFLICT 260 260
FT CONFLICT 284 284
FT CONFLICT 312 312
FT CONFLICT 338 338
FT CONFLICT 342 342
FT CONFLICT 346 346
FT CONFLICT 376 376
FT CONFLICT 526 526
FT CONFLICT 527 527
FT CONFLICT 535 535
SQ SEQUENCE 549 AA; 62670 MW; 3A2DD93A955E79D3 CRC64;
Query Match 66.8%; Score 1763.5; DB 1; Length 549;
Best Local Similarity 65.2%; Pred. No. 2.5e-117;
Matches 315; Conservative 58; Mismatches 105; Indels 5; Gaps 2;
Oy 2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGTAVWIPAYKGLSQSDNGYGFYDLYD 61
Dy 39 NGTMMQYFEWYLPDDGTLTKVANEANNLSLIGITALWLPPAYKGTSDVGYGVYDLYD 98
Oy 62 LGFEQOQGTWRTKYGTGKSELDQDAGSLHSRNVQYGVVNLNHNKAGADATEDVTAVERNPA 121
Dy 99 LGFEQKQGAVRTKYGTQAYQLQAIQAHAAGMVOYADVDFDHKGAGDGTWDAVEVNP 158

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QY 122 NRNOETSEYQIKAWTDFFRPGNGNTYSDFKWHYHFDGADWDESKISRIKPFREGKA 181
Db 159 DRNOEISGTYQIQAWTKFPFPGNGNTYSSFKRWYHFDGVDWDESKRSRIYKPRGIGKA 218
QY 182 WMEVSSSENGNYDLYMYADVDYDHPDVAETKKGWIWYANELSLDGFRIIDAKHKKPSFL 241
Db 219 WMEVDTENGNYDLYMYADLDMDHPVVTTELKSGWKYVNTNIDGFRDLDAVKHKIKFSFF 278
QY 242 RDMVQAVROATKEMFTVAEYQWONAGKLENLTKTSFNQSVFDPVPLHFNLOAASSQGG 301
Db 279 PDLSDVRSQTKPLFTTGYEWSYDINKLHNYIMKTNGTMSLFDAPLHNFVTKASKG 338
QY 302 YDMRLLDGTVYSRUPEKAVTVEVNHDTOPGOSLESTVQTFKPLAYAFILTRBSGYPQV 361
Db 339 FDMRTLMTNTLMKDPTLATVFDVNDHTEPGALQSWDPMFKPLAYAFILTRBSGYPV 398
QY 362 FYGDMYGTGTSBK-BIPSLKDNIBPILKARKEYAYGPHDYIDHPDVIGWTRBGDSAA 420
Db 399 FYGDIYGI----PQYNIPSLKSDIPLLIARDYAYGQHDYLDHSDIIGWTRBGVTEKP 454
QY 421 KSLGALITDGGGSKRWYAGLKNAGETWYDITGNRSVTYVIGSDGWFPHVNDGVSIVY 480
Db 455 GSGLAALITDGGGSKRWYVYQKHAGKVFYDLTGNRSDTVTINSDBGWGFVKVSGSVW 514
QY 481 VQK 483
Db 515 VPR 517
RESULT 5
ID AMY2_SALTY
AC P26613; STANDARD; PRT; 494 AA.
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYA OR STM1963.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=SJW1103;
RC MEDLINE=93015717; PubMed=1400215;
RX Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RL "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
RN J. Bacteriol. 174:6644-6652(1992).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan B., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
RN [3]
RN SEQUENCE OF 1-6 FROM N.A.
RP STRAIN=SJW1103;
RC MEDLINE=92407478; PubMed=1527488;
RX Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RA "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes";
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [4]
RP SEQUENCE OF 476-494 FROM N.A.

RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIb, including a
RT large non-coding region.";
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC EMBL; L01643; AAA27110.1; -;
DR EMBL; AE008787; AAL20875.1; -;
DR EMBL; M85241; AAA27079.1; -;
DR EMBL; L13280; AAA1970.1; -;
DR PIR; B45738; B45738.
DR HSSP; P06278; 1VJS.
DR StyGene; SG10011; amyA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alp_amy1_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Complete proteome.
FT ACT_SITE 235 BY SIMILARITY.
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 332 332 BY SIMILARITY.
FT METAL 104 104 CALCIUM (BY SIMILARITY).
FT METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 462 462 L -> S (IN REF. 1).
SQ SEQUENCE 494 AA; 56522 MW; 5C1E862FEDD5847C CRC64;
Query Match 38.6%; Score 1017; DB 1; Length 494;
Best Local Similarity 41.3%; Pred. NO. 1.3e-64;
Matches 203; Conservative 76; Mismatches 198; Indels 14; Gaps 5;
QY 2 NCTLMQYFETWYTPNDGQHWKRLQNDALHSLDIGITAVWIPAYKGLSOSDN-GYCPYDLY 60
Db 3 NPTLLQYFHWYYPDGGKLUWSELAEADGLNDIGINMWLWLPACKGASGGYGVGYDYDLP 62
QY 61 DLGEFQKGTVRTKYTKSELQDAIGSLHSRNVOYGVVNLNKHAGADATEDVTAVEVNP 120
Db 63 DLGEFDQGTIATKYGDKRQLLTALDKKNIAVLLDVVNVHKGADKERRIVQVRVQ 122
QY 121 ANRNOETSEYQIKAWTDFFRPGNGNTYSDFKWHYHFDGADWDESKISRIKPFREG-- 178
Db 123 DDRTOIDNIIIECEGWTYTFPARAGQYSNFIMDYHCFSGIDHIENPDEDGIFKIVNDYT 182
QY 179 GKAMDWEYSSSENGNYDLYMYADVDYDHPDVAETKKGWIWYANELSLDGFRIIDAKHKKF 238
Db 183 GDGWNQVDDENGFDYLMGENIDFRNHAHVEEIKYARWVMEQTHCDGFRDLDAVKHHPA 242
QY 239 SFRLDWVQAVQATGKEMFTVAEYQWONAGKLENLTKTSFNQSVFDPVPLHFNLOAASSQ 298
Db 243 WYKXEWIEHVQAVAPKPLFVAEYWSHEVDKLTQYIDQVDGKTLFDPAPLQMKPFHASRQ 302
QY 299 GGGYDMRLLDGTVYSRUPEKAVTVEVNHDTOPGOSLESTVQTFKPLAYAFILTRBSG 358
Db 303 GAEDYMRHIFTGLIVEADPPFAVTLVANHDTQPLQALEAPVPEWPKFLAYAILLRENGV 362
QY 359 PQVIFYGDMYGTK-----GTSPEKIPSLKDNIEPTILKARKEYAYGPHDYIDHPDVIG 410

QY	409	IGWTRGDSAAKSLAALITDPGGSKRWYAGLKNAGETWYDITGNRSDTVKIGSDGWG	468
Db	420	IAFSGSTDEFF--PGCVVMSNGDDGEKTHLGENYGNKTRDFLGNRQERVVTDNGEA	477
QY	469	EFHVNDSGVSIVV	481
Db	478	TFPCNGSGSVWV	490

RESULT 7				
AM3A_ORYSA				
ID	AM3A_ORYSA	STANDARD;	PRT;	440 AA.
AC	P27932;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-			
DE	glucan glucanohydrolase).			
GN	AMY1.2 OR AMY3A.			
OS	Oryza sativa (Rice).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Ehrhartoideae; Oryzeae; Oryza.			
OX	NCBI_TaxID=4530;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. Japonica M202; TISSUE=Etiolated leaf;			
FX	MEDLINE=91329692; PubMed=1714318;			
RA	Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;			
RT	"Characterization of an alpha-amylase multigene cluster in rice.;"			
RL	Plant Mol. Biol. 16:579-591(1991).			
CC	!- FUNCTION: Important for breakdown of endosperm starch during			
CC	germination			
CC	!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic			
CC	linkages in oligosaccharides and polysaccharides.			
CC	!- COPACITOR: Binds 3 calcium ions per subunit (By similarity).			
CC	!- SUBUNIT: Monomer.			
CC	!- TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.			
CC	!- DEVELOPMENTAL STAGE: Expressed at a high level during germination			
CC	in the aleurones cells under the control of the plant hormone			
CC	gibberellic acid and in the developing grains at a low level.			
CC	!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swets Institute of Bioinformatics and the EMBL outstation			
CC	at the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announcement/			
CC	or send an email to license@sb-sib.ch).			
CC	-----			
CC	EMBL; X56336; CAA39776.1; --			
CC	PIR; S14958; S14958.			
DR	HSP; P04063; IAVA.			
DR	Gramene; P27932; --			
DR	InterPro; IPR006589; Alp_ami1_cat_sub.			
DR	InterPro; IPR006047; Alpha_ami1_cat.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Pfam; PF00128; alpha-amylase; 1.			
DR	PRINTS; PR00110; ALPHAMYLASE.			
DR	SMART; SM00642; Amy1; 1.			
KW	Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;			
KW	Signal; Multigene family.			
FT	SIGNAL	1	26	POTENTIAL.
FT	CHAIN	27	440	ALPHA-AMYLASE ISOZYME 3A.
FT	ACT_SITE	207	207	BY SIMILARITY.
FT	ACT_SITE	315	315	BY SIMILARITY.
FT	METAL	119	119	CALCIUM 1 (BY SIMILARITY).
FT	METAL	145	145	CALCIUM 2 (BY SIMILARITY).
FT	METAL	155	155	CALCIUM 3 (BY SIMILARITY).
FT	METAL	166	166	CALCIUM 3 (BY SIMILARITY).
FT	METAL	169	169	CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT				SIMILARITY)


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FT METAL 143 143 CALCIUM 2 (BY SIMILARITY).
FT METAL 153 153 CALCIUM 3 (BY SIMILARITY).
FT METAL 164 164 CALCIUM 3 (BY SIMILARITY).
FT METAL 167 167 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 168 168 CALCIUM 1 (BY SIMILARITY).
FT METAL 169 169 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 172 172 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 174 174 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 437 AA; 48637 MW; BD304250B40C7A8B CRC64;

Query Match 12.3%; Score 324; DB 1; Length 437;
Best Local Similarity 24.9%; Pred. No. 1.1e-15;
Matches 108; Conservative 56; Mismatches 140; Indels 130; Gaps 15;

QY 5 LMQYFEWTPNDQHWKR-LQNDAEHLSDIGTAWIPPAVKGLSOSDNGPGPYDLVDLG 63
Db 29 LFGFNWESWKKQGWYNFLSHVDYIAATGVTWVLP--PSHSVAPQGYMPGRLYDLD 86
QY 64 EFQGGTVRTKYTKGSELQDAIGLSHSRNVOYGVVNLNKHAGADATEDVTAVEVNPANR 123
Db 87 -----ASKYGTGAELSLIAAFHSKSIKCVADIVNHC----- 120
QY 124 NQETSEYQIKAWTDPRFPGRGNTYSDPKWHYHFDGADWDESKISRIKFRGEGKAWD 183
Db 121 -----ADYKDSRGYICFEFGTTPDSRLD 143
QY 184 W---EVSENGNY-----DYLMYADVDYDHPVVAETKKGIGWVANELSLDGR 229
Db 144 WGPDMICDDTYQNGRHRGTGADGAPDIDHLNTRVQTLSDLNWLKLVGDFDGR 203
QY 230 IDAAKHIFSLRDMVQAVRQATKEMFTVAEYQN-----NAGKLENYL 274
Db 204 LDFAGYSATVAKTYVDNTDPS-----FVVAEISWNMYDNGEPPSNQDGRQELVNW 258
QY 275 NKTSPNSQVFVPLHFNLAQASSGGVDMRRLDGT-----VVSHPKAVTFVFNHDT 329
Db 259 QAVGGPASAFDTTKGELORA-VQG---ELWRMKDNGKAPGMIGWLPKAVTFIDNHDT 314
QY 330 QPGQSLESTVOTWFKP-----LAVAFILTRSGYQVFGYDMGTGKTSKPEIPLSKDNI 384
Db 315 -----GSTQNSWFFPDKVMQRYAYILT-HPGVPCIFYDHFVDM-----NLKQEI 358
QY 385 EPILKARKEYAYGP 398
Db 359 STLAAVRSRGIHP 372

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RESULT 10

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ID AMYB PAEPO STANDARD; PRT; 1196 AA.
AC P21543;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Beta/alpha-amylase precursor [includes: Beta-amylase (EC 3.2.1.2);
Alpha-amylase (EC 3.2.1.1)].
OS Paenibacillus polymyxa (Bacillus polymyxa).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=1406;
RN [1]
SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=87165765; PubMed=2435707;
RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "Cloning and nucleotide sequence of the gene coding for enzymatically
RT active fragments of the Bacillus polymyxa beta-amylase.";
RL J. Bacteriol. 169:1564-1570(1987).
RN [2]
RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.

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RC STRAIN=72;
RX MEDLINE=89123046; PubMed=2464578;
RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "A single gene directs synthesis of a precursor protein with beta-
RT and alpha-amylase activities in Bacillus polymyxa.";
RL J. Bacteriol. 171:375-382(1989).
RN [3]
RP SEQUENCE OF 1-776 FROM N.A.
RC STRAIN=ATCC 8523;
RX MEDLINE=87231094; PubMed=2438660;
RA Rhodes C., Strasser J., Friedberg F.;
RT "Sequence of an active fragment of B. polymyxa beta amylase.";
RL Nucleic Acids Res. 15:3934-3934(1987).
RN [4]
RP DISULFIDE BOND AND MUTAGENESIS OF CYSTEINE RESIDUES.
RX MEDLINE=91215008; PubMed=1827035;
RA Uozumi N., Matsuoka T., Tsukagoshi N., Uda S.;
RT "Structural and functional roles of cysteine residues of Bacillus
RT polymyxa beta-amylase.";
RL Biochemistry 30:4594-4599(1991).
CC -I- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 Kda ALPHA-AMYLASE AFTER
CC SECRETION.
CC -I- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
CC polysaccharides so as to remove successive maltose units from the
CC non-reducing ends of the chains.
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: In the N-terminal section; belongs to family 14 of
CC glycosyl hydrolases.
CC -I- SIMILARITY: In the C-terminal section; belongs to family 13 of
CC glycosyl hydrolases.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M15817; AAA85446.1; -.
CC EMBL; Y00150; CAA68344.1; -.
CC FIR; A29130; A29130.
CC HSP; P36924; 1B9Z.
CC InterPro; IPR006589; Alp_amyl_cat_sub.
CC InterPro; IPR006048; Alpha_amyl_C.
CC InterPro; IPR006047; Alpha_amyl_cat.
CC InterPro; IPR005085; CBM 25.
CC InterPro; IPR006046; Glyco_hydro_13.
CC InterPro; IPR001554; Glyco_hydro_14.
CC Pfam; PF00128; alpha-amylase; 1.
CC Pfam; PF02806; alpha-amylase_C; 1.
CC Pfam; PF03423; CBM 25; 2.
CC Pfam; PF01373; Glyco_hydro_14; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC PRINTS; PR00750; BETAAMYLASE.
CC SMART; SM00642; Amy; 1.
CC SMART; SM00632; Amy; C; 1.
CC PROSITE; PS00506; BETA_AMYLASE 1; 1.
CC PROSITE; PS00679; BETA_AMYLASE 2; 1.
CC Multicatalytic enzyme; Hydrolase; Glycosidase; Signal;
KW Polysaccharide degradation; Repeat.
FT SIGNAL 1 35
FT CHAIN 36 1196 BETA/ALPHA-AMYLASE.
FT DOMAIN 36 454 BETA-AMYLASE.
FT REPEAT 455 558
FT REPEAT 565 668
FT DOMAIN 669 1196 ALPHA-AMYLASE.
FT DISULFID 118 126
FT ACT_SITE 198 198 BY SIMILARITY.

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FT ACT SITE 394 394 BY SIMILARITY.
FT MUTAGEN 118 118 C->S: 5-FOLD DECREASE IN ACTIVITY.
FT MUTAGEN 126 126 C->V: 20-FOLD DECREASE IN ACTIVITY.
FT MUTAGEN 358 358 C->S: 60-FOLD DECREASE IN ACTIVITY.
FT CONFLICT 1 1 M -> MGL (IN REF. 3).
FT CONFLICT 67 67 N -> S (IN REF. 3).
FT CONFLICT 100 100 N -> D (IN REF. 3).
FT CONFLICT 154 154 S -> N (IN REF. 3).
FT CONFLICT 177 177 E -> Q (IN REF. 3).
FT CONFLICT 227 228 NA -> KS (IN REF. 3).
FT CONFLICT 330 330 G -> S (IN REF. 3).
FT CONFLICT 425 425 N -> S (IN REF. 3).
FT CONFLICT 493 493 D -> A (IN REF. 3).
FT CONFLICT 532 532 S -> L (IN REF. 3).
FT CONFLICT 559 559 A -> T (IN REF. 3).
FT CONFLICT 665 665 A -> T (IN REF. 3).
FT CONFLICT 681 681 A -> N (IN REF. 3).
FT CONFLICT 686 686 T -> A (IN REF. 3).
FT CONFLICT 725 728 AFTS -> VFSP (IN REF. 3).
FT CONFLICT 736 736 N -> K (IN REF. 3).
FT CONFLICT 741 741 N -> S (IN REF. 3).
FT CONFLICT 758 758 S -> N (IN REF. 3).
SQ SEQUENCE 1196 AA; 130893 MW; A41EAGB70F257064 CRC64;

Query Match 12.2%; Score 323; DB 1; Length 1196;
Best Local Similarity 21.5%; Pred. No. 4.8e-15;
Matches 112; Conservative 82; Mismatches 162; Indels 164; Gaps 24;

Qy 10 EWTNPNGQHWKRLONDAEHLSDIGITAVMTPPAYKGLSQ-SDNGYGPYLDLGEFQOK 68
Db 779 KWH-----GGPQGIINKLDYIKNGFTAIWTPVMQSEVAYHYTYDFY----- 826
Qy 69 GTVTKYTKSGLQDAIGLSHRNVQVGVVLLNHKAGADATEDVTAVEVPANRNOETS 128
Db 827 -AVDGLGTMDKQLQELVKRAHKNAIAVWDVVVNHGT----- 862
Qy 129 BEYQKAWTDFRPGRGNTVSDP-KWTHYHPDG-----ADWDSRKISRIKFRGEGKAWD 183
Db 863 -----DFQ-PGNGFAKAPFDKADWYHNGDITDGDVNSNQ----- 897
Qy 184 WEYSENGNDYLMYADVDDHPDVAETKKGWYANELSLDGFRIIDAAKHIFSLRD 243
Db 898 WKI--ENG--DVAGLDLHNHPATANELKWKILNLTGIDGLRLDTVKHVPKGFLOD 953
Qy 244 WVOAVROATKEMPTAEYVWONNAGLENLYNLTSTFNQSVDFVPLHFNLOAASQGGGYD 303
Db 954 FDQAA-----NTTWGEIHEGDPAVYGDY---TRYLDAALDFPMYTIKDFV---GHDQS 1002
Qy 304 MRLLDGTVVSRRHPEKAVT---FVENHDT-----QPQSLESSTVQWFKPLAYAFI 351
Db 1003 MRKIKDRYSDDRYRDAQTNGVFIIDNHDVRFRLNDASGKPGANYDKWPQL---KAALGFT 1059
Qy 352 LTRESGYPOVPYGMGTGTSKPSKIEISLKNIEPILKARKEYAYGQHDYIDHPDVIGW 411
Db 1060 LT-SRGPIIYQGTQGYSG---GDDPANRENMN-----FNAHDLVQYIAKLYN 1105
Qy 412 TREGDSSAAKSLAALITDGGSGKRMVAGLKNAGETWYD-----ITGNRSSTVTKGS 464
Db 1106 VRNHPAL-----QNGSQR-----EKWVDSFSYFQSRKNGDEAIVFIN 1144
Qy 465 DGW-----GEF-----HVNDGSVSI 479
Db 1145 NSWNSTRTIGNFNDLSNGTRLTNLQNSDSVQINNGSITV 1184

RESULT 11
ID AM3B ORYSA STANDARD; PRT; 438 AA.
AC P27937;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
```

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DE glucanohydrolase).
GN AMY1.6 OR AMY3B.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amylase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Sutliff T.D., Huang N., Rodriguez R.L.;
RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Germinating seeds.
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurones cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56337; CAA39777.1; -.
DR EMBL; M24941; AAA33897.1; -.
DR PIR; S14957; S14957.
DR HSP; P04063; IAVA.
DR Gramene; P27937; -.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 438 ALPHA-AMYLASE ISOZYME 3B.
FT ACT_SITE 205 205 BY SIMILARITY.
FT ACT_SITE 313 313 BY SIMILARITY.
FT METAL 117 117 CALCIUM 1 (BY SIMILARITY).
FT METAL 134 134 CALCIUM 2 (BY SIMILARITY).
FT METAL 137 137 CALCIUM 2 (BY SIMILARITY).
FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
FT METAL 143 143 CALCIUM 3 (BY SIMILARITY).
FT METAL 153 153 CALCIUM 3 (BY SIMILARITY).
FT METAL 164 164 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 167 167 SIMILARITY).
FT METAL 168 168 CALCIUM 1 (BY SIMILARITY).
FT METAL 169 169 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 172 172 SIMILARITY).
FT METAL 174 174 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 174 174 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 438 AA; 48591 MW; B9DE0DBSABC63F9C CRC64;

Query Match 12.1%; Score 319; DB 1; Length 438;
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Best Local Similarity 24.5%; Pred. No. 2.6e-15;
Matches 108; Conservative 54; Mismatches 136; Indels 142; Gaps 16;

QY 5 LMQYFEWYTPNDGQHWR-----LQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPY 57
Db 29 LFQGFNW-----ESWKKQGGWYNFLGHVDDIAATGVTHWLP--PSHSVAPQGYMPG 80
QY 58 DLYDLGEFQKGTVRTKYTKSELQDAIGSLHSRNVQVGVVNLNKKAGADATEDVTA 117
Db 81 RLYDL-----ASKYGTGAELSLIAAFHSKGIKCVADIVNHC-----120
QY 118 VNPANRNETSEYQIKAWTDFFRPGRGNTYSDFKWHYHFDGADWDSRKRISRFKRG 177
Db 121 -----ADYKDSRGYCIPEGGT 137
QY 178 EKGAWD-----EVSSENGNY-----DYLMAVDYDHPDVVAETKKGWYANEL 223
Db 138 PDSRLDWPDMICSDDTYSNGRHRDTCADFGAPDIDLHNTVRVQTELSDLNWLKSDV 197
QY 224 SLDFRIDAAKHKFSFLRDWVQAVRQATGKEMFTVAEYQW-----NAG 268
Db 198 GFDGRLDFAKGYSAAVAKTYDNTDPS-----FVVAEWSNMYDGNBPSWQDGDQ 252
QY 269 KLENLNTKTSFNQSVDFPLHFNLOAASSQGGYDMRELLGT-----VVSRRHPEKAVTF 323
Db 253 ELVWQAQVGGPASAFDTTKGELQA-VQG---ELWRMKDGNKGKAPGMIGWLPEKAVTF 308
QY 324 VENHDTQPGQSLSTVQTFKP-----LAYAFILTRSGYPQVFGDMYKGTGTSPEIP 378
Db 309 IDNHDT-----GSTQNSWPPSPDKVMQGYAVILT-HPGVPCIFYDHFVDM-----352
QY 379 SIKONIEPILKARKEYAYGP 398
Db 353 LKQIEISTLAARSRNEIHP 372

RESULT 12
AM3D_ORYSA
ID AM3D_ORYSA STANDARD; PRT; 435 AA.
AC DT27933;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
DE AMY1.3 OR AMY3D.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Rhizophorales; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
RC MEDLINE=91088278; PubMed=2263460;
RA Huang N., Koizumi N., Reini S., Rodriguez R.L.;
RT "Structural organization and differential expression of rice alpha-
RT amylase genes."
RL Nucleic Acids Res. 18:7007-7014 (1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POS137).
RX MEDLINE=90318322; PubMed=2370848;
RA O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutliff T.D.,
RA Rodriguez R.L.;
RT "The alpha-amylase genes in Oryza sativa: characterization of cDNA
RT clones and mRNA expression during seed germination."
RL Mol. Gen. Genet. 221:235-244 (1990).
CC -1- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.

-!- TISSUE SPECIFICITY: Is expressed in all tissues, except in
immature seeds. Is the most abundant alpha-amylase isozyme in
callus.
-!- DEVELOPMENTAL STAGE: Expressed at a high level during germination
in the aleurones cells under the control of the plant hormone
gibberellic acid and in the developing grains at a low level.
-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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EMBL; M59351; AAA33895.1; -.
EMBL; M24287; AAA33886.1; -.
PIR; S12625; S12625.
HSP; P04063; IAVA.
Gramene; P27933; -.
InterPro; IPR006589; Alp_amy1_cat_sub.
InterPro; IPR006047; Alpha_amy1_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Amy1; 1.
Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
Signal; Multigene family.
SIGNAL 1 25
CHAIN 26 435
ACT_SITE 203 203
ACT_SITE 311 311
METAL 116 116
METAL 133 133
METAL 136 136
METAL 138 138
METAL 141 141
METAL 151 151
METAL 162 162
METAL 167 167
METAL 170 170
METAL 172 172
CONFLICT 73 74
CONFLICT 137 137
SEQUENCE 435 AA; 47911 MW; 1BBD6AB195BA0D6E CRC64;
Query Match 12.1%; Score 318; DB 1; Length 435;
Best Local Similarity 28.0%; Pred. No. 3e-15;
Matches 111; Conservative 42; Mismatches 134; Indels 110; Gaps 17;

QY 5 LMQYFEWYTPNDGQHWR-----LQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPY 57
Db 28 LFQGFNW-----ESWKKQGGWYNFLKHQVDDIAKAGVTHWLP--PSHSVAPQGYMPG 79
QY 58 DLYDLGEFQKGTVRTKYTKSELQDAIGSLHSRNVQVGVVNLNKKAG--ADATEDVTA 115
Db 80 RLYDL-----ASKYGTGAELSLIAAFHKGVCQVADVNVNHRCAEKDARGVYCV 131
QY 116 VNPANRNETSEYQIKAWTDFFRPGRGNTYSDFKWHYHFDGADWDSRKRISRFK 175
Db 132 FEGGTFDLR-----NGPGMICSDDTQYSDGTCH-----RD 162
QY 176 RGEKAWDWEVSSSENGVDYLMYADVDYDHPDVVAETKKGWYANELSDGFRIDAAKH 235
Db 163 TCEG-----FGAAPDIDLHNPVRQELTDLNWLKSDVDFGFWLDFAKG 207
QY 236 IKFGLRDWQAVQATGKEMFTVAEYQW-----NNAG-----LENYLNKTSFN 280
Db 208 YSTDIKMYVESC-----KPGFVVAEIVNSLSYNGDGKPAANQDQGRQLVNWVNVGGP 262

```

QY 281 QSVDFVPLHFNLAQASSGGYDMRRLLDGT-----VVSRRPERKAVTFVENHDTQPGQSL 335
DB 263 AMTFDTTKGLQ-AGVQ---ELWRLRDGNGKAPGMIGLWLPKAVTFVDNHD----- 312
QY 336 ESTVOTWFKP-----LAYAFILTRSGYQVQVYGYDMY 367
DB 313 GSTOKLWFFPSDKVMQGYAYILT-HPGVPCIFYDHMF 348

RESULT 13
AM3E_ORYSA
ID _AM3E_ORYSA STANDARD; PRT; 437 AA.
AC P27934;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase isozyme 3E precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase).
GN AMY1.4 OR AMY3E.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=cv. Japonica M202; TISSUE=Etisolated leaf;
RX MEDLINE=91088278; PubMed=2263460;
RA Huang N., Koizumi N., Reil S., Rodriguez R.L.;
RT "Structural organization and differential expression of rice alpha-
RT amylase genes";
RL Nucleic Acids Res. 18:7007-7014(1990).
CC -!- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- TISSUE SPECIFICITY: More abundant in germinating seeds than in
CC young roots, young leaves and callus.
CC -!- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurones cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; M59352; AAA33896.1; -;
DR PIR; J00946; J00946.
DR HSP; P04063; LAVA.
DR Gramene; P27934;
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 25
FT CHAIN 26 437
FT ACT_SITE 204 204
FT ACT_SITE 312 312
FT METAL 116 116
FT METAL 133 133
FT METAL 136 136
FT METAL 138 138
FT POTENTIAL.
FT CHAIN 26 437
FT ACT_SITE 204 204
FT ACT_SITE 312 312
FT METAL 116 116
FT METAL 133 133
FT METAL 136 136
FT METAL 138 138
FT ALPHA-AMYLASE ISOZYME 3E.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT CALCIUM 1 (BY SIMILARITY).
FT CALCIUM 2 (BY SIMILARITY).
FT CALCIUM 2 (BY SIMILARITY).
FT CALCIUM 2 (BY SIMILARITY).

FT METAL 142 142 CALCIUM 2 (BY SIMILARITY).
FT METAL 152 152 CALCIUM 3 (BY SIMILARITY).
FT METAL 163 163 CALCIUM 3 (BY SIMILARITY).
FT METAL 166 166 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 168 168 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 171 171 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 173 173 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 437 AA; 48707 MW; C0E8276CCEA16602 CRC64;
Query Match 12.0%; Score 315.5; DB 1; Length 437;
Best Local Similarity 24.9%; Pred. No. 4.5e-15;
Matches 122; Conservative 54; Mismatches 146; Indels 167; Gaps 21;
QY 5 LMQVFEWYTPNDGQHKKR-----LQDAEHLSDIGITAVWIPPPAYKGLSQSDNGVGPY 57
DB 28 LFOGFNW-----ESMRKQGGWYNFLHEKVEEIASTGATHWLPF--PSHSVSPQGMGP 79
QY 58 DLYDLGFEQKGTVRTKYTKSELODAIGSLHSRNVQVGVVVLNKHAGADATEDVTAVE 117
DB 80 RLYDL-----ASKYGEAEELKSLIEAFHDKNVECLADIVNHR----- 119
QY 118 VNPANRQETSEYQIKAWTDFRPPGRGNTYSDFKWHYHFDGADWDESRRISRFKRG 177
DB 120 -----ADYKDSRGVYCVFEGGT 136
QY 178 EGRADW-----EVSENGNYD-----YLMYADVDYDHPDVVAETKKWGIWYANEL 223
DB 137 PDGLRDGPMICSDDTQYNGRGRDGTAGFGAAPDIDLHLPVQBELTDWLNWLRDLD 196
QY 224 SLDFGRIDAARKHKFSLRDWQAVROATGKEMFTVAEYQW-----NNAGK----- 269
DB 197 GFDGWRDLDFAGYSAPLARIYVDNTNP-----FVGEIWSLLIYNGDKRSTNQDADQ 251
QY 270 -LENYLNTKTSFNOSVDFVPLHFNLAQASSGGYDMRRLLDGT-----VVSRRPERKAVTF 323
DB 252 ELVNWVEGVGKPTAFDFTTKGILQAA-VQG---ELWRLHDGNGKAPGLMGWMDQAVTF 307
QY 324 VENHDTQPGQSLSTVOTWFKP-----LAYAFILTRSGYQVQVYGYDMYTKGTSKPEIP 378
DB 308 VDNDHTGSTQSL-----WPFPSDKVMQGYAYILT-HPGVPCIFYDHVF--DMNLQHEIA 358
QY 379 SL-----KDNIEPILKARKEY-----AYGPHD-----YIDH-P 406
DB 359 TLAIRSRNGIHAEESTDLILKAEGDIYVAMIDGKVIKLGPRYDAGGIIPSDFFVVAHGN 418
QY 407 DVGWTRREG 415
DB 419 DYCVMKEG 427

RESULT 14
AM33 WHEAT
ID _AM33 WHEAT STANDARD; PRT; 413 AA.
AC P0817;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase AMY3 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase).
GN AMY1.1 OR ALPHA-AMY3.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Chinese Spring;
RA Baulcombe D.C., Huttly A.K., Martienssen R.A., Barker R.F.,
RA Jarvis M.G.;


```
FT ACT_SITE 204 204 BY SIMILARITY.
FT ACT_SITE 229 229 BY SIMILARITY.
FT ACT_SITE 315 315 BY SIMILARITY.
FT METAL 116 116 CALCIUM 1 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 136 136 CALCIUM 2 (BY SIMILARITY).
FT METAL 138 138 CALCIUM 2 (BY SIMILARITY).
FT METAL 142 142 CALCIUM 2 (BY SIMILARITY).
FT METAL 152 152 CALCIUM 3 (BY SIMILARITY).
FT METAL 163 163 CALCIUM 3 (BY SIMILARITY).
FT METAL 166 166 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 167 167 CALCIUM 1 (BY SIMILARITY).
FT METAL 168 168 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 171 171 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 173 173 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 438 AA; 47796 MW; 2393FDAC51E80F51 CRC64;

Query Match 11.7%; Score 307.5; DB 1; Length 438;
Best Local Similarity 25.2%; Pred. No. 1.7e-14;
Matches 110; Conservative 51; Mismatches 131; Indels 145; Gaps 18;

Qy 5 LMQYFEWYTNDCQHWKR-----LQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPY 57
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
28 LFQGFNN-----ESWQSGGWYNNMMGVDDIAAGVTHWLP--PSHSVSNEGYMPG 79
Qy 58 DLVDLGEFQKGTVRTKYTKYKSELODAIGLSHSRNQVYGDVVLNKKAGADATEDVTAVE 117
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
80 RLVDID-----ASKYGAELKSLIGALHGKGVQVQAIADIVNHR----- 119
Qy 118 VNPANRNQETSEYQIKAWTDFFPPGRGNTYSDFKWHYHFDGADWDESRKISRIFKFRG 177
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
120 -----ADYKDSRCIYCFEGGT 136
Qy 178 EGRKAWD-----EVSENGY-----DYLMYADVDPVDPVAVETKKWGIWYANEL 223
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
137 SDGRLDWGPIMICRDDTKYSDGTANLDTGADFAAAPDIDLNDRVQRELKWLILWKSDDL 196
Qy 224 SLGDFRIDAAKHIFSLRDWVQVQVQATGKEMFTVAEYQNNNA-----GK----- 269
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
197 GFDAWRLDFARGYSPENAKVYIDGTSPS-----LAVAEVMDNMATGGDKPNYDQDAHRQ 251
Qy 270 -LENYLNKTSFNOS---VFDVPLHFNLOAASSQGGGYDMRRLDGT-----VVSRRHPEKA 320
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
252 NLVNWVDKVGGAASAGWVFDTTKGILNAA-VEG---ELWRLIDPQKAPGVGWWPAXA 307
Qy 321 VTFVENHDTQPGQSLSTVQWFKP-----LAYAFILTRBSGYQVYFQVGYDMYGTGTSPK 375
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
308 ATFVDNHT-----GSTQAMWPFPSDKVMQGYAYILT-HPGIPCFYDFHFFNW----- 354
Qy 376 EIPSLKDNIEPILKARK 392
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
355 ---GFKDQIAALVAIRK 368
```

Search completed: October 7, 2004, 00:13:23
Job time : 9.47121 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.3093 Seconds
(without alignments)
3290.816 Million cells updates/sec

Title: US-09-925-576C-10
Perfect score: 2638
Sequence: 1 VNGTLMQYFEWYTPNDGQHW.....SDGWGEFHVNDGVSIVYQK 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2071	78.5	519	2 Q9RQT8	Q9RQT8 cytophaga s
2	1957	74.2	513	16 Q81A84	Q81A84 bacillus ce
3	1957	74.2	533	2 Q9AQ54	Q9AQ54 bacillus me
4	1924	72.9	513	16 Q81YJ4	Q81YJ4 bacillus an
5	1842	69.8	516	2 Q82839	Q82839 bacillus sp
6	1772.5	67.2	549	2 Q31193	Q31193 bacillus st
7	1771.5	67.2	549	2 Q9KWY6	Q9KWY6 bacillus st
8	1767.5	67.0	521	2 P71034	P71034 bacillus sp
9	1757.5	66.6	613	2 Q59222	Q59222 bacillus sp
10	1619.5	61.4	501	2 Q93148	Q93148 bacillus sp
11	1478.5	56.0	507	16 Q87HG6	Q87HG6 vibrio para
12	1369	51.9	481	16 Q89YF1	Q89YF1 bacteroides
13	1253	47.5	493	2 Q03657	Q03657 bacillus ci
14	1217	46.1	484	16 Q97Q49	Q97Q49 streptococc
15	1214.5	46.0	486	16 Q8D708	Q8D708 streptococc
16	1214.5	46.0	488	16 Q8E696	Q8E696 streptococc

17	1214.5	46.0	488	16 Q8E0M2	Q8E0M2 streptococc
18	1212	45.9	484	16 Q8DPC8	Q8DPC8 streptococc
19	1206	45.7	492	16 Q8YU21	Q8YU21 anabaena sp
20	1193.5	45.2	484	2 O50583	O50583 streptococc
21	1191.5	45.2	486	2 O68875	O68875 streptococc
22	1180.5	44.7	485	2 Q53786	Q53786 streptococc
23	1136	43.1	491	16 Q9CG59	Q9CG59 lactococcus
24	1061.5	40.2	529	3 Q877B1	Q877B1 aspergillus
25	1054	40.0	506	16 Q8U916	Q8U916 agrobacteri
26	1010	38.3	494	16 Q8Z5S5	Q8Z5S5 salmonella
27	1004	38.1	495	16 Q8FGL8	Q8FGL8 escherichia
28	1003	38.0	495	16 Q8XBB6	Q8XBB6 escherichia
29	993	37.6	495	16 Q7UAB0	Q7UAB0 shigella fl
30	991	37.6	495	16 Q83R40	Q83R40 shigella fl
31	496	18.8	469	1 O50200	O50200 thermococcu
32	494.5	18.7	461	1 Q8NKR5	Q8NKR5 thermococcu
33	483	18.3	457	1 Q93647	Q93647 thermococcu
34	480.5	18.2	461	1 Q33476	Q33476 pyrococcus
35	476.5	18.1	460	1 Q9P9L0	Q9P9L0 pyrococcus
36	476.5	18.1	460	1 O08452	O08452 pyrococcus
37	476.5	18.1	461	1 Q8NKR4	Q8NKR4 thermococcu
38	476.5	18.1	473	17 Q8U3I9	Q8U3I9 pyrococcus
39	464.5	17.6	432	14 Q8JZK3	Q8JZK3 uncultured
40	351.5	13.3	826	10 Q9CAR6	Q9CAR6 arabidopsis
41	351.5	13.3	887	10 Q94A41	Q94A41 arabidopsis
42	334.5	12.7	906	10 Q8LQK4	Q8LQK4 oryza sativ
43	326	12.4	420	10 Q9ZP43	Q9ZP43 phaseolus v
44	324.5	12.3	421	10 Q7X9T1	Q7X9T1 phaseolus a
45	322	12.2	416	10 Q8LJQ6	Q8LJQ6 musa acumin

ALIGNMENTS

RESULT 1

Q9RQT8 ID Q9RQT8 PRELIMINARY; PRT; 519 AA.
AC Q9RQT8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Raw starch digesting amylase precursor.
OS Cytophaga sp.
OC Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
OC Flexibacteraceae; Cytophaga.
OX NCBI_TaxID=29535;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeang C.L., Chen L.S., Chen M.Y.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067653; AAF00567.1; -
DR HSSP; P06278; IVJS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW SIGNAL.
FT SIGNAL
FT CHAIN 1 57 POTENTIAL.
FT SIGNAL 58 519 RAW STARCH DIGESTING AMYLASE.
SQ SEQUENCE 519 AA; 58337 MW; 3E6B88A4DF98B163 CRC64;

Query Match 78.5%; Score 2071; DB 2; Length 519;

Best local Similarity 75.3%; Pred. No. 2.1e-134;

Matches 363; Conservative 49; Mismatches 70; Indels 0; Gaps 0;

Qy 2 NGTLMQYFEWYTPNDGQHWKRLQNDGHLSDIGITAVWIPPAYKGLSQSDNGYGPYLYD 61

Db 38 NGTMMQYFEWYTPNDGQWRLRTPAYKGLSQSDNGYGPYLYD 97

QY 62 LGFEQKGTVRTKYGKSELODAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 121
DB 98 LGFEQKGTVRTKYGKSELODAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 157
QY 122 NRNQETSEYQIKAWTDFFRPPGRGNTYSDFKWHWHYHFDGADWDSRKRIFKFRGEGKA 181
DB 158 NRNQETSEYQIKAWTDFFRPPGRGNTYSDFKWHWHYHFDGADWDSRKRIFKFRGEGKA 217
QY 182 WDEVESSSENGNYDYLMAVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFKSF 241
DB 218 WDEVESSSENGNYDYLMAVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFKSF 277
QY 242 RDMQVAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLOAASSOGGG 301
DB 278 RDMQVAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLOAASSOGGG 337
QY 302 YDMRLLDGTVVSRRHPEKAVTFVFNHDTQPGQSLSTVQTFKPLAYAFILTRSSGYPQV 361
DB 338 YDMRLLDGTVVSRRHPEKAVTFVFNHDTQPGQSLSTVQTFKPLAYAFILTRSSGYPQV 397
QY 362 FYGDMYGTGTSPEIPSLKDNIEPILKARKEYAYGPOHDIYDHPDVIGWTRGDSAAK 421
DB 398 FYGDMYGTGTSPEIPSLKDNIEPILKARKEYAYGPOHDIYDHPDVIGWTRGDSAAK 457
QY 422 SGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEHFNDSVYIV 481
DB 458 SGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEHFNDSVYIV 517
QY 482 QK 483
DB 518 QQ 519

RESULT 2

ID Q81AS4 PRELIMINARY; PRT; 513 AA.
AC Q81AS4;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Glucan 1,4-alpha-maltohexaosidase (EC 3.2.1.98).
GN BC3482.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haeckel R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyripides N.,
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis".
RL Nature 423:87-91(2003).
DR EMBL; AEO17009; AAPI041.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BFF9FF6 CRC64;

Query Match 74.2%; Score 1957; DB 16; Length 513;
Best Local Similarity 71.8%; Pred. No. 1.5e-126;
Matches 346; Conservative 48; Mismatches 88; Indels 0; Gaps 0;

QY 2 NGTLMQYFEWYTPNDGQHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 61
DB 52 NGTLMQYFEWYTPNDGQHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 111
QY 62 LGFEQKGTVRTKYGKSELODAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 121

DB 32 NGTLMQYFEWYTPNDGQHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 91
QY 62 LGFEQKGTVRTKYGKSELODAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 121
DB 92 LGFEQKGTVRTKYGKSELODAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 151
QY 122 NRNQETSEYQIKAWTDFFRPPGRGNTYSDFKWHWHYHFDGADWDSRKRIFKFRGEGKA 181
DB 152 NRNQETSEYQIKAWTDFFRPPGRGNTYSDFKWHWHYHFDGADWDSRKRIFKFRGEGKA 211
QY 182 WDEVESSSENGNYDYLMAVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFKSF 241
DB 212 WDEVESSSENGNYDYLMAVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFKSF 271
QY 242 RDMQVAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLOAASSOGGG 301
DB 272 RDMQVAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLOAASSOGGG 331
QY 302 YDMRLLDGTVVSRRHPEKAVTFVFNHDTQPGQSLSTVQTFKPLAYAFILTRSSGYPQV 361
DB 332 YDMRLLDGTVVSRRHPEKAVTFVFNHDTQPGQSLSTVQTFKPLAYAFILTRSSGYPQV 391
QY 362 FYGDMYGTGTSPEIPSLKDNIEPILKARKEYAYGPOHDIYDHPDVIGWTRGDSAAK 421
DB 392 FYGDMYGTGTSPEIPSLKDNIEPILKARKEYAYGPOHDIYDHPDVIGWTRGDSAAK 451
QY 422 SGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEHFNDSVYIV 481
DB 452 SGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEHFNDSVYIV 511
QY 482 QK 483
DB 512 QQ 513

RESULT 3

ID Q9AQ54 PRELIMINARY; PRT; 533 AA.
AC Q9AQ54;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Alpha-amylase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.,
RT "Cloning of maltopentaose-producing amylase from Bacillus megaterium
RT KSM B-404".
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220440; AAK00598.1; -.
DR HSP; P06278; 1VJ3.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

Query Match 74.2%; Score 1957; DB 2; Length 533;
Best Local Similarity 72.0%; Pred. No. 1.6e-156;
Matches 347; Conservative 45; Mismatches 90; Indels 0; Gaps 0;

QY 2 NGTLMQYFEWYTPNDGQHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 61
DB 52 NGTLMQYFEWYTPNDGQHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 111
QY 62 LGFEQKGTVRTKYGKSELODAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 121

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Db 112 LGFENQKGTVRTKYGKTAQLKSAIDALHKKNIIDVYGDVNVNHHKGGADYTTTAVTAVEVDPS 171
QY 122 NRNQETSEBYQIKAWTDTRFPGRGNTYSDFKWHTYHFDGADWDSRKRISIKFRGREGKA 181
Db 172 NRNVESGDVEISAWTGFNPFGRGDSYSNFKWYHFDGTDWDEGRKLNRIYKFRGIGKA 231
QY 182 WDEVSSENGNYDLYMAYDVYDHPDVVAETKKWGIWYANELSJDGFRIDAAXHIKPSFL 241
Db 232 WDEVSSENGNYDLYMAYDVYDHPDVVAETKKWGIWYANELSJDGFRIDAAXHIKPSFL 291
QY 242 RDWQVAVRQATGKEMFTVAEYQWNNACKLENLYNKTSPNQSVDVPLHFNLAQASSQGG 301
Db 292 RDWVNVHQGTGKEMFTVAEYQWNNACKLENLYNKTSPNQSVDVPLHFNLAQASSQGG 351
QY 302 YDMRRLDGTWVSRRHPEKAVTFVENHDTQPGQSLSTVQWTFKPLAYAFILTRREGSQA 361
Db 352 YDMRRLDGTWVSRRHPEKAVTFVENHDTQPGQSLSTVQWTFKPLAYAFILTRREGSQA 411
QY 362 FYGDMYGTGKTSPEIKSLKONTIEPILKARKEVAYGQHDYIDHPDVIGWTRREGSQA 421
Db 412 FYGDMYGTGKTSPEIKSLKONTIEPILKARKEVAYGQHDYIDHPDVIGWTRREGSQA 471
QY 422 SGLAALITDGGGSKMYAGLKNAGETWYDITGNRSSTVTKIGSDGGEFFHNDGSVIYV 481
Db 472 SGLAALITDGGGSKMYAGLKNAGETWYDITGNRSSTVTKIGSDGGEFFHNDGSVIYV 531
QY 482 QK 483
Db 532 QR 533

RESULT 4
Q81YJ4 ID Q81YJ4 PRELIMINARY; PRT; 513 AA.
AC Q81YJ4
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN AMYS OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasee N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ostad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Niemman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86 (2003).
DR EMBL; AE017035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; Alp_amyl_cat_sub.
DR SMART; SM00642; alpha-amylase; 1.
KW Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

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Query Match 72.9%; Score 1924; DB 16; Length 513;
 Best Local Similarity 70.7%; Pred. No. 2.8e-124;

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Matches 341; Conservative 48; Mismatches 93; Indels 0; Gaps 0;
QY 2 NGTLMQYFEWYTPNDGQHKRLQNDABHLSDIGITAVIPPAYKGLSQSNGYGPYDLYD 61
Db 32 NGTLMQYFEWYAPSDRNHNRLRTDAENLAQKIGTSWIPPAYKGTQNDVGYCAYDLYD 91
QY 62 LGFQOKGTVRTKYGKSELODAIGSIHSRNVOYGDVNLHKKAGADATDVTAVEVNP 121
Db 92 LGFQOKGTVRTKYGKSELODAIGSIHSRNVOYGDVNLHKKAGADATDVTAVEVNP 151
QY 122 NRNQETSEBYQIKAWTDTRFPGRGNTYSDFKWHTYHFDGADWDSRKRISIKFRGREGKA 181
Db 152 NRNVESGDVEISAWTGFNPFGRGDSYSNFKWYHFDGTDWDEGRKLNRIYKFRGIGKA 211
QY 182 WDEVSSENGNYDLYMAYDVYDHPDVVAETKKWGIWYANELSJDGFRIDAAXHIKPSFL 241
Db 212 WDEVSSENGNYDLYMAYDVYDHPDVVAETKKWGIWYANELSJDGFRIDAAXHIKPSFL 271
QY 242 RDWQVAVRQATGKEMFTVAEYQWNNACKLENLYNKTSPNQSVDVPLHFNLAQASSQGG 301
Db 272 RDWVNVHQGTGKEMFTVAEYQWNNACKLENLYNKTSPNQSVDVPLHFNLAQASSQGG 331
QY 302 YDMRRLDGTWVSRRHPEKAVTFVENHDTQPGQSLSTVQWTFKPLAYAFILTRREGSQA 361
Db 332 YDMRRLDGTWVSRRHPEKAVTFVENHDTQPGQSLSTVQWTFKPLAYAFILTRREGSQA 391
QY 362 FYGDMYGTGKTSPEIKSLKONTIEPILKARKEVAYGQHDYIDHPDVIGWTRREGSQA 421
Db 392 FYGDMYGTGKTSPEIKSLKONTIEPILKARKEVAYGQHDYIDHPDVIGWTRREGSQA 451
QY 422 SGLAALITDGGGSKMYAGLKNAGETWYDITGNRSSTVTKIGSDGGEFFHNDGSVIYV 481
Db 452 SGLAALITDGGGSKMYAGLKNAGETWYDITGNRSSTVTKIGSDGGEFFHNDGSVIYV 511
QY 482 QK 483
Db 512 QQ 513

RESULT 5
O82839 ID O82839 PRELIMINARY; PRT; 516 AA.
AC O82839
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-1378;
RX MEDLINE=98342096; PubMed=9675143;
RA Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,
RA Ozaki K., Ito S.;
RT "Improved thermostability of a Bacillus alpha-amylase by deletion of
RT an arginine-glycine residue is caused by enhanced calcium binding.";
RL Biochem. Biophys. Res. Commun. 248:372-377 (1998).
DR EMBL; AB008763; BAA32431.1; -.
DR HSPB; P62778; IVD5.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

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Query Match 69.8%; Score 1842; DB 2; Length 516;
 Best Local Similarity 66.8%; Pred. No. 1.3e-118;

Matches	324;	Conservative	67;	Mismatches	86;	Indels	8;	Gaps	3;
QY	2	NCTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPAYAKGLSDMGYGYFDLYD	61						
Db	37	NCTMMQYFEWHLPLNDGNHNRLRDDAANLKSIGITAVWIPPAWKGTQNDVGYGAYDLYD	96						
QY	62	LGEFOOKGTVRKYTKTSELQDAIGLSHSRNVQVYGDVVLNHHKAGADATEDVTAVENPA	121						
Db	97	LGEFNQKGTVRKYTKYTRQLQGAVTSLKNGGIQVYGDVVMNHHKGGADGTEMVNAFEVNR	156						
QY	122	NRNQTSBEYQIKAWTDFFRFGCRGNTYDGFKWHYHFDGADWDERSKI-SRIKFRGEGK	180						
Db	157	NRNQISGEYITAEWTKDFPGRGNTHSNFKRWYHFDGTDWDSRQLQNKLIYFRGTGK	216						
QY	181	AWDWEVSSENGYDLYMAYDVYDHPDVVAETKKGWIYANELSLDQFRIDAAKHIKFSF	240						
Db	217	AWDWEVDIENGNDYLYMAYADTDMOHPEVINELRNWGVYVYTTLLDQFRIDAVAKHIKYS	276						
QY	241	LRDWQVQVRQATGKEMFTVAEYVQWQNAKLENYLNKTSFNQSVFDPVPLHNLQAASSQGG	300						
Db	277	TRDMLTHVRNTGKPMFAVAFKNDLAAIENYLNKTSWNHSVFDPVPLHNLNYSNMSG	336						
QY	301	GYDMRRLDGVTVSRHPKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAIFLTRESGYQP	360						
Db	337	YFDMRNLINGSVVOKHPITHAVTFVDNHDSPQGEALSFVQSWFKPLAYAILLTREQGYPS	396						
QY	361	VFYGDWVG--TKGTSPEIKPSLKNIEPILKARKEYAGQHDYIDHPDVIWGTREGDSS	418						
Db	397	VFYGDYGIPTG-----VPSMKSKIDPLQARQYAYAGTQHDYFDHHDIIIGWTREGDSS	451						
QY	419	AAKSGLAALITDGGGSKRMYAGLKNAGETWYDITGNRSDTVKISGDGSGEHHVNDGSVS	478						
Db	452	HPNSGLATIMSDGPGGNKMYVGKHAGQVWRDITGNRSRTVTINADGWNFTVNGGAVS	511						
QY	479	IYVOK 483							
Db	512	VWVAK 516							
RESULT	6								
ID	O31193	PRELIMINARY;	PRT;	549	AA.				
AC	O31193,								
DT	01-JAN-1998	(TrEMBLrel. 05, Created)							
DT	01-JAN-1998	(TrEMBLrel. 05, Last sequence update)							
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)							
DE	Alpha amylase.								
GN	AMI.								
OS	Bacillus stearothermophilus.								
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.								
OX	NCBI_TaxID=1422;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=ATCC 31195;								
RL	da Silva A.C.R., Fernandes E., Pueyo M.T.;								
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.								
DR	EMBL: AF032864; AAB86961.1; -								
DR	P1R: A54541; A54541.								
DR	HGSP; P06278; IJVS.								
DR	GO: GO:0004556; F:alpha-amylase activity; IEA.								
DR	GO: GO:0005375; P:carbohydrate metabolism; IEA.								
DR	InterPro: IPR006047; Alpha amyl cat.								
DR	InterPro: IPR006589; Alp amyl cat sub.								
DR	InterPro: IPR006046; Glyco_hydro_13.								
DR	Pfam: PF00128; alpha-amylase; 1.								
DR	PRINTS; P00110; ALPHAAMYLASE.								
DR	SMART; SM00642; Aamy; 1.								
SQ	SEQUENCE 549 AA; 62651 MW; 2CA689BEDACC4D262 CRC64;								

QY	2	NGTLMQYFEWYTPNDGQWHRKLQNDGAHLSIDIGITAVTPIPPAYKGLGSQSDMGNGYGPYDLYD	61
Db	39	NGTMMQYFEWYLPDGTLTWKVANEANLSSLGITALMLPPAYKGTSRSDYGYGYDLYD	98
QY	62	LGEFQOKGTVRTKYGKTSKSELDGAISLHSGNVOYQTDVVLNHKAGADATDVTAVENPA	121
Db	99	LGEFQOKGTVRTKYGKTSKSELDGAISLHSGNVOYQTDVVLNHKAGADATDVTAVENPA	155
QY	122	NRNQTSEBYQIKAWTDFRPRGRGNTYSDFKWHWHYFDGADWDSRKISRIKFRGSGKA	181
Db	159	DRNQEIISTGVIQIQAWTKFDPPRGNTYSSFKRWTHFDGVDWDSRKLSRIYKFRGIGKA	218
QY	192	WDNEVSSNGNYDLYMYADVVDYDHPDVAETKKGWGIWYANELSLDGFRIDAARKHKSFL	241
Db	219	WDNEVDTENGNYDLYMYADLDMDHPVETLKNWGWVNTTNDGFRDLDAVKHKFSFF	276
QY	242	RDWVOAQRQATGKEMFTVAEYEQNNAGKLENLYNKTSSFNQSVDFVPLHFNLOAASSOGGG	301
Db	279	PDWLUSYVRSQTGKPLFTVGEYWSYDINKLUHNYITNTGMSLDFAPLHNKFPYTASKGGGA	338
QY	302	YDMRRLDGTGVVSRHPEKAVTFFVENHDTQPGQSLESTVQTWFKPLAYAFILITRESGYPOV	361
Db	339	FDMRTLMTNLMDKQPTLAVTFVDNHDTEPQALQSWDPMFKPLAYAFILITRQEGYPCV	398
QY	362	FYGDMYGKTSKSPK-BIPSLKNIIEPILKARKEYAYGQHDYIDHPDVGWTRGDSAA	420
Db	399	FYGDYGI-----PQYNIPSLKSIDPELLTARRDAYGQTDYLDHSDIIGWTRGVTKEP	454
QY	421	KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSPTVKIGSDGGEHFVNDGVSIIY	480
Db	455	GSGLAALITDGPQGSKMYVGVQHGAGKVFYDLTGNSDVTVTINSNGGEFVNGGVSIVW	514
QY	481	VQK 483	
Db	515	VPR 517	
RESULT 7			
Q9KWY6	AC	Q9KWY6 PRELIMINARY; PRT; 549 AA.	
AC	Q9KWY6		
DT	01-OCT-2000	(TrEMBLrel. 15, Created)	
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Alpha-amylase (EC 3.2.1.1).		
OS	Bacillus stearothermophilus.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.		
OX	NCBI_TaxID=1422;		
FP	[1]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=US100;		
EA	Bejar S.;		
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; Y17557; CAB93517.1; -.		
DR	PIR; A54541; A54541.		
DR	HSP; P06278; 1VJ5.		
DR	GO; GO:0004556; P:alpha-amylase activity; IEA.		
DR	GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	InterPro; IPR006047; Alpha_amy1_cat.		
DR	InterPro; IPR006589; Alp_amy1_cat_sub.		
DR	InterPro; IPR006046; Glyco_hydro_I3.		
DR	Pfam; PF00128; alpha-amylase; 1.		
DR	PRINTS; PR00110; ALPHAMYLASE.		
DR	SMART; SM00642; Amy; 1.		
DR	Glycosidase; Hydrolase.		
QW	SEQUENCE 549 AA; 62582 MW; 8DA3B66DF9120BCE CRC64;		

Query Match 67.2%; Score 1771.5; DB 2; Length 549;
Best Local Similarity 65.4%; Pred. No. 9.9e-114;
Matches 316; Conservative 58; Mismatches 104; Indels 5; Gaps 2

QY 2 NGTLMQYFEWTTDNGDQHWKRLQNDABHLSDIGITAWTPPYKGLSDNDCGYPDYLDY 61

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Db 39 NGTMOQFEWYLPDDGLTWTKVANEANLSSGLITLWLPAYKTSRSDVGVGYDLYD 98
QY 62 LGSEFOQKGTVRTKYGTSELDQDAIGSLHSRNVOYGVVNLHKGADATEDVTAVERNPA 121
Db 99 LGSEFOQKGTVRTKYGTSELDQDAIGSLHSRNVOYGVVNLHKGADATEDVTAVERNPA 158
QY 122 NRQETSEBYOIKAWTDFFRPPGRGNTYSDPKWYHFDGADWDDESRIKISIFKPERGEGA 181
Db 159 DRNQETSGTYOIQAWTKFDFPPGRGNTYSSPKWYHFDGADWDDESRIKISIFKPERGEGA 218
QY 182 WDNVESSNGNDYLYMADVDYDHPDVAETKKGWYANLSDGFRIDAAGHIFKFSPL 241
Db 219 WDNVEVTENGNDYLYMADVDYDHPDVAETKKGWYANLSDGFRIDAAGHIFKFSPL 278
QY 242 RDWQAVRQATGKEMFTVAEYQNNAGKLENLYNKTSFNQSVDFVPLHFNLAASSQGGG 301
Db 279 PDWLSYVRSQTKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNFYFTASKSGGA 338
QY 302 YDMRRLDGTVSRHPEKAVTFVENHDTOPQOSLESTVQWTFKPLAYAFILITRESGYPOV 361
Db 339 FDMRTLTMTLMDQPTLAVTFVDNHDTEPQALQSWVDWPFKPLAYAFILITRQEGYPCV 398
QY 362 FYGDMYTKGTSPK-EIPSLKDNIEPLTKARKEYAYGPOHDYIDHDPDVGWTRGDSAA 420
Db 399 FYGDIYGI-----POYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGVTTEKP 454
QY 421 KSGLAALITDPGCGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGVSIVY 480
Db 455 GSGLAALITDPGCGSKMYVKGQHAGKVFDYLTGNRSDTVTITSDGWEFHVNDGVSIVW 514
QY 481 VQK 483
Db 515 VPR 517

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RESULT 8

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ID P71034 PRELIMINARY; PRT; 521 AA.
AC AC Q59222
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase precursor.
OS Bacillus sp. MK 716.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=54116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MK 716;
RA Sidhu G.S., Chakrabarti T.;
RT "Molecular cloning and expression of the gene encoding for
thermostable alpha-amylase of a thermophilic bacterial isolate.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75445; AAB18785.1; -.
DR HSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 521 AA; 59311 MW; 5612A88596D922E1 CRC64;

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Query Match 67.0%; Score 1767.5; DB 2; Length 521;
 Best Local Similarity 65.2%; Pred. No. 1.7e-113;
 Matches 315; Conservative 58; Mismatches 105; Indels 5; Gaps 2;

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QY 2 NGTMOQFEWYLPDDGLTWTKVANEANLSDGFRIDAAGHIFKFSPL 61
Db 39 NGTMOQFEWYLPDDGLTWTKVANEANLSSGLITLWLPAYKTSRSDVGVGYDLYD 98
QY 62 LGSEFOQKGTVRTKYGTSELDQDAIGSLHSRNVOYGVVNLHKGADATEDVTAVERNPA 121
Db 99 LGSEFOQKGTVRTKYGTSELDQDAIGSLHSRNVOYGVVNLHKGADATEDVTAVERNPA 158
QY 122 NRQETSEBYOIKAWTDFFRPPGRGNTYSDPKWYHFDGADWDDESRIKISIFKPERGEGA 181
Db 159 DRNQETSGTYOIQAWTKFDFPPGRGNTYSSPKWYHFDGADWDDESRIKISIFKPERGEGA 218
QY 182 WDNVESSNGNDYLYMADVDYDHPDVAETKKGWYANLSDGFRIDAAGHIFKFSPL 241
Db 219 WDNVEVTENGNDYLYMADVDYDHPDVAETKKGWYANLSDGFRIDAAGHIFKFSPL 278
QY 242 RDWQAVRQATGKEMFTVAEYQNNAGKLENLYNKTSFNQSVDFVPLHFNLAASSQGGG 301
Db 279 PDWLSYVRSQTKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNFYFTASKSGGA 338
QY 302 YDMRRLDGTVSRHPEKAVTFVENHDTOPQOSLESTVQWTFKPLAYAFILITRESGYPOV 361
Db 339 FDMRTLTMTLMDQPTLAVTFVDNHDTEPQALQSWVDWPFKPLAYAFILITRQEGYPCV 398
QY 362 FYGDMYTKGTSPK-EIPSLKDNIEPLTKARKEYAYGPOHDYIDHDPDVGWTRGDSAA 420
Db 399 FYGDIYGI-----POYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGVTTEKP 454
QY 421 KSGLAALITDPGCGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGVSIVY 480
Db 455 GSGLAALITDPGCGSKMYVKGQHAGKVFDYLTGNRSDTVTITSDGWEFHVNDGVSIVW 514
QY 481 VQK 483
Db 515 VPR 517

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RESULT 9

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ID Q59222 PRELIMINARY; PRT; 613 AA.
AC AC Q59222;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase [EC 3.2.2.1].
OS Bacillus sp. TS-23.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=38441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TS-23;
RA Lin L.-L., Chu W.S., Hsu W.H.;
RT Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RL EMBL; U22045; AAA63900.1; -.
DR HSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0008477; F:purine nucleosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF00686; CBM_20; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR PRODOM; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 613 AA; 69537 MW; 14684A30FC2895E8 CRC64;

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Query Match 66.6%; Score 1757.5; DB 2; Length 613;

Db 86 DLGEFDQKGTIRTKYGTQKDELKMKIDELHKYHIAVYLDVNLNHHKAGDGFTEKPMVVEVDPK 145
QY 121 ANRNETSEEEYQIKAWTDFFRPPGNGTYSDPKWHYHFDGADWDSRKTIRIFKFRGEGKA 180
Db 146 DNRNIELGDKW-LEAWVEFPNGRNDKYSNPHWTYHFDGVDWDAGKKAIFKFRGEGK 204
QY 181 ADWEVSSSENGNYDYLMDYADVDYDHPDVVAETKKGWYIYANELSLDGFRIIDAAKHIFSF 240
Db 205 ADWEVSSSENGNYDYLMDYADVDYDHPDVVAETKKGWYIYANELSLDGFRIIDAAKHIFSF 264
QY 241 LRWVQAVROATGKEMFTVAEYQWQNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 300
Db 265 LQEWIDHLRWKTKLEFTVGEYWNVDYVNLHNFITKTSGMSLFDAPLHNFNFYASKSGG 324
QY 301 GYDMLRLDGTWVSRHPEKAVTFVENHDTQPGQSLSTVQWTFKPLAYAFITLTRESGYPQ 360
Db 325 NYDMRQIMNGTLMKDNPKVAVTLVENHDTQPGQSLSTVQWTFKPLAYAFITLTRESGYPQ 384
QY 361 VFYDGYGTGK-----GTSPEIKDNTPEILKARKEYAYGQPHDYIDHPDVIGWTR 414
Db 385 VFYDGYGTGK-----GTSPEIKDNTPEILKARKEYAYGQPHDYIDHPDVIGWTR 440
QY 415 GDSAAKSGLAALITDGGSGKRYAGLKNAGETWYDITGNRSPTVKIGSDGWGEFHVND 474
Db 441 GDAEHFNS-NAVIMSDGPGGTGKMYTG--KPSTRYVDKLGIRTEVWTDANGMAEFVNG 497
QY 475 GSVSIYV 481
Db 498 GSVSVVW 504

RESULT 12

Q89YPI PRELIMINARY; PRT; 481 AA.
AC Q89YPI
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase precursor.
GN B74690.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VPI-5482 / ATCC 29148;
RC MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
DR EMBL; AE016946; AA079795.1; .
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EE1A CRC64;

Query Match 51.9%; Score 1369; DB 16; Length 481;
Best Local Similarity 51.0%; Pred. No. 4.4e-86;
Matches 246; Conservative 83; Mismatches 149; Indels 4; Gaps 2;
QY 2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSNGYGYDLYD 61
Db 3 NGVMQYFEWHLNDGKLMQIKEDALHLDIGITAVWIPPAYKADQDEGYATYDLYD 62
QY 62 LGFEQKGTVRTKYGTSKELQDAIGSLHSRNQVQYGVNHNHKGADATEDVTAVEVNP 121

Db 63 LGFEQKGTIRTKYGTQKDELKMKIDELHKYHIAVYLDVNLNHHKAGDGFTEKPMVVEVDPK 122
QY 122 NRNETSEEEYQIKAWTDFFRPPGNGTYSDPKWHYHFDGADWDSRKTIRIFKFRGEGKA 181
Db 123 ERYKALGEPFEIQGTGTSFHRKXKHSDFKWHYHFDGADWDSRKTIRIFKFRGEGKA 182
QY 182 WDWEVSSSENGNYDYLMDYADVDYDHPDVVAETKKGWYIYANELSLDGFRIIDAAKHIFSF 241
Db 183 WSEGVDSSENGNYDYLMDYADVDYDHPDVVAETKKGWYIYANELSLDGFRIIDAAKHIFSF 242
QY 242 RDWVQAVROATGKEMFTVAEYQWQNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 301
Db 243 AQFLDAVRSRGNDFYAVGEYWNVDYVNLHNFITKTSGMSLFDAPLHNFNFYASKSGG 302
QY 302 YDMLRLDGTWVSRHPEKAVTFVENHDTQPGQSLSTVQWTFKPLAYAFITLTRESGYPQ 361
Db 303 YDMLRLDGTWVSRHPEKAVTFVENHDTQPGQSLSTVQWTFKPLAYAFITLTRESGYPQ 362
QY 362 FYDGYGTGKSPKEIPSLKDNTEPILKARKEYAYGQPHDYIDHPDVIGWTRGDSAAK 421
Db 363 FYDGYGTGKSPKEIPSLKDNTEPILKARKEYAYGQPHDYIDHPDVIGWTRGDSAAK 421
QY 422 SGLAALITDGGSGKRYAGLKNAGETWYDITGNRSPTVKIGSDGWGEFHVNDGSIYV 481
Db 419 SGLVFLMSNDEAGSKIMSLGKHKGEVWHEITGTSISEITLDEEGNGEFSVESRNLA 478
QY 482 QK 483
Db 479 KK 480

RESULT 13

Q03657 PRELIMINARY; PRT; 493 AA.
AC Q03657
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
GN AMYE.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RA Marcel T.;
RL Nucleic Acids Res. 0:0-0(0).
DR EMBL; X60779; CAA43194.1; .
DR PIR; S15713; S15713.
DR HSP; P06278; IVS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_I3.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 493 AA; 56537 MW; FECCD2F805BB4694 CRC64;

Query Match 47.5%; Score 1253; DB 2; Length 493;
Best Local Similarity 47.2%; Pred. No. 4.5e-78;
Matches 226; Conservative 74; Mismatches 177; Indels 2; Gaps 1;
QY 2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSNGYGYDLYD 61
Db 4 NHTMQYFEWHLNADGQHWKRLAEAPELAKAGIDTAVWPPVYKVAEDTGYGYDLYD 63
QY 62 LGFEQKGTVRTKYGTSKELQDAIGSLHSRNQVQYGVNHNHKGADATEDVTAVEVNP 121
Db 64 LGFEQKGTVRTKYGTSKELQDAIGSLHSRNQVQYGVNHNHKGADATEDVTAVEVNP 123
QY 122 NRNETSEEEYQIKAWTDFFRPPGNGTYSDPKWHYHFDGADWDSRKTIRIFKFRGEGKA 181


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Db 124 DRTKEISEPPEIGWTKFTFPGRGDQYSSFKWNSHFNGFDFDARBEERTGVFRIAGENKK 183
QY 182 WDNEVSSSENGNYDLYMADVDYDHPDVVAETKKWGIWYANELSLDGFRIIDAAKHIFSFL 241
Db 184 WNNVDDDFNGYDLYMFANIDYDHPDVVRREMDWGKWLIDTLCGGFRDLAIKIHNEFI 243
QY 242 RDWQVAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLAQASSQGGG 301
Db 244 KEFAAEAMIRKRGQDFYIVGFWNSLNDACREFLDVDYQIDLFDVSLHYKLEASLGRD 303
QY 302 YDMRRLDGTVSRHPEKATVFVNHDTQPGQSLSTVQWTFPPLAYAFILITRESGYPQV 361
Db 304 FDLISKIFDDTLVQTHPTAVTFVDNHDSPHEALESWIGDFKPSAYALTLLRDGYPV 363
QY 362 FYGDMYGTGTSPEKIPSLKDNTEPILKARKEYAGPQHDYIDHPDVIGWTRGDSAAK 421
Db 364 FYGDIYIGIG--PEPDGKKEIIDLISARCNKAYGEQEDYFPHANTIGWRGVREEIG 421
QY 422 SGLAALITDGPFGSKRMVAGLNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSVSIY 480
Db 422 SGCAVVISNGDDGKRMFGEHRAGEVWDLTKSCDDQITIEEDGWATFHVCGGVSVW 480

RESULT 14
Q97Q49 PRELIMINARY; PRT; 484 AA.
AC Q97Q49;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase.
GN SP1382.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzaple E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Lofcus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RL Science 293:498-506(2001).
DR ENBL; AE007435; AAK75480.1; -.
DR PIR; G95160; G95160.
DR TIGR; SP1382; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.
KW Complete proteome.
SQ SEQUENCE 484 AA; 55918 MW; 4E90A450A90EFB8C CRC64;
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Best Local Similarity 47.0%; Pred. No. 1.3e-75;
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QY 2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIPPAKYGLSQSDNGYGPVDLYD 61
Db 3 NQTLMQYFEWYLPDGGQHWKRLAENAPHLAHLGSHVWMPFAPKATNEKDVIGVTDLFD 62
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QY 62 LGEFQOKGTVRTKYTKSELQDAIGSLHNRNVQVYGVVNLNHKAGADATDVTAVEVNP 121
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QY 122 NRNQETSEYQIKAWTDFPFGRGWYSDPKWHVHFDGADWDESKISRIKFRGEGKA 181
Db 123 DRTVELGEPFTINGWTSFTFDGRQDTYNGFHHWHYHFTGTDYDAKRSKSGIYLIQDNKG 182
QY 182 WQWE--VSSSENGNYDLYMADVDYDHPDVVAETKKWGIWYANELSLDGFRIIDAAKHIFS 239
Db 183 WANEELVDNENGYDLYMADLDKHEPVIQNIYDADWFMETTVGAFRLDAVKHIDSF 242
QY 240 FIRDWQVAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLAQASSQG 299
Db 243 FMRNFTRDMKEKYGDDFYVGFGEFNPDKKANLDYLEKTEHEHFDLVVRLHQNLFASQAG 302
QY 300 GGYDMRRLDGTVSRHPEKATVFVNHDTQPGQSLSTVQWTFKPLAYAFILITRESGYP 359
Db 303 ANYDLRGIFDLSLVELUKPKAVTFVDNHDTRQGALESTVEEFKPAAYALILLRQGLP 362
QY 360 QVFGDMYGTGTSPEKIPSLKDNTEPILKARKEYAGPQHDYIDHPDVIGWTRGDSAA 419
Db 363 CVFYGDYIGISQYAGQ--DFKEILLDRLLAIRKOLAYGEQNDYFDHANCIGWYRSGAEN- 419
QY 420 AKSGLAALITDGPFGSKRMVAGLNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSVSI 479
Db 420 -QSPVAVLISNDQENSKSMFVGQEWNTQTFVLLGNHQGVTTIDEEGYGQFPVSARSVS 478
QY 480 Y 480
Db 479 W 479

RESULT 15
Q8DT08 PRELIMINARY; PRT; 486 AA.
AC Q8DT08;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Intracellular alpha-amylase (EC 3.2.1.1).
GN AMYA OR SMU.1590.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT pathogen."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
DR ENBL; AB014990; AAN59233.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Aamy; 1.
KW Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 486 AA; 56457 MW; EF482B92FB37C4D8 CRC64;
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Best Local Similarity 44.6%; Pred. No. 2e-75;
Matches 216; Conservative 88; Mismatches 175; Indels 5; Gaps 3;

QY 2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIPPAKYGLSQSDNGYGPVDLYD 61
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Db 63 LGFENQGTVRTKYGSREDYLNVALKEQEIMPISDIVLNHKGAKERFQVVKVNP 122
Qy 122 NRQETSEYQIKAWTDPRFGRGNTYSDFKWHYHFDGADWDSRKISIFKFRGEGKA 181
Db 123 NRQEKISEPYEIEGTQFNFPGRQDNYSDFKWHYHFTGVYDALHNENGIYMLGDNKG 182
Qy 182 W--DWEYSSNGNYDYLWYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKS 239
Db 183 WASQENIDQNGNYDYLWYDDIDFKHPEVQEHLDWVAFLETSGVGGRDLDAIKHDKT 242
Qy 240 FLRDWQAVQATCKEMFTVAEYQNNAGKLENYLNKTSFNQSVFDPVPLHFNQAASSQG 299
Db 243 FMAQFIRYIIEHLKADLYVFEYWKDSHFDTIDLHSDVDLQFDLIDVNLHMSLEACQKG 302
Qy 300 GGYDMRLLDGTVVSRRHPEKAVTFVENHDTQPQGSLESTVQTFKPLAYAFILTRSGYP 359
Db 303 SDFDLSTILDDSLMKSHDPFAVTFVDNHDQRQALESTVAENFKPLAYGLILRQEGIP 362
Qy 360 QVFGDMYKTSKPKEIPSLKONIEPILKARKEYAYGPQHDYIDHDPDVTGWTREGDSSA 419
Db 363 CVFYGDYIGISGEPAQE--SFQTVLDKLLYIRQYHVYGSQEDYFDYANCIGWTCIGDEE- 419
Qy 420 AKSGLAALITDGGGSKRMVAGLKNAGETWVDITGNESDVTYKIGSDGWBGFHNDGVSII 479
Db 420 HPDGVAVIISNGEANCRRMMNGEFNRNKFVDYLYLNCTTEVILDDQGWGDFPVQEAISLA 479
Qy 480 YVQK 483
Db 480 WVNK 483
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:12:34 ; Search time 14.9658 Seconds
(without alignments)
1666.155 Million cell updates/sec

Title: US-09-925-576C-10
Perfect score: 2638
Sequence: 1 VNGTLMQYFEWYTPNDGQHW.....SDGWBGFHNDGVSIVYQK 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2638	100.0	483	4	US-09-291-023A-16
2	2638	100.0	483	4	US-09-537-168-6
3	2638	100.0	483	4	US-09-381-687-6
4	2638	100.0	483	4	US-09-540-715A-16
5	2638	100.0	514	1	US-08-720-899-4
6	2638	100.0	514	1	US-08-459-610-4
7	2638	100.0	514	2	US-08-343-804-4
8	2638	100.0	514	2	US-08-687-399-4
9	2638	100.0	514	2	US-08-600-908A-4
10	2638	100.0	514	3	US-08-683-838A-4
11	2638	100.0	514	3	US-09-264-097-4
12	2638	100.0	514	4	US-09-636-252A-4
13	2638	100.0	520	1	US-08-468-700-36
14	2638	100.0	520	1	US-08-645-971-4
15	2638	100.0	520	2	US-08-468-220-34
16	2638	100.0	520	2	US-08-468-698-34
17	2638	100.0	520	2	US-08-704-706A-36
18	2638	100.0	520	3	US-08-890-383-5
19	2638	100.0	520	3	US-08-914-679A-5
20	2638	100.0	520	3	US-08-985-659-37
21	2638	100.0	520	3	US-08-194-664A-34
22	2638	100.0	520	5	PCT-US94-01553A-34
23	2638	100.0	520	5	PCT-US95-10426-34
24	2624	99.5	480	3	US-09-182-859-4
25	2624	99.5	480	3	US-09-170-670-5
26	2624	99.5	480	3	US-09-193-068-5
27	2624	99.5	480	3	US-09-183-412-5

ALIGNMENTS

RESULT 1

US-09-291-023A-16
; Sequence 16, Application US/09291023A

; Patent No. 6309871

; GENERAL INFORMATION:

; APPLICANT: Outtrup, Helle

; APPLICANT: Borchert, Torben

; APPLICANT: Nielsen, Bjarne

; APPLICANT: Nielsen, Vibeke

; APPLICANT: Hoeck, Lisbeth

; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A

; FILE OF INVENTION: Encoding Same

; FILE REFERENCE: 5821.010-US

; CURRENT APPLICATION NUMBER: US/09/291,023A

; CURRENT FILING DATE: 1999-04-13

; PRIOR APPLICATION NUMBER: DK 1999 00438

; PRIOR FILING DATE: 1999-03-31

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 16

; LENGTH: 483

; TYPE: PRT

; ORGANISM: Bacillus

US-09-291-023A-16

Query Match 100.0%; Score 2638; DB 4; Length 483;

Best Local Similarity 100.0%; Pred. No. 2.1e-231;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVTWIPPAKGLSQSDNGVGPYDLY 60

Qy 61 DLGEFQKQGVTRKYGTGKSELODAIGSLHSERNVQVTVGVVNLNKHAGADATEDVTAVEVNP 120

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Db 301 GYDMRLLDGTVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILITRESGYPQ 360
Qy 361 VFYGDYMGTKGTSPEKPSLKNIEPILKARKEYAYGPOHDYIDHPDVIWGTREGDSSAA 420
Db 361 VFYGDYMGTKGTSPEKPSLKNIEPILKARKEYAYGPOHDYIDHPDVIWGTREGDSSAA 420
Qy 421 KSLAALITDGPGRKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
Db 421 KSLAALITDGPGRKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
Qy 481 VQK 483
Db 481 VQK 483

RESULT 2
US-09-537-168-6
; Sequence 6, Application US/09537168
; Patent No. 6410295
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/09/537,168
; CURRENT FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: PA 1999 00437
; EARLIER FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: 60/127,427
; EARLIER FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-09-537-168-6
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Query Match 100.0%; Score 2638; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.1e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Qy 61 DLGEFQOQGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
Db 61 DLGEFQOQGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
Qy 121 ANRNQETSEEVQIKAWTDFFPGRGNTYSDPKWHWHFDGADWDESRKISRIFKPRGEGK 180
Db 121 ANRNQETSEEVQIKAWTDFFPGRGNTYSDPKWHWHFDGADWDESRKISRIFKPRGEGK 180
Qy 181 AWDWEVSSNGNYDLYMADVVDYDHPDVVAETKKGWIWYANELSLDGRIDAAKHIKFSF 240
Db 181 AWDWEVSSNGNYDLYMADVVDYDHPDVVAETKKGWIWYANELSLDGRIDAAKHIKFSF 240
Qy 241 LRDWVQAVRQATGKEMFTVAEYQNNAGKLENLYNKTSFNQSVDFVPLHFNLAQASSQGG 300
Db 241 LRDWVQAVRQATGKEMFTVAEYQNNAGKLENLYNKTSFNQSVDFVPLHFNLAQASSQGG 300
Qy 301 GYDMRLLDGTVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILITRESGYPQ 360
Db 301 GYDMRLLDGTVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILITRESGYPQ 360
Qy 361 VFYGDYMGTKGTSPEKPSLKNIEPILKARKEYAYGPOHDYIDHPDVIWGTREGDSSAA 420
Db 361 VFYGDYMGTKGTSPEKPSLKNIEPILKARKEYAYGPOHDYIDHPDVIWGTREGDSSAA 420
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Qy 421 KSLAALITDGPGRKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
Db 421 KSLAALITDGPGRKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
Qy 481 VQK 483
Db 481 VQK 483

RESULT 3
US-09-381-687-6
; Sequence 6, Application US/09381687
; Patent No. 6486113
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yuji
; APPLICANT: IKAWA, Kaori
; APPLICANT: ITO, Susumu
; APPLICANT: IGARASHI, Kazuaki
; APPLICANT: HAGIHARA, Hiroshi
; APPLICANT: HAYASHI, Yasuhiro
; APPLICANT: ABAKI, Hiroyuki
; APPLICANT: OZAKI, Katsuya
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
; FILE REFERENCE: 2173-0115P
; CURRENT APPLICATION NUMBER: US/09/381,687
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 483
; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
US-09-381-687-6
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Query Match 100.0%; Score 2638; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.1e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Qy 61 DLGEFQOQGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
Db 61 DLGEFQOQGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
Qy 121 ANRNQETSEEVQIKAWTDFFPGRGNTYSDPKWHWHFDGADWDESRKISRIFKPRGEGK 180
Db 121 ANRNQETSEEVQIKAWTDFFPGRGNTYSDPKWHWHFDGADWDESRKISRIFKPRGEGK 180
Qy 181 AWDWEVSSNGNYDLYMADVVDYDHPDVVAETKKGWIWYANELSLDGRIDAAKHIKFSF 240
Db 181 AWDWEVSSNGNYDLYMADVVDYDHPDVVAETKKGWIWYANELSLDGRIDAAKHIKFSF 240
Qy 241 LRDWVQAVRQATGKEMFTVAEYQNNAGKLENLYNKTSFNQSVDFVPLHFNLAQASSQGG 300
Db 241 LRDWVQAVRQATGKEMFTVAEYQNNAGKLENLYNKTSFNQSVDFVPLHFNLAQASSQGG 300
Qy 301 GYDMRLLDGTVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILITRESGYPQ 360
Db 301 GYDMRLLDGTVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILITRESGYPQ 360
Qy 361 VFYGDYMGTKGTSPEKPSLKNIEPILKARKEYAYGPOHDYIDHPDVIWGTREGDSSAA 420
Db 361 VFYGDYMGTKGTSPEKPSLKNIEPILKARKEYAYGPOHDYIDHPDVIWGTREGDSSAA 420
Qy 421 KSLAALITDGPGRKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
Db 421 KSLAALITDGPGRKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
Qy 481 VQK 483
Db 481 VQK 483
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Db 481 VQK 483

RESULT 4

US-09-540-715A-16
; Sequence 16, Application US/09540715A

; Patent No. 6623948

; GENERAL INFORMATION:

; APPLICANT: Outtrup, Helle

; APPLICANT: Borchart, Torben

; APPLICANT: Nielsen, Bjarne

; APPLICANT: Nielsen, Vibeke

; APPLICANT: Hoeck, Lisbeth

; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A

; FILE REFERENCE: 5821.010-US

; CURRENT APPLICATION NUMBER: US/09/540,715A

; CURRENT FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/291,023

; PRIOR FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 16

; LENGTH: 483

; TYPE: PRT

; ORGANISM: Bacillus

US-09-540-715A-16

Query Match 100.0%; Score 2638; DB 4; Length 483;

Best Local Similarity 100.0%; Pred. No. 2.1e-231;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VNGTLMQYFEWYTPNDQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	60
Db	1	VNGTLMQYFEWYTPNDQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	60
Qy	61	DLGEFOQKGTVRTKYGTSEYQIKAWTDPRPGRGNTYSDFKWHYHFDGADWDESKISRIKFRGEGK	120
Db	61	DLGEFOQKGTVRTKYGTSEYQIKAWTDPRPGRGNTYSDFKWHYHFDGADWDESKISRIKFRGEGK	120
Qy	121	ARNQETSEYQIKAWTDPRPGRGNTYSDFKWHYHFDGADWDESKISRIKFRGEGK	180
Db	121	ARNQETSEYQIKAWTDPRPGRGNTYSDFKWHYHFDGADWDESKISRIKFRGEGK	180
Qy	181	ADWEVSSSENGNDYLMYADVDPDVAETKKGWYANELSLDGFRIIDAAKHIFSF	240
Db	181	ADWEVSSSENGNDYLMYADVDPDVAETKKGWYANELSLDGFRIIDAAKHIFSF	240
Qy	241	LRDWQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASSQGG	300
Db	241	LRDWQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASSQGG	300
Qy	301	GYDMRRLDGTWVSRHPEKAVTFVENHDTQPGQSLSTVQTFWPKPLAYAFILITRESGYPQ	360
Db	301	GYDMRRLDGTWVSRHPEKAVTFVENHDTQPGQSLSTVQTFWPKPLAYAFILITRESGYPQ	360
Qy	361	VFYGDMYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPDHYIDHPDVIWGTREGDSSAA	420
Db	361	VFYGDMYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPDHYIDHPDVIWGTREGDSSAA	420
Qy	421	KSLGAAALITDGPGGSKRMAYAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSYSIY	480
Db	421	KSLGAAALITDGPGGSKRMAYAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSYSIY	480
Qy	481	VQK 483	
Db	481	VQK 483	

RESULT 5

US-08-720-899-4

; Sequence 4, Application US/08720899

; Patent No. 5753460

GENERAL INFORMATION:

; APPLICANT: Bisgaard-Frantzen, Henrik

; APPLICANT: Borchart, Torben Vedel

; APPLICANT: Svendsen, Allan

; APPLICANT: Thellersen, Marianne

; APPLICANT: Van der Zee, Pia

; TITLE OF INVENTION: AMYLASE VARIANTS

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5753460o No. 5753460disk of No. 5753460th America, Inc.

; STREET: 405 Lexington Avenue, 64th Floor

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/720,899

; FILING DATE: 10-OCT-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/343,804

; FILING DATE: 22-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lowney Dr., Karen A.

; REGISTRATION NUMBER: 31,274

; REFERENCE/DOCKET NUMBER: 4054.214-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 514 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-720-899-4

Query Match

100.0%; Score 2638; DB 1; Length 514;

Best Local Similarity 100.0%; Pred. No. 2.3e-231;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VNGTLMQYFEWYTPNDQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	60
Db	32	VNGTLMQYFEWYTPNDQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	91
Qy	61	DLGEFOQKGTVRTKYGTSEYQIKAWTDPRPGRGNTYSDFKWHYHFDGADWDESKISRIKFRGEGK	120
Db	92	DLGEFOQKGTVRTKYGTSEYQIKAWTDPRPGRGNTYSDFKWHYHFDGADWDESKISRIKFRGEGK	151
Qy	121	ARNQETSEYQIKAWTDPRPGRGNTYSDFKWHYHFDGADWDESKISRIKFRGEGK	180
Db	152	ARNQETSEYQIKAWTDPRPGRGNTYSDFKWHYHFDGADWDESKISRIKFRGEGK	211
Qy	181	ADWEVSSSENGNDYLMYADVDPDVAETKKGWYANELSLDGFRIIDAAKHIFSF	240
Db	212	ADWEVSSSENGNDYLMYADVDPDVAETKKGWYANELSLDGFRIIDAAKHIFSF	271
Qy	241	LRDWQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASSQGG	300
Db	272	LRDWQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASSQGG	331
Qy	301	GYDMRRLDGTWVSRHPEKAVTFVENHDTQPGQSLSTVQTFWPKPLAYAFILITRESGYPQ	360
Db	332	GYDMRRLDGTWVSRHPEKAVTFVENHDTQPGQSLSTVQTFWPKPLAYAFILITRESGYPQ	391
Qy	361	VFYGDMYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPDHYIDHPDVIWGTREGDSSAA	420
Db	392	VFYGDMYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPDHYIDHPDVIWGTREGDSSAA	451

Qy 421 KSLAALITDGGSKMYAGLKNAGETWYDITGNRSDTVKIGDQGWGFHNDGVSIVY 480
Db 452 KSLAALITDGGSKMYAGLKNAGETWYDITGNRSDTVKIGDQGWGFHNDGVSIVY 511
Qy 481 VQK 483
Db 512 VQK 514

RESULT 6
US-08-459-610-4
; Sequence 4, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5801043o No. 5801043disk of No. 5801043th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,610
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-610-4

Query Match 100.0%; Score 2638; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDQGHKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGYDLY 60
Db 32 VNGTLMQYFEWYTPNDQGHKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGYDLY 91
Qy 61 DLGEFQKGVTRTKYGTGKSELQDAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVERN 120
Db 92 DLGEFQKGVTRTKYGTGKSELQDAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVERN 151
Qy 121 ANRNQETSEYQIKAWTDFFPGRGNTYSDFKWHWHFDGADWDSRKISRIFKRGEGK 180
Db 152 ANRNQETSEYQIKAWTDFFPGRGNTYSDFKWHWHFDGADWDSRKISRIFKRGEGK 211
Qy 181 ANDWEVSENGNYDYLMYADVDVDPVVAETKKGWIWYANBELSLDGFRIIDAAKHKFSF 240

Db 212 ANDWEVSENGNYDYLMYADVDVDPVVAETKKGWIWYANBELSLDGFRIIDAAKHKFSF 271
Qy 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASQGG 300
Db 272 LRDWQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASQGG 331
Qy 301 GYDMRLLDGTVVSRRHPEKAVTFVENHDTQPGQSLESTVQTPKPLAYAFILTRREGYPQ 360
Db 332 GYDMRLLDGTVVSRRHPEKAVTFVENHDTQPGQSLESTVQTPKPLAYAFILTRREGYPQ 391
Qy 361 VFYGDMYGTGTSPTKPSLKDNIPIILKARKEYAYGPOHDYIDHDPVIGWTRREGSSAA 420
Db 392 VFYGDMYGTGTSPTKPSLKDNIPIILKARKEYAYGPOHDYIDHDPVIGWTRREGSSAA 451
Qy 421 KSLAALITDGGSKMYAGLKNAGETWYDITGNRSDTVKIGDQGWGFHNDGVSIVY 480
Db 452 KSLAALITDGGSKMYAGLKNAGETWYDITGNRSDTVKIGDQGWGFHNDGVSIVY 511
Qy 481 VQK 483
Db 512 VQK 514

RESULT 7
US-08-343-804-4
; Sequence 4, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5830837o No. 5830837disk of No. 5830837th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,804
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-343-804-4

Query Match 100.0%; Score 2638; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDQGHKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGYDLY 60

Db 32 VNGTLMQYFEWYTPNDQGHKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPVDLY 91
Qy 61 DLGEFOQKGTVRTKYGTSELDQDAIGSLHSRNQVYGDVVLNKHKAGADATEDVTAVEVNP 120
Db 92 DLGEFOQKGTVRTKYGTSELDQDAIGSLHSRNQVYGDVVLNKHKAGADATEDVTAVEVNP 151
Qy 121 ANRNETSEBYQIKAWTDFFPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGK 180
Db 152 ANRNETSEBYQIKAWTDFFPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGK 211
Qy 181 AWDWEVSSNGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHIFSF 240
Db 212 AWDWEVSSNGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHIFSF 271
Qy 241 LRWDVQAVROATKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDPVPLHFNLAQSSQGG 300
Db 272 LRWDVQAVROATKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDPVPLHFNLAQSSQGG 331
Qy 301 GYDMRLLDGTVVSRRHPEKAVTFVNHDTOPGOSLESTVQWTFKPLAYAFILTRRESYPO 360
Db 332 GYDMRLLDGTVVSRRHPEKAVTFVNHDTOPGOSLESTVQWTFKPLAYAFILTRRESYPO 391
Qy 361 VFYGDYMTGKTSPEKPSLKNIEPILKARKEYAYGPDHYIDHPDVIWGTREGDSAA 420
Db 392 VFYGDYMTGKTSPEKPSLKNIEPILKARKEYAYGPDHYIDHPDVIWGTREGDSAA 451
Qy 421 KSGLAALITDGPQSGKMYAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 480
Db 452 KSGLAALITDGPQSGKMYAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 511
Qy 481 VQK 483
Db 512 VQK 514

RESULT 8

US-08-687-399-4
; Sequence 4, Application US/08687399
; Patent No. 5928381
; GENERAL INFORMATION:
; APPLICANT: Toft, Annette H.
; APPLICANT: Marcher, Dorte
; APPLICANT: Pedersen, Hanne H.
; APPLICANT: Nilsen, Thomas E.
; TITLE OF INVENTION: A Combined Desizing and Bleaching
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59283810 No. 59283810disk of No. 59283810th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 008
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4127.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-687-399-4
Query Match 100.0%; Score 2638; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VNGTLMQYFEWYTPNDQGHKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPVDLY 60
Db 32 VNGTLMQYFEWYTPNDQGHKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPVDLY 91
Qy 61 DLGEFOQKGTVRTKYGTSELDQDAIGSLHSRNQVYGDVVLNKHKAGADATEDVTAVEVNP 120
Db 92 DLGEFOQKGTVRTKYGTSELDQDAIGSLHSRNQVYGDVVLNKHKAGADATEDVTAVEVNP 151
Qy 121 ANRNETSEBYQIKAWTDFFPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGK 180
Db 152 ANRNETSEBYQIKAWTDFFPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGK 211
Qy 181 AWDWEVSSNGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHIFSF 240
Db 212 AWDWEVSSNGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHIFSF 271
Qy 241 LRWDVQAVROATKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDPVPLHFNLAQSSQGG 300
Db 272 LRWDVQAVROATKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDPVPLHFNLAQSSQGG 331
Qy 301 GYDMRLLDGTVVSRRHPEKAVTFVNHDTOPGOSLESTVQWTFKPLAYAFILTRRESYPO 360
Db 332 GYDMRLLDGTVVSRRHPEKAVTFVNHDTOPGOSLESTVQWTFKPLAYAFILTRRESYPO 391
Qy 361 VFYGDYMTGKTSPEKPSLKNIEPILKARKEYAYGPDHYIDHPDVIWGTREGDSAA 420
Db 392 VFYGDYMTGKTSPEKPSLKNIEPILKARKEYAYGPDHYIDHPDVIWGTREGDSAA 451
Qy 421 KSGLAALITDGPQSGKMYAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 480
Db 452 KSGLAALITDGPQSGKMYAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 511
Qy 481 VQK 483
Db 512 VQK 514
RESULT 9
US-08-600-908A-4
; Sequence 4, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59891690 No. 59891690disk of No. 59891690th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-600-908A-4

Query Match 100.0%; Score 2638; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Db 32 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 91
QY 61 DLGEFQOQGTVRTKYGTKSELQDAIGSLHSRNVQYGDVVLNHNKAGADATEDVTAVEVNP 120
Db 92 DLGEFQOQGTVRTKYGTKSELQDAIGSLHSRNVQYGDVVLNHNKAGADATEDVTAVEVNP 151
QY 121 ANRNETSEEEYQIKAWTDPRPGRGNTYSDPKWHYHFDGADWDSRKSIRIFKFRGEGK 180
Db 152 ANRNETSEEEYQIKAWTDPRPGRGNTYSDPKWHYHFDGADWDSRKSIRIFKFRGEGK 211
QY 181 AWDWEVSSNGNYDYLMDYADVDPVVAETKKGWIWYANELSLDGFRIIDAAKHKFSF 240
Db 212 AWDWEVSSNGNYDYLMDYADVDPVVAETKKGWIWYANELSLDGFRIIDAAKHKFSF 271
QY 241 LRDWVQAVROATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVFDPVPLHFNLAQASSQG 300
Db 272 LRDWVQAVROATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVFDPVPLHFNLAQASSQG 331
QY 301 GYDMRRLDGTVVSRRHPEKAVTFVENHDTOPGOSLESTVQTFKPLAYAFILTRREGYPQ 360
Db 332 GYDMRRLDGTVVSRRHPEKAVTFVENHDTOPGOSLESTVQTFKPLAYAFILTRREGYPQ 391
QY 361 VFYGDYGTGTSPEKIPSLKDNIEPILKARKEYAYGQHDYIDHPDVIGTWREGDSSAA 420
Db 392 VFYGDYGTGTSPEKIPSLKDNIEPILKARKEYAYGQHDYIDHPDVIGTWREGDSSAA 451
QY 421 KSGLAALITDGPCKGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 480
Db 452 KSGLAALITDGPCKGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 511
QY 481 VQK 483
Db 512 VQK 514

RESULT 10
US-08-683-838A-4
; Sequence 4, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bigg rd-Frantzen, Henrik
; APPLICANT: Borcherdt, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6022724o No. 6022724disk of No. 6022724th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,838A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-683-838A-4

Query Match 100.0%; Score 2638; DB 3; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Db 32 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 91
QY 61 DLGEFQOQGTVRTKYGTKSELQDAIGSLHSRNVQYGDVVLNHNKAGADATEDVTAVEVNP 120
Db 92 DLGEFQOQGTVRTKYGTKSELQDAIGSLHSRNVQYGDVVLNHNKAGADATEDVTAVEVNP 151
QY 121 ANRNETSEEEYQIKAWTDPRPGRGNTYSDPKWHYHFDGADWDSRKSIRIFKFRGEGK 180
Db 152 ANRNETSEEEYQIKAWTDPRPGRGNTYSDPKWHYHFDGADWDSRKSIRIFKFRGEGK 211
QY 181 AWDWEVSSNGNYDYLMDYADVDPVVAETKKGWIWYANELSLDGFRIIDAAKHKFSF 240
Db 212 AWDWEVSSNGNYDYLMDYADVDPVVAETKKGWIWYANELSLDGFRIIDAAKHKFSF 271
QY 241 LRDWVQAVROATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVFDPVPLHFNLAQASSQG 300
Db 272 LRDWVQAVROATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVFDPVPLHFNLAQASSQG 331
QY 301 GYDMRRLDGTVVSRRHPEKAVTFVENHDTOPGOSLESTVQTFKPLAYAFILTRREGYPQ 360
Db 332 GYDMRRLDGTVVSRRHPEKAVTFVENHDTOPGOSLESTVQTFKPLAYAFILTRREGYPQ 391
QY 361 VFYGDYGTGTSPEKIPSLKDNIEPILKARKEYAYGQHDYIDHPDVIGTWREGDSSAA 420
Db 392 VFYGDYGTGTSPEKIPSLKDNIEPILKARKEYAYGQHDYIDHPDVIGTWREGDSSAA 451
QY 421 KSGLAALITDGPCKGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 480
Db 452 KSGLAALITDGPCKGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 511
QY 481 VQK 483
Db 512 VQK 514

RESULT 11
US-09-264-097-4
; Sequence 4, Application US/09264097
; Patent No. 6287826
; GENERAL INFORMATION:
; APPLICANT: No. 6287826man, Barrie Edmund

```


APPLICANT: Hendriksen, Hanne Vang
TITLE OF INVENTION: Enzymatic Preparation of Glucose Syrup
FILE OF INVENTION: From Starch
FILE REFERENCE: 5278.200-US
CURRENT APPLICATION NUMBER: US/09/264,097
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: PA 0321/98
EARLIER FILING DATE: 1998-03-09
EARLIER APPLICATION NUMBER: 60/079,209
EARLIER FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 514
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-09-264-097-4

Query Match 100.0%; Score 2638; DB 3; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	60
Db	32	VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	91
Qy	61	DLGFEQKGTVRTKYGTKSELODAIGSLHSRNVQVGDVVLNHKAGADATEDVTAVERN	120
Db	92	DLGFEQKGTVRTKYGTKSELODAIGSLHSRNVQVGDVVLNHKAGADATEDVTAVERN	151
Qy	121	ANRNQETSEYQIKAWTDPRFPGRGNTYSDPKWHWHYHFDGADWDESKISRIKFRGEGK	180
Db	152	ANRNQETSEYQIKAWTDPRFPGRGNTYSDPKWHWHYHFDGADWDESKISRIKFRGEGK	211
Qy	181	ADWEVSENGNYDYLMDVVDYDHPDVAETKKGWIKWYANELSLDGFRIIDAAKHIFSF	240
Db	212	ADWEVSENGNYDYLMDVVDYDHPDVAETKKGWIKWYANELSLDGFRIIDAAKHIFSF	271
Qy	241	LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVDFVPLHFNLAQSSQGG	300
Db	272	LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVDFVPLHFNLAQSSQGG	331
Qy	301	GYDMRLLDGTVVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAFILTRREGSYPQ	360
Db	332	GYDMRLLDGTVVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAFILTRREGSYPQ	391
Qy	361	VFYGDMYGTGTSPEKIPSLKONIEPILKARKEYAYGQHDYIDHPDVIGWTRREGDSSAA	420
Db	392	VFYGDMYGTGTSPEKIPSLKONIEPILKARKEYAYGQHDYIDHPDVIGWTRREGDSSAA	451
Qy	421	KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSNTVKIGSDGWFHNDGVSIIY	480
Db	452	KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSNTVKIGSDGWFHNDGVSIIY	511
Qy	481	VQK 483	
Db	512	VQK 514	

RESULT 12
US-09-636-252A-4
Sequence 4, Application US/09636252A
Patent No. 6440716
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/636,252A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18

NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 514
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-09-636-252A-4

Query Match 100.0%; Score 2638; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	60
Db	32	VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	91
Qy	61	DLGFEQKGTVRTKYGTKSELODAIGSLHSRNVQVGDVVLNHKAGADATEDVTAVERN	120
Db	92	DLGFEQKGTVRTKYGTKSELODAIGSLHSRNVQVGDVVLNHKAGADATEDVTAVERN	151
Qy	121	ANRNQETSEYQIKAWTDPRFPGRGNTYSDPKWHWHYHFDGADWDESKISRIKFRGEGK	180
Db	152	ANRNQETSEYQIKAWTDPRFPGRGNTYSDPKWHWHYHFDGADWDESKISRIKFRGEGK	211
Qy	181	ADWEVSENGNYDYLMDVVDYDHPDVAETKKGWIKWYANELSLDGFRIIDAAKHIFSF	240
Db	212	ADWEVSENGNYDYLMDVVDYDHPDVAETKKGWIKWYANELSLDGFRIIDAAKHIFSF	271
Qy	241	LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVDFVPLHFNLAQSSQGG	300
Db	272	LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVDFVPLHFNLAQSSQGG	331
Qy	301	GYDMRLLDGTVVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAFILTRREGSYPQ	360
Db	332	GYDMRLLDGTVVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAFILTRREGSYPQ	391
Qy	361	VFYGDMYGTGTSPEKIPSLKONIEPILKARKEYAYGQHDYIDHPDVIGWTRREGDSSAA	420
Db	392	VFYGDMYGTGTSPEKIPSLKONIEPILKARKEYAYGQHDYIDHPDVIGWTRREGDSSAA	451
Qy	421	KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSNTVKIGSDGWFHNDGVSIIY	480
Db	452	KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSNTVKIGSDGWFHNDGVSIIY	511
Qy	481	VQK 483	
Db	512	VQK 514	

RESULT 13
US-08-468-700-36
Sequence 36, Application US/08468700
Patent No. 5736499
GENERAL INFORMATION:
APPLICANT: COLIN MITCHINSON
APPLICANT: CAROL A. REQUADT
APPLICANT: TRACI H. ROPP
APPLICANT: LEIF P. SOLHEIM
TITLE OF INVENTION: MUTANT ALPHA-AMYLASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

```
; APPLICATION NUMBER: US/08/468,700
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 252
; ATTORNEY/AGENT INFORMATION:
; NAME: Stone, Christopher
; REGISTRATION NUMBER: 35,696
; REFERENCE/DOCKET NUMBER: G2275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 742-7555
; TELEFAX: (415) 742-7217
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus amyloliquefaciens
; US-08-468-700-36

Query Match      100.0%; Score 2638; DB 1; Length 520;
Best Local Similarity 100.0%; Pred. No. 2.4e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
DB 38 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 97
QY 61 DLGEFOQKGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNKHAGADATEDVAVEVNP 120
DB 98 DLGEFOQKGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNKHAGADATEDVAVEVNP 157
QY 121 ANRNOETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYFDGADWDESKISRIFKFRGEGK 180
DB 158 ANRNOETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYFDGADWDESKISRIFKFRGEGK 217
QY 181 ADWEVSSSENGNDYLMYADVDDHPDVVAETKKWGIWYANELSLDGFRIIDAAKHIFKFSF 240
DB 218 ADWEVSSSENGNDYLMYADVDDHPDVVAETKKWGIWYANELSLDGFRIIDAAKHIFKFSF 277
QY 241 LRDWQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSFNQSVFVPLHFNLAQASSQGG 300
DB 278 LRDWQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSFNQSVFVPLHFNLAQASSQGG 337
QY 301 GYDMRRLDGTGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTFWFKPLAYAFILTRREGSYPQ 360
DB 338 GYDMRRLDGTGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTFWFKPLAYAFILTRREGSYPQ 397
QY 361 VFYGDWMTGTSKPEIPSLKDNIEPLKARKEYAYGPOHDYIDHPDVIGTWREGDSSAA 420
DB 398 VFYGDWMTGTSKPEIPSLKDNIEPLKARKEYAYGPOHDYIDHPDVIGTWREGDSSAA 457
QY 421 KSGLAALITDGGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSGWGEFHVNDGVSIIY 480
DB 458 KSGLAALITDGGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSGWGEFHVNDGVSIIY 517
QY 481 VQK 483
DB 518 VQK 520

RESULT 14
US-08-468-700-4
; Sequence 4, Application US/08645971
; Patent No. 5763385
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Alpha-Amylases Having Altered
; CALCIUM BINDING PROPERTIES
; NUMBER OF SEQUENCES: 5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,971
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus amyloliquefaciens
; US-08-645-971-4

Query Match      100.0%; Score 2638; DB 1; Length 520;
Best Local Similarity 100.0%; Pred. No. 2.4e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
DB 38 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 97
QY 61 DLGEFOQKGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNKHAGADATEDVAVEVNP 120
DB 98 DLGEFOQKGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNKHAGADATEDVAVEVNP 157
QY 121 ANRNOETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYFDGADWDESKISRIFKFRGEGK 180
DB 158 ANRNOETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYFDGADWDESKISRIFKFRGEGK 217
QY 181 ADWEVSSSENGNDYLMYADVDDHPDVVAETKKWGIWYANELSLDGFRIIDAAKHIFKFSF 240
DB 218 ADWEVSSSENGNDYLMYADVDDHPDVVAETKKWGIWYANELSLDGFRIIDAAKHIFKFSF 277
QY 241 LRDWQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSFNQSVFVPLHFNLAQASSQGG 300
DB 278 LRDWQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSFNQSVFVPLHFNLAQASSQGG 337
QY 301 GYDMRRLDGTGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTFWFKPLAYAFILTRREGSYPQ 360
DB 338 GYDMRRLDGTGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTFWFKPLAYAFILTRREGSYPQ 397
QY 361 VFYGDWMTGTSKPEIPSLKDNIEPLKARKEYAYGPOHDYIDHPDVIGTWREGDSSAA 420
DB 398 VFYGDWMTGTSKPEIPSLKDNIEPLKARKEYAYGPOHDYIDHPDVIGTWREGDSSAA 457
QY 421 KSGLAALITDGGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSGWGEFHVNDGVSIIY 480
DB 458 KSGLAALITDGGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSGWGEFHVNDGVSIIY 517
QY 481 VQK 483
DB 518 VQK 520

RESULT 15
US-08-468-220-34
; Sequence 34, Application US/08468220
; Patent No. 5824532
; GENERAL INFORMATION:
; APPLICANT: Antrim, Richard L.
; APPLICANT: Barnett, Christopher
; APPLICANT: Mitchinson, Colin
; APPLICANT: Power, Scott D.
; APPLICANT: Requaft, Carol
; APPLICANT: Solheim, Leif P.
; TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International, Inc.
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
```

Search completed: October 7, 2004, 00:47:12
Job time : 16.9658 secs

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,220
FILING DATE: 06-JUN-95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/016,395
FILING DATE: 11-FEB-93
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC220D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7555
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-220-34

Query Match 100.0%; Score 2638; DB 2; Length 520;
Best Local Similarity 100.0%; Pred. No. 2.4e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKYGLSQSDNGYGPYDLY	60
Db	38	VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKYGLSQSDNGYGPYDLY	97
QY	61	DLGEFQKQGTVRTKYGTKSELQDAIGSLHSRNVQYGDVVLNHNKAGADATEDVTAVEVNP	120
Db	98	DLGEFQKQGTVRTKYGTKSELQDAIGSLHSRNVQYGDVVLNHNKAGADATEDVTAVEVNP	157
QY	121	ANRQETSEYQIKAWTDPRPGRGNTYSDFKWHYHFDGADWDESRKISRIFKFRGEGK	180
Db	158	ANRQETSEYQIKAWTDPRPGRGNTYSDFKWHYHFDGADWDESRKISRIFKFRGEGK	217
QY	181	AWDWEVSSENGNDYLMYADVVDYDHPDVVAETKKWGIWYANELSLDGFRIIDAAKHKPSF	240
Db	218	AWDWEVSSENGNDYLMYADVVDYDHPDVVAETKKWGIWYANELSLDGFRIIDAAKHKPSF	277
QY	241	LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVFDPVPLHFNLAQSSQGG	300
Db	278	LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVFDPVPLHFNLAQSSQGG	337
QY	301	GYDMRRLDGTTVSRHPEKAVTFVENHDTQPGQSLSTVQTFWPKPLAYAFILITRESGYPQ	360
Db	338	GYDMRRLDGTTVSRHPEKAVTFVENHDTQPGQSLSTVQTFWPKPLAYAFILITRESGYPQ	397
QY	361	VFYGDMYGTGTSKPEIPLSKNDIEPIILKARKEYAYGPQHDYIDHPDVIGWTRREGDSAA	420
Db	398	VFYGDMYGTGTSKPEIPLSKNDIEPIILKARKEYAYGPQHDYIDHPDVIGWTRREGDSAA	457
QY	421	KSGLAALITDGPGGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEHVNDSVSIY	480
Db	458	KSGLAALITDGPGGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEHVNDSVSIY	517
QY	481	VQK 483	
Db	518	VQK 520	

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:19:14 ; Search time 53.2274 Seconds
(without alignments)
2920.093 Million cell updates/sec

Title: US-09-925-576C-10
Perfect score: 2638
Sequence: 1 VNGTLMQYFEWYTPNDGQHW.....SDGWGBFHVNDGSVIVQK 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 segs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2638	100.0	483	9	US-09-854-346-10
2	2638	100.0	483	9	US-09-918-543-10
3	2638	100.0	483	10	US-09-925-576C-10
4	2638	100.0	483	14	US-10-146-327-6
5	2638	100.0	483	16	US-10-477-725-10
6	2638	100.0	514	14	US-10-184-771-4
7	2624	99.5	480	9	US-09-769-864-5
8	2624	99.5	480	12	US-10-665-667-5
9	2624	99.5	480	12	US-10-644-187-4
10	2624	99.5	480	12	US-10-327-837-5
11	2624	99.5	480	14	US-10-186-042-4
12	2486	94.2	483	14	US-10-184-771-13
13	2201	83.4	481	14	US-10-146-327-2
14	2193	83.1	512	14	US-10-081-872-114
15	2193	83.1	512	14	US-10-105-733-8

16	2193	83.1	512	14	US-10-081-739A-8	Sequence 8, Appli
17	2193	83.1	512	15	US-10-385-305-114	Sequence 114, App
18	2187	82.9	512	14	US-10-199-922-2	Sequence 2, Appli
19	2184	82.8	483	9	US-09-769-864-4	Sequence 8, Appli
20	2184	82.8	483	9	US-09-854-346-8	Sequence 4, Appli
21	2184	82.8	483	9	US-09-918-543-8	Sequence 8, Appli
22	2184	82.8	483	9	US-09-918-543-30	Sequence 30, Appli
23	2184	82.8	483	10	US-09-925-576C-8	Sequence 8, Appli
24	2184	82.8	483	12	US-10-665-667-4	Sequence 4, Appli
25	2184	82.8	483	12	US-10-644-187-2	Sequence 2, Appli
26	2184	82.8	483	12	US-10-327-837-4	Sequence 4, Appli
27	2184	82.8	483	14	US-10-146-327-4	Sequence 4, Appli
28	2184	82.8	483	14	US-10-186-042-2	Sequence 2, Appli
29	2184	82.8	483	16	US-10-399-161-6	Sequence 6, Appli
30	2184	82.8	483	16	US-10-477-725-8	Sequence 8, Appli
31	2184	82.8	512	14	US-10-184-771-2	Sequence 2, Appli
32	1931	73.2	513	14	US-10-081-872-146	Sequence 146, App
33	1931	73.2	513	15	US-10-385-305-146	Sequence 146, App
34	1930	73.2	513	14	US-10-081-872-70	Sequence 70, Appli
35	1930	73.2	513	15	US-10-385-305-70	Sequence 70, Appli
36	1925	73.0	478	14	US-10-081-872-166	Sequence 166, App
37	1925	73.0	478	15	US-10-385-305-166	Sequence 166, App
38	1870	70.9	485	9	US-09-769-864-2	Sequence 2, Appli
39	1870	70.9	485	9	US-09-769-864-8	Sequence 8, Appli
40	1870	70.9	485	9	US-09-854-346-4	Sequence 4, Appli
41	1870	70.9	485	9	US-09-902-188A-2	Sequence 2, Appli
42	1870	70.9	485	9	US-09-918-543-4	Sequence 4, Appli
43	1870	70.9	485	9	US-09-795-211-2	Sequence 2, Appli
44	1870	70.9	485	10	US-09-925-576C-4	Sequence 4, Appli
45	1870	70.9	485	12	US-10-665-667-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-854-346-10
; Sequence 10, Application US/09854346
; Patent No. US20020068352A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020068352A1ozymes A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Jorgensen, Christel Thea
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Alpha-amylase variants with altered 1.6 activity
; FILE REFERENCE: 6140.200-US
; CURRENT APPLICATION NUMBER: US/09/854.346
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-09-854-346-10

Query Match		100.0%;	Score 2638;	DB 9;	Length 483;
Best Local Similarity		100.0%;	Pred. No. 2.5e-238;		
Matches 483;		Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
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Db	1	VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIWPYPAYKGLSQSDNGYGPYDLY	60		
Qy	61	DLGSEFOQKTVRTKYTKGKSELODAIGSLHSENNVQYGVVNLHNKAGADATDVAVEVNP	120		
Db	61	DLGSEFOQKTVRTKYTKGKSELODAIGSLHSENNVQYGVVNLHNKAGADATDVAVEVNP	120		
Qy	121	ANRNOETSEEVQIKAWTDFFRPGKNTYSDFPKWHYHFDGADWDSESRKISIFKFRGEGK	180		
Db	121	ANRNOETSEEVQIKAWTDFFRPGKNTYSDFPKWHYHFDGADWDSESRKISIFKFRGEGK	180		
Qy	181	AWDWEVSENGNYDLYMVDVDPVAVETKKGIWYANELSLDGFRIIDAKHIKFSF	240		

Db 181 ANDWEVSSNGNYDLYMADVDYDHPDVVAETKKWGIWYANELSLDGFPRIDAARKHKFSF 240
|||
Qy 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYLNKTSFNQSVDFVPLHFNLAQASSQGG 300
|||
Db 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYLNKTSFNQSVDFVPLHFNLAQASSQGG 300
|||
Qy 301 GYDMRRLDGTGTVSRHPKAVTFVENHDTQPGSLSTVQTFWFKPLAYAFILITRESGYPQ 360
|||
Db 301 GYDMRRLDGTGTVSRHPKAVTFVENHDTQPGSLSTVQTFWFKPLAYAFILITRESGYPQ 360
|||
Qy 361 VFYGDYMTGKTSPEKIPSLKDNTEPILKARKEYAYGPHDYIDHPDVIGWTRGDSAA 420
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Db 361 VFYGDYMTGKTSPEKIPSLKDNTEPILKARKEYAYGPHDYIDHPDVIGWTRGDSAA 420
|||
Qy 421 KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
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Db 421 KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
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Qy 481 VQK 483
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Db 481 VQK 483
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RESULT 2

US-09-918-543-10
; Sequence 10, Application US/09918543
; Patent No. US20020155574A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020155574Allozymes A/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kjaerulff, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fuglsang, Claus Crone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062.200-US
; CURRENT APPLICATION NUMBER: US/09/918,543
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-09-918-543-10

Query Match 100.0%; Score 2638; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.5e-238;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
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Qy 61 DLGEFOQKGTVRTKYGTKSELQDAIGSLHSRNVQVGVVNLNKHAGADATEDVTAVERN 120
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Db 61 DLGEFOQKGTVRTKYGTKSELQDAIGSLHSRNVQVGVVNLNKHAGADATEDVTAVERN 120
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Qy 121 ANRNQETSEYQIKAWTDFFPGRGNTYSDPKWHWHFPGADWDESRKISRIFKFRGEK 180
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Db 121 ANRNQETSEYQIKAWTDFFPGRGNTYSDPKWHWHFPGADWDESRKISRIFKFRGEK 180
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Qy 181 ANDWEVSSNGNYDLYMADVDYDHPDVVAETKKWGIWYANELSLDGFPRIDAARKHKFSF 240
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Db 181 ANDWEVSSNGNYDLYMADVDYDHPDVVAETKKWGIWYANELSLDGFPRIDAARKHKFSF 240
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Qy 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYLNKTSFNQSVDFVPLHFNLAQASSQGG 300
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Db 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYLNKTSFNQSVDFVPLHFNLAQASSQGG 300
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Qy 301 GYDMRRLDGTGTVSRHPKAVTFVENHDTQPGSLSTVQTFWFKPLAYAFILITRESGYPQ 360
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Db 301 GYDMRRLDGTGTVSRHPKAVTFVENHDTQPGSLSTVQTFWFKPLAYAFILITRESGYPQ 360
|||

Qy 361 VFYGDYMTGKTSPEKIPSLKDNTEPILKARKEYAYGPHDYIDHPDVIGWTRGDSAA 420
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Db 361 VFYGDYMTGKTSPEKIPSLKDNTEPILKARKEYAYGPHDYIDHPDVIGWTRGDSAA 420
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Qy 421 KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
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Db 421 KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
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Qy 481 VQK 483
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Db 481 VQK 483
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RESULT 3

US-09-925-576C-10
; Sequence 10, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-09-925-576C-10

Query Match 100.0%; Score 2638; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.5e-238;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
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Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
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Qy 61 DLGEFOQKGTVRTKYGTKSELQDAIGSLHSRNVQVGVVNLNKHAGADATEDVTAVERN 120
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Db 61 DLGEFOQKGTVRTKYGTKSELQDAIGSLHSRNVQVGVVNLNKHAGADATEDVTAVERN 120
|||
Qy 121 ANRNQETSEYQIKAWTDFFPGRGNTYSDPKWHWHFPGADWDESRKISRIFKFRGEK 180
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Db 121 ANRNQETSEYQIKAWTDFFPGRGNTYSDPKWHWHFPGADWDESRKISRIFKFRGEK 180
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Qy 181 ANDWEVSSNGNYDLYMADVDYDHPDVVAETKKWGIWYANELSLDGFPRIDAARKHKFSF 240
|||
Db 181 ANDWEVSSNGNYDLYMADVDYDHPDVVAETKKWGIWYANELSLDGFPRIDAARKHKFSF 240
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Qy 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYLNKTSFNQSVDFVPLHFNLAQASSQGG 300
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Db 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYLNKTSFNQSVDFVPLHFNLAQASSQGG 300
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Qy 301 GYDMRRLDGTGTVSRHPKAVTFVENHDTQPGSLSTVQTFWFKPLAYAFILITRESGYPQ 360
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Qy 361 VFYGDYMTGKTSPEKIPSLKDNTEPILKARKEYAYGPHDYIDHPDVIGWTRGDSAA 420
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Db 361 VFYGDYMTGKTSPEKIPSLKDNTEPILKARKEYAYGPHDYIDHPDVIGWTRGDSAA 420
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Qy 421 KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
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Db 421 KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
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Qy 481 VQK 483
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Db 481 VQK 483
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RESULT 4
US-10-146-327-6
; Sequence 6, Application US/10146327
; Publication No. US20030044954A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kiaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/10/146,327
; CURRENT FILING DATE: 2002-05-15
; PRIOR FILING DATE: US/09/537,168
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PA 1999 00437
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/127,427
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-10-146-327-6

Query Match      100.0%; Score 2638; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.5e-238;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY 60
Qy 61 DLGEFQKQGVTRTKYGTGKSELQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVERN 120
Db 61 DLGEFQKQGVTRTKYGTGKSELQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVERN 120
Qy 121 ANRNETSEBYQIKAWTDFFPPGNGNTYSDPKWHWHYHFDGADWDESKISRIKFRGEGK 180
Db 121 ANRNETSEBYQIKAWTDFFPPGNGNTYSDPKWHWHYHFDGADWDESKISRIKFRGEGK 180
Qy 181 AWDWEVSENGNDYLMYADVVDYDHPDVVAETKKGWYANELSLDGFRIIDAAKHIFSP 240
Db 181 AWDWEVSENGNDYLMYADVVDYDHPDVVAETKKGWYANELSLDGFRIIDAAKHIFSP 240
Qy 241 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFDPVPLHFNLAASSQGG 300
Db 241 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFDPVPLHFNLAASSQGG 300
Qy 301 GYDMRRLDGTWVSRHPEKAVTFVENHDTOPGQSLESTVQTFWPKPLAYAFILITRESGY 360
Db 301 GYDMRRLDGTWVSRHPEKAVTFVENHDTOPGQSLESTVQTFWPKPLAYAFILITRESGY 360
Qy 361 VFYGDYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPHDYIDHPDVIGWTRGDSAA 420
Db 361 VFYGDYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPHDYIDHPDVIGWTRGDSAA 420
Qy 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGGEHFNVDGVSIIY 480
Db 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGGEHFNVDGVSIIY 480
Qy 481 VQK 483
Db 481 VQK 483

RESULT 5
US-10-477-725-10
; Sequence 10, Application US/10477725
; Publication No. US20040096952A1
; GENERAL INFORMATION:
; APPLICANT: NOVOZYMES A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Thisted, Thomas
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: Alpha-amylase variant with altered properties
; FILE REFERENCE: 10182.204-US
; CURRENT APPLICATION NUMBER: US/10/477,725
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-10-477-725-10

Query Match      100.0%; Score 2638; DB 16; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.5e-238;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY 60
Qy 61 DLGEFQKQGVTRTKYGTGKSELQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVERN 120
Db 61 DLGEFQKQGVTRTKYGTGKSELQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVERN 120
Qy 121 ANRNETSEBYQIKAWTDFFPPGNGNTYSDPKWHWHYHFDGADWDESKISRIKFRGEGK 180
Db 121 ANRNETSEBYQIKAWTDFFPPGNGNTYSDPKWHWHYHFDGADWDESKISRIKFRGEGK 180
Qy 181 AWDWEVSENGNDYLMYADVVDYDHPDVVAETKKGWYANELSLDGFRIIDAAKHIFSP 240
Db 181 AWDWEVSENGNDYLMYADVVDYDHPDVVAETKKGWYANELSLDGFRIIDAAKHIFSP 240
Qy 241 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFDPVPLHFNLAASSQGG 300
Db 241 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFDPVPLHFNLAASSQGG 300
Qy 301 GYDMRRLDGTWVSRHPEKAVTFVENHDTOPGQSLESTVQTFWPKPLAYAFILITRESGY 360
Db 301 GYDMRRLDGTWVSRHPEKAVTFVENHDTOPGQSLESTVQTFWPKPLAYAFILITRESGY 360
Qy 361 VFYGDYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPHDYIDHPDVIGWTRGDSAA 420
Db 361 VFYGDYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPHDYIDHPDVIGWTRGDSAA 420
Qy 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGGEHFNVDGVSIIY 480
Db 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGGEHFNVDGVSIIY 480
Qy 481 VQK 483
Db 481 VQK 483

RESULT 6
US-10-184-771-4
; Sequence 4, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borcherdt, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
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; PRIOR APPLICATION NUMBER: US/09/636,252
 ; PRIOR FILING DATE: 2000-08-10
 ; PRIOR APPLICATION NUMBER: 08/683,838
 ; PRIOR FILING DATE: 1996-07-18
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 514
 ; TYPE: PRT
 ; ORGANISM: B. amyloliquefaciens
 US-10-184-771-4

Query Match 100.0%; Score 2638; DB 14; Length 514;
 Best Local Similarity 100.0%; Pred. No. 2.7e-238;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
 DB 32 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 91
 QY 61 DLGFEQKGTVRTKYGTGKSELQDAIGSLHSRNVOYGDVVLNKHAGADATEDVTAVERN 120
 DB 92 DLGFEQKGTVRTKYGTGKSELQDAIGSLHSRNVOYGDVVLNKHAGADATEDVTAVERN 151
 QY 121 ANRQETSEYQIKAWTDFRPPGRGNTYSDFKWHYHFDGADWDESKISRIIPKFRGEGK 180
 DB 152 ANRQETSEYQIKAWTDFRPPGRGNTYSDFKWHYHFDGADWDESKISRIIPKFRGEGK 211
 QY 181 AWDWEVSSNGNYDYLKADVDYDHPDVVAETKKGWGWYANELSLDGFRIIDAAKHIFSP 240
 DB 212 AWDWEVSSNGNYDYLKADVDYDHPDVVAETKKGWGWYANELSLDGFRIIDAAKHIFSP 271
 QY 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASSQGG 300
 DB 272 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASSQGG 331
 QY 301 GYDMRLLDGTVVSRRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAYAFILTRREGSYPQ 360
 DB 332 GYDMRLLDGTVVSRRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAYAFILTRREGSYPQ 391
 QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRREGSSAA 420
 DB 392 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRREGSSAA 451
 QY 421 KSGLAALITDGGGSKMYAGLKNAGETWYDITGNRSNTVKIGSDGWGEFHVNDGVSIIY 480
 DB 452 KSGLAALITDGGGSKMYAGLKNAGETWYDITGNRSNTVKIGSDGWGEFHVNDGVSIIY 511
 QY 481 VQK 483
 DB 512 VQK 514

RESULT 7
 US-09-769-864-5
 ; Sequence 5, Application US/09769864
 ; Patent No. US20010039253A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Borchert, Torben V.
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Nielsen, Bjarne
 ; APPLICANT: Nissen, Torben L.
 ; APPLICANT: Kjaerulff, Soren
 ; TITLE OF INVENTION: Alpha-Amulase Mutants
 ; FILE REFERENCE: 5368.200-US
 ; CURRENT APPLICATION NUMBER: US/09/769,864
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 09/183,412
 ; PRIOR FILING DATE: 1998-10-30
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 5

; LENGTH: 480
 ; TYPE: PRT
 ; ORGANISM: Bacillus amyloliquefaciens
 US-09-769-864-5
 Query Match 99.5%; Score 2624; DB 9; Length 480;
 Best Local Similarity 100.0%; Pred. No. 5.1e-237;
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
 DB 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
 QY 61 DLGFEQKGTVRTKYGTGKSELQDAIGSLHSRNVOYGDVVLNKHAGADATEDVTAVERN 120
 DB 61 DLGFEQKGTVRTKYGTGKSELQDAIGSLHSRNVOYGDVVLNKHAGADATEDVTAVERN 120
 QY 121 ANRQETSEYQIKAWTDFRPPGRGNTYSDFKWHYHFDGADWDESKISRIIPKFRGEGK 180
 DB 121 ANRQETSEYQIKAWTDFRPPGRGNTYSDFKWHYHFDGADWDESKISRIIPKFRGEGK 180
 QY 181 AWDWEVSSNGNYDYLKADVDYDHPDVVAETKKGWGWYANELSLDGFRIIDAAKHIFSP 240
 DB 181 AWDWEVSSNGNYDYLKADVDYDHPDVVAETKKGWGWYANELSLDGFRIIDAAKHIFSP 240
 QY 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASSQGG 300
 DB 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASSQGG 300
 QY 301 GYDMRLLDGTVVSRRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAYAFILTRREGSYPQ 360
 DB 301 GYDMRLLDGTVVSRRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAYAFILTRREGSYPQ 360
 QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRREGSSAA 420
 DB 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRREGSSAA 420
 QY 421 KSGLAALITDGGGSKMYAGLKNAGETWYDITGNRSNTVKIGSDGWGEFHVNDGVSIIY 480
 DB 421 KSGLAALITDGGGSKMYAGLKNAGETWYDITGNRSNTVKIGSDGWGEFHVNDGVSIIY 480

RESULT 8
 US-10-665-667-5
 ; Sequence 5, Application US/10665667
 ; Publication No. US20040038368A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Borchert, Torben V.
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Nielsen, Bjarne
 ; APPLICANT: Nissen, Torben L.
 ; APPLICANT: Kjaerulff, Soren
 ; TITLE OF INVENTION: Alpha-Amulase Mutants
 ; FILE REFERENCE: 5368.200-US
 ; CURRENT APPLICATION NUMBER: US/10/665,667
 ; CURRENT FILING DATE: 2003-09-19
 ; PRIOR APPLICATION NUMBER: US/09/769,864
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 09/183,412
 ; PRIOR FILING DATE: 1998-10-30
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 480
 ; TYPE: PRT
 ; ORGANISM: Bacillus amyloliquefaciens
 US-10-665-667-5

Query Match 99.5%; Score 2624; DB 12; Length 480;
 Best Local Similarity 100.0%; Pred. No. 5.1e-237;
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIIPPAYKGLSQSDNGYGPYDLY 60
|
|
|
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIIPPAYKGLSQSDNGYGPYDLY 60
|
|
|
QY 61 DLGEFOQKGTVRTKYGTKSELDQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP 120
|
|
|
Db 61 DLGEFOQKGTVRTKYGTKSELDQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP 120
|
|
|
QY 121 ANRNETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYHFDGADWDESKIRIFKFRGEGK 180
|
|
|
Db 121 ANRNETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYHFDGADWDESKIRIFKFRGEGK 180
|
|
|
QY 181 AWDWEVSSENGNDYLMYADVDDHPDVVAETKKGWIWYANELSLDGFRIIDAAKHIFSF 240
|
|
|
Db 181 AWDWEVSSENGNDYLMYADVDDHPDVVAETKKGWIWYANELSLDGFRIIDAAKHIFSF 240
|
|
|
QY 241 LRWDVQAVRQATCKEMFTVAEYQNNAGKLENLYNKTSEFNQSVDFVPLHFNLAASQGG 300
|
|
|
Db 241 LRWDVQAVRQATCKEMFTVAEYQNNAGKLENLYNKTSEFNQSVDFVPLHFNLAASQGG 300
|
|
|
QY 301 GYDMRLLDGTVVSRRPEKAVTFVFNHDTQPGOSLESTVQTFKPLAYAFILTRREGYPQ 360
|
|
|
Db 301 GYDMRLLDGTVVSRRPEKAVTFVFNHDTQPGOSLESTVQTFKPLAYAFILTRREGYPQ 360
|
|
|
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIQWTRREGDSAA 420
|
|
|
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIQWTRREGDSAA 420
|
|
|
QY 421 KSGLAALITDPGCGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGVSIIY 480
|
|
|
Db 421 KSGLAALITDPGCGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGVSIIY 480
|
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|
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RESULT 9

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US-10-644-187-4
; Sequence 4, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Prantzen, Henrik
; APPLICANT: Borchert, Torben
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; PRIOR FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Bacillus amylioliquefaciens
US-10-644-187-4
```

```
Query Match 99.5%; Score 2624; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 5.1e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIIPPAYKGLSQSDNGYGPYDLY 60
|
|
|
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIIPPAYKGLSQSDNGYGPYDLY 60
|
|
|
QY 61 DLGEFOQKGTVRTKYGTKSELDQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP 120
|
|
|
```

```
Db 61 DLGEFOQKGTVRTKYGTKSELDQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP 120
|
|
|
QY 121 ANRNETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYHFDGADWDESKIRIFKFRGEGK 180
|
|
|
Db 121 ANRNETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYHFDGADWDESKIRIFKFRGEGK 180
|
|
|
QY 181 AWDWEVSSENGNDYLMYADVDDHPDVVAETKKGWIWYANELSLDGFRIIDAAKHIFSF 240
|
|
|
Db 181 AWDWEVSSENGNDYLMYADVDDHPDVVAETKKGWIWYANELSLDGFRIIDAAKHIFSF 240
|
|
|
QY 241 LRWDVQAVRQATCKEMFTVAEYQNNAGKLENLYNKTSEFNQSVDFVPLHFNLAASQGG 300
|
|
|
Db 241 LRWDVQAVRQATCKEMFTVAEYQNNAGKLENLYNKTSEFNQSVDFVPLHFNLAASQGG 300
|
|
|
QY 301 GYDMRLLDGTVVSRRPEKAVTFVFNHDTQPGOSLESTVQTFKPLAYAFILTRREGYPQ 360
|
|
|
Db 301 GYDMRLLDGTVVSRRPEKAVTFVFNHDTQPGOSLESTVQTFKPLAYAFILTRREGYPQ 360
|
|
|
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIQWTRREGDSAA 420
|
|
|
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIQWTRREGDSAA 420
|
|
|
QY 421 KSGLAALITDPGCGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGVSIIY 480
|
|
|
Db 421 KSGLAALITDPGCGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGVSIIY 480
|
|
|
```

RESULT 10

```
US-10-327-837-5
; Sequence 5, Application US/10327837
; Publication No. US20030211959A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgaard-Prantzen, Henrik
; APPLICANT: Oultup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Hoeck, Lisbeth Hedegaard
; APPLICANT: Nielsen, Vibeke Skovgaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 480
; TYPE: PRT
; ORGANISM: B. amylioliquefaciens
US-10-327-837-5
```

```
Query Match 99.5%; Score 2624; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 5.1e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIIPPAYKGLSQSDNGYGPYDLY 60
|
|
|
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIIPPAYKGLSQSDNGYGPYDLY 60
|
|
|
QY 61 DLGEFOQKGTVRTKYGTKSELDQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP 120
|
|
|
Db 61 DLGEFOQKGTVRTKYGTKSELDQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP 120
|
|
|
QY 121 ANRNETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYHFDGADWDESKIRIFKFRGEGK 180
|
|
|
Db 121 ANRNETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYHFDGADWDESKIRIFKFRGEGK 180
|
|
|
QY 181 AWDWEVSSENGNDYLMYADVDDHPDVVAETKKGWIWYANELSLDGFRIIDAAKHIFSF 240
|
|
|
Db 181 AWDWEVSSENGNDYLMYADVDDHPDVVAETKKGWIWYANELSLDGFRIIDAAKHIFSF 240
|
|
|
```

QY 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 300
 DB 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 300
 QY 301 GYDMRRLDGTVVSRHPEKAVTFVFNHDTOPGQSLESTVQWFKPLAYAFILITRESGYPO 360
 DB 301 GYDMRRLDGTVVSRHPEKAVTFVFNHDTOPGQSLESTVQWFKPLAYAFILITRESGYPO 360
 QY 361 VFYGDYMTGKTSPEKIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTRGDSAA 420
 DB 361 VFYGDYMTGKTSPEKIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTRGDSAA 420
 QY 421 KSLGAAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
 DB 421 KSLGAAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480

RESULT 11

US-10-186-042-4
 ; Sequence 4, Application US/10186042
 ; Publication No. US20030171236A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Bisgard-Frantzen, Henrik
 ; TITLE OF INVENTION: Alpha-Amylase Mutants
 ; FILE REFERENCE: 4796.204-US
 ; CURRENT APPLICATION NUMBER: US/10/186,042
 ; PRIOR FILING DATE: 2002-06-28
 ; PRIOR APPLICATION NUMBER: US/09/672,459
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 09/182,859
 ; PRIOR FILING DATE: 1998-10-29
 ; PRIOR APPLICATION NUMBER: 0515/96
 ; PRIOR FILING DATE: 1996-04-30
 ; PRIOR APPLICATION NUMBER: 0712/96
 ; PRIOR FILING DATE: 1996-06-28
 ; PRIOR APPLICATION NUMBER: 0775/96
 ; PRIOR FILING DATE: 1996-07-11
 ; PRIOR APPLICATION NUMBER: 1263/96
 ; PRIOR FILING DATE: 1996-11-08
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; TYPE: PRT
 ; ORGANISM: Bacillus amyloliquefaciens
 US-10-186-042-4

Query Match 99.5%; Score 2624; DB 14; Length 480;
 Best Local Similarity 100.0%; Pred. No. s.le-237;
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVMIPPAYKGLSQSDNGYGYDLY 60
 DB 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVMIPPAYKGLSQSDNGYGYDLY 60
 QY 61 DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHAGADATEDVTAVERN 120
 DB 61 DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHAGADATEDVTAVERN 120
 QY 121 ANRNOETSEYQIKAWTDPRFPGRGNTYSDFKWHYHFDGADWDESKISRIFKPRGEGK 180
 DB 121 ANRNOETSEYQIKAWTDPRFPGRGNTYSDFKWHYHFDGADWDESKISRIFKPRGEGK 180
 QY 181 AWDWEVSSENGNYDLYMAYADVDYDHPDVVAETKKWGIWYANELSLDGFPRIDAAKHKPSF 240
 DB 181 AWDWEVSSENGNYDLYMAYADVDYDHPDVVAETKKWGIWYANELSLDGFPRIDAAKHKPSF 240
 QY 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 300
 DB 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 300

QY 301 GYDMRRLDGTVVSRHPEKAVTFVFNHDTOPGQSLESTVQWFKPLAYAFILITRESGYPO 360
 DB 301 GYDMRRLDGTVVSRHPEKAVTFVFNHDTOPGQSLESTVQWFKPLAYAFILITRESGYPO 360
 QY 361 VFYGDYMTGKTSPEKIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTRGDSAA 420
 DB 361 VFYGDYMTGKTSPEKIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTRGDSAA 420
 QY 421 KSLGAAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
 DB 421 KSLGAAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
 RESULT 12
 US-10-184-771-13
 ; Sequence 13, Application US/10184771
 ; Publication No. US20030170769A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Bisgard-Frantzen, Henrik
 ; APPLICANT: Borchert, Torben Vedel
 ; TITLE OF INVENTION: Alpha-Amylase Mutants
 ; FILE REFERENCE: 0776/1F216-US2
 ; CURRENT APPLICATION NUMBER: US/10/184,771
 ; PRIOR FILING DATE: 2002-06-28
 ; PRIOR APPLICATION NUMBER: US/09/636,252
 ; PRIOR FILING DATE: 2000-08-10
 ; PRIOR APPLICATION NUMBER: 08/683,838
 ; PRIOR FILING DATE: 1996-07-18
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 13
 ; LENGTH: 483
 ; TYPE: PRT
 ; ORGANISM: Bascillius
 US-10-184-771-13

Query Match 94.2%; Score 2486; DB 14; Length 483;
 Best Local Similarity 93.4%; Pred. No. 4.5e-224;
 Matches 451; Conservative 16; Mismatches 16; Indels 0; Gaps 0;
 QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVMIPPAYKGLSQSDNGYGYDLY 60
 DB 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVMIPPAYKGLSQSDNGYGYDLY 60
 QY 61 DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHAGADATEDVTAVERN 120
 DB 61 DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHAGADATEDVTAVERN 120
 QY 121 ANRNOETSEYQIKAWTDPRFPGRGNTYSDFKWHYHFDGADWDESKISRIFKPRGEGK 180
 DB 121 ANRNOETSEYQIKAWTDPRFPGRGNTYSDFKWHYHFDGADWDESKISRIFKPRGEGK 180
 QY 181 AWDWEVSSENGNYDLYMAYADVDYDHPDVVAETKKWGIWYANELSLDGFPRIDAAKHKPSF 240
 DB 181 AWDWEVSSENGNYDLYMAYADVDYDHPDVVAETKKWGIWYANELSLDGFPRIDAAKHKPSF 240
 QY 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 300
 DB 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 300
 QY 301 GYDMRRLDGTVVSRHPEKAVTFVFNHDTOPGQSLESTVQWFKPLAYAFILITRESGYPO 360
 DB 301 GYDMRRLDGTVVSRHPEKAVTFVFNHDTOPGQSLESTVQWFKPLAYAFILITRESGYPO 360
 QY 361 VFYGDYMTGKTSPEKIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTRGDSAA 420
 DB 361 VFYGDYMTGKTSPEKIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTRGDSAA 420
 QY 421 KSLGAAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
 DB 421 KSLGAAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480

QY 481 VQK 483
||:
Db 481 VQR 483

RESULT 13

US-10-146-327-2
; Sequence 2, Application US/10146327
; Publication NO. US20030044954A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Biegaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/10/146,327
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/537,168
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PA 1999 00437
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/127,427
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-10-146-327-2

Query Match 83.4%; Score 2201; DB 14; Length 481;
Best Local Similarity 81.6%; Pred. No. 2.4e-197;
Matches 394; Conservative 38; Mismatches 49; Indels 2; Gaps 1;
QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAAHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAAHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRTKYGTSGELQDAIGSLHNRNVQVGVVNLNKHAGADATEDVTAVEVNP 120
Db 61 DLGEFHQKGTVRTKYGTSGELQSAIKSLHNRDINVYGVVNLNKHGGADATEDVTAVEVDP 120
QY 121 ANRNOETSEBYQIKAWTDFFPGRGNTYSDPKWYHFDGADWDSEKISRIKFRGEGK 180
Db 121 ADNRVLSGHLIKAWTHFFPGRGSTYSDPKWYHFDGTDWDESKRLARIYKF--QKG 178
QY 181 AWDWEVSSNGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHKFSF 240
Db 179 TWDEVSNEFNGNDYLMYADFDYDHPDVAEIKWGTWYANELQDGFRLDVAKHKFSF 238
QY 241 LRDMVQAVROATGKEMFTVAEYQNNAGKLENLYNKTSFNQSVDPVPLHFNLAQASQGG 300
Db 239 LRDMVNVREKTKGEMFTVAEYNSDLGALENLYNKTNFNHNSVDFVPLHYQFHAASQGG 298
QY 301 GYDMRLLDGTVVSRHPEKAVTFVNHDTOPGQSLESTVQTPKPLAYAIFILITRESGYPQ 360
Db 299 GYDMRKLNGTVVSKHPLKAVTFVNDHDTOPGQSLESTVQTPKPLAYAIFILITRESGYPQ 358
QY 361 VFYGDWYGTGTSKPEIPSLKDNIEPIILKARKEYAVGPDHYDHPDVIQWTRGDSAA 420
Db 359 VFYGDWYGTGDSQREIPALKKHIEPIILKARKQYAGQADHYDHHDIVQWTRGDSVA 418
QY 421 KSGLAALITDPGSGKEMYAGLNAGETWYDITGNRSDTVKIGSDGWFHFNVDGVSIIY 480
Db 419 NSGLAALITDPGGAKEYVGRQNAGETWHDITGNRSEPPVINSEGEHFHVGSGVSIIY 478
QY 481 VQK 483
||:
Db 479 VQR 481

RESULT 14

US-10-081-872-114
; Sequence 114, Application US/10081872
; Publication No. US2003012534A1
; GENERAL INFORMATION:
; APPLICANT: Callen, Walter
; APPLICANT: Richardson, Toby
; APPLICANT: Frey, Gerhard
; APPLICANT: Short, Jay M.
; APPLICANT: Mathur, Eric J.
; APPLICANT: Gray, Kevin A.
; APPLICANT: Kerovuo, Janne S.
; APPLICANT: Slupska, Malgorzata
; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
; FILE REFERENCE: 09010-108001
; CURRENT APPLICATION NUMBER: US/10/081,872
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,495
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/270,496
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/291,122
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Environmental
US-10-081-872-114

Query Match 83.1%; Score 2193; DB 14; Length 512;
Best Local Similarity 80.7%; Pred. No. 1.5e-196;
Matches 390; Conservative 43; Mismatches 48; Indels 2; Gaps 1;
QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAAHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Db 32 LNTGLMQYFEWYTPNDGQHWKRLQNDASAYLAEGITAVWIPPAYKGLSQSDNGYGPYDLY 91
QY 61 DLGEFOQKGTVRTKYGTSGELQDAIGSLHNRNVQVGVVNLNKHAGADATEDVTAVEVNP 120
Db 92 DLGEFHQKGTVRTKYGTSGELQSAIKSLHNRDINVYGVVNLNKHGGADATEDVTAVEVDP 151
QY 121 ANRNOETSEBYQIKAWTDFFPGRGNTYSDPKWYHFDGADWDSEKISRIKFRGEGK 180
Db 152 ADNRVLSGSHRIKAWTHFFPGRGSTYSDPKWYHFDGTDWDESKRLARIYKF--QKG 209
QY 181 AWDWEVSSNGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHKFSF 240
Db 210 AWDWEVSNENGNDYLMYADIDYDHPDVAEIKWGTWYANELQDGFRLDVAKHKFSF 269
QY 241 LRDMVQAVROATGKEMFTVAEYQNNAGKLENLYNKTSFNQSVDPVPLHFNLAQASQGG 300
Db 270 LRDMVNVREKTKGEMFTVAEYQNDLGALENLYNKTNFNHNSVDFVPLHYQFHAASQGG 329
QY 301 GYDMRLLDGTVVSRHPEKAVTFVNHDTOPGQSLESTVQTPKPLAYAIFILITRESGYPQ 360
Db 330 GYDMRKLNGTVVSKHPLKAVTFVNDHDTOPGQSLESTVQTPKPLAYAIFILITRESGYPQ 389
QY 361 VFYGDWYGTGTSKPEIPSLKDNIEPIILKARKEYAVGPDHYDHPDVIQWTRGDSAA 420
Db 390 VFYGDWYGTGDSQREIPALKKHIEPIILKARKQYAGQADHYDHHDIVQWTRGDSVA 449
QY 421 KSGLAALITDPGSGKEMYAGLNAGETWYDITGNRSDTVKIGSDGWFHFNVDGVSIIY 480
Db 450 NSGLAALITDPGGAKEYVGRQNAGETWHDITGNRSEPPVINSEGEHFHVGSGVSIIY 509
QY 481 VQK 483
||:
Db 510 VQR 512

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:46:32 ; Search time 8.50628 Seconds
(without alignments)
2968.867 Million cell updates/sec

Title: US-09-925-576C-12

Perfect score: 2708

Sequence: 1 HHNGTGTWQYFEWYLPND.....ADGNGFVNGSVSIWVAK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2613	96.5	518	1 AMT6_BACS7	P19571 bacillus sp
2	1887	69.7	512	1 AMY_BACLI	P06278 bacillus li
3	1859.5	68.7	549	1 AMY_BACST	P06279 bacillus st
4	1847	68.2	514	1 AMY_BACAM	P00692 bacillus am
5	1105	40.8	494	1 AMY2_SALTY	P26613 salmonella
6	1075	39.7	495	1 AMY2_ECOLI	P26612 escherichia
7	320	11.8	1196	1 AMYB_PAEFO	P21543 paenibacill
8	283.5	10.5	421	1 AMYA_VIGMU	P17859 vigna mungo
9	270.5	10.0	551	1 AMT4_PBSA	P22963 pseudomonas
10	270	10.0	440	1 AM3A_ORYSA	P27932 oryza sativ
11	267	9.9	548	1 AMT4_PSEST	P23507 pseudomonas
12	264	9.7	368	1 AMY3_HORVU	P04747 hordeum vul
13	263.5	9.7	435	1 AM3D_ORYSA	P27933 oryza sativ
14	262	9.7	427	1 AMY2_HORVU	P04063 hordeum vul
15	259	9.6	719	1 AMYM_BACST	P19531 bacillus st
16	256.5	9.5	428	1 AMY1_ORYSA	P17654 oryza sativ
17	256.5	9.5	438	1 AMY1_HORVU	P00693 hordeum vul
18	254	9.4	429	1 AMY6_HORVU	P04750 hordeum vul
19	253	9.3	437	1 AM3C_ORYSA	P27939 oryza sativ
20	253	9.3	438	1 AM3B_ORYSA	P27937 oryza sativ
21	252.5	9.3	710	1 CDGT_THERU	P26827 thermoanaer
22	250.5	9.3	413	1 AMY3_WHEAT	P08117 triticum ae
23	247.5	9.1	713	1 CDGT_PAEWA	P31835 paenibacill
24	246.5	9.1	498	1 AMYA_ASAPW	Q02905 aspergillus
25	246.5	9.1	499	1 AMYB_ASAPW	Q02906 aspergillus
26	243.5	9.0	499	1 AMYA_ASPOP	P10529 aspergillus
27	243	9.0	437	1 AM3E_ORYSA	P27934 oryza sativ
28	243	9.0	713	1 CDGT_BACSP	P30921 bacillus sp
29	242.5	9.0	442	1 MGTA_THENA	O86956 thermotoga
30	241.5	8.9	718	1 CDGT_BACCI	P30920 bacillus ci
31	240.5	8.9	499	1 AMY ASPSH	P30292 aspergillus
32	240	8.9	528	1 AMY_BACCI	P08137 bacillus ci
33	234	8.6	712	1 CDGT_BACS3	P09121 bacillus sp

RESULT 1

ID	AMT6_BACS7	STANDARD;	PRT;	518 AA.
AC	P19571;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (G6-amylase)			
DE	(Maltotetraose-producing amylase) (Exo-maltohexaohydrolase).			
OS	Bacillus sp. (strain 707).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1416;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.			
RX	MEDLINE=88162814; PubMed=3258152;			
RA	Takamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;			
RT	"Nucleotide sequence of the maltotetraose-producing amylase gene from an alkalophilic Bacillus sp. #707 and structural similarity to			
RT	liquefying type alpha-amylases."			
RL	Biochem. Biophys. Res. Commun. 151:25-31(1988).			
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages in amylose polysaccharides so as to remove successive maltotetraose residues from the non-reducing chain ends.			
CC	-1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By similarity).			
CC	-1- PATHWAY: Starch degradation.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; M18862; AAA22231.1; ..			
DR	PIR; A27705; A27705.			
DR	HSP; P06278; 1VUS.			
DR	InterPro; IPR006589; Alp_amy1_cat_sub.			
DR	InterPro; IPR006047; Alpha_amy1_cat.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Pfam; PF00128; alpha-amylase; 1.			
DR	PRINTS; PR00110; ALPHAMYLASE.			
DR	SMART; SM00642; Amy; 1.			
DR	HydroLase; Glycosidase; Carbohydrate metabolism; Signal.			
FT	SIGNAL 1 33			
FT	CHAIN 34 518			
FT	ACT_SITE 269 269			
FT	BY SIMILARITY.			
FT	ACT_SITE 273 273			
FT	BY SIMILARITY.			
FT	ACT_SITE 366 366			
FT	METAL 139 139			
FT	METAL 196 196			
FT	METAL 219 219			
FT	GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE.			
FT	BY SIMILARITY.			
FT	BY SIMILARITY.			
FT	CALCIUM 1 (BY SIMILARITY).			
FT	CALCIUM 2 AND SODIUM (BY SIMILARITY).			
FT	CALCIUM 2 (VIA CARBONYL OXYGEN) (BY SIMILARITY).			

ALIGNMENTS

P31747 bacillus sp
P31746 bacillus sp
P17692 bacillus sp
P31797 bacillus st
P05618 bacillus sp
P21567 saccharomyc
P80099 thermotoga
P33379 bacillus ci
Q05884 streptomyces
P27935 oryza sativ
P27941 oryza sativ
P14014 bacillus li

34 233.5 8.6 718 1 CDGT_BACSS
35 233 8.6 703 1 CDGT_BACS2
36 232 8.6 713 1 CDGT_BACS8
37 226.5 8.4 711 1 CDGT_BACST
38 226 8.3 713 1 CDGT_BACS0
39 225 8.3 494 1 AMY1_SACFI
40 224.5 8.3 441 1 MGTA_THENA
41 224 8.3 713 1 CDGT_BACCI
42 223.5 8.3 919 1 AMY_STRLI
43 222.5 8.2 443 1 AM2A_ORYSA
44 222.5 8.2 445 1 AMC2_ORYSA
45 222.5 8.2 718 1 CDGT_BACLI

FT	METAL	221	221	CALCIUM 2 AND SODIUM (BY SIMILARITY).
FT	METAL	232	232	CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT	METAL	238	238	CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT	METAL	240	240	CALCIUM 2 (BY SIMILARITY).
FT	METAL	242	242	CALCIUM 2 (BY SIMILARITY).
FT	METAL	273	273	CALCIUM 1 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
SQ	SEQUENCE	518 AA;	59009 MW;	3A961E21612682C4 CRC64;
Query Match				
Best Local Similarity		96.5%;	Score 2613;	DB 1; Length 518;
Matches		463; Conservative	13; Mismatches	9; Indels 0; Gaps 0;
Qy	1	HHNGTGTMOYFEWYLPNDGNHNRRLSDASNLKDGISAVWT	PPPAWKASQNDVGGA	60
Db	34	HHNGTGTMOYFEWYLPNDGNHNRRLSDASNLKDGITAVW	PPPAWKASQNDVGGA	93
Qy	61	YDLVGLGFENKGTIRTKYGRNLOQAVNALKSGIQVYGDV	VVMNHKGGADATEMVR	120
Db	94	YDLVGLGFENKGTIRTKYGRNLOQAVNALKSGIQVYGDV	VVMNHKGGADATEMVR	153
Qy	121	EVNPNRNQEVSGEYTTIEAWTKFDPGRGNTHSNFKRWYH	FDGVDWQSKLNNRIYKF	180
Db	154	EVNPNRNQEVSGEYTTIEAWTKFDPGRGNTHSNFKRWYH	FDGVDWQSKLNNRIYKF	213
Qy	181	RGDGKGDWEVDTEGNYDILMYADIDMDHPEVNVNELRN	NGWVYNTLGLDGFRI	240
Db	214	RGHGKAWDWEVDTEGNYDILMYADIDMDHPEVNVNELRN	NGWVYNTLGLDGFRI	273
Qy	241	IKYSFTDWINHVRSATGKNFAVAEFKNDGLGAIENYLNK	TWNHSHVDFVPLHYNLYNA	300
Db	274	IKYSFTDWINHVRSATGKNFAVAEFKNDGLGAIENYLNK	TWNHSHVDFVPLHYNLYNA	333
Qy	301	SKSGGNYDMRQIFNGTIVVQHPMAVTFVDNHDSDQPEAL	ESFVEWFKPLAVALTLTRE	360
Db	334	SKSGGNYDMRQIFNGTIVVQHPMAVTFVDNHDSDQPEAL	ESFVEWFKPLAVALTLTRE	393
Qy	361	QGTPSVFYGYGYPHPTGVPAMKSKIDPILAEARKYAYG	QNDYLDHNNIIGWTREGNTA	420
Db	394	QGTPSVFYGYGYPHPTGVPAMKSKIDPILAEARKYAYG	QNDYLDHNNIIGWTREGNTA	453
Qy	421	HPNSGLATIMSDGAGGKMWFGVGRNKGQVWTDITGNR	AGTGTINADGWNFSVNGGSVS	480
Db	454	HPNSGLATIMSDGAGGKMWFGVGRNKGQVWTDITGNR	AGTGTINADGWNFSVNGGSVS	513
Qy	481	IWNK 485		
Db	514	IWNK 518		

RESULT 2

AMY_BACLI	ID	AMY_BACLI	STANDARD;	PRT;	512 AA.
AC	P06278;	O84171;			
DT	01-JAN-1988	(Rel. 06, Created)			
DT	01-JAN-1988	(Rel. 06, Last sequence update)			
DT	15-MAR-2004	(Rel. 43, Last annotation update)			
DE	Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan				
DE	Glucanohydrolase) (BLA).				
GN	AMYS OR AMYL				
OS	Bacillus licheniformis.				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=1402;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 27811;				
RX	MEDLINE=86111694; PubMed=2418011;				
RA	Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,				
RA	Trukagoshi N., Uda S.;				
RT	"Complete nucleotide sequence of a gene coding for heat- and				
RT	pH-stable alpha-amylase of Bacillus licheniformis: comparison of the				
RT	amino acid sequences of three bacterial liquefying alpha-amylases				
RT	deduced from the DNA sequences."				

RL	J. Biochem.	98:1147-1156(1985).			
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86195857; PubMed=3009417;				
RA	Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,				
RA	Carmona C., Requadt C.;				
RT	"Structural genes encoding the thermophilic alpha-amylases of				
RT	Bacillus stearothermophilus and Bacillus licheniformis."				
RL	J. Bacteriol.	166:635-643(1986).			
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	Shahosseini M., Ziaei A.A., Ghaemi N., Pourbabeai A.A.;				
RA	"An unusual DNA sequence encoded a hyperthermostable alpha-amylase."				
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE OF 1-104 FROM N.A.				
RX	MEDLINE=84185455; PubMed=6609154;				
RA	Stephens M.A., Orlepp S.A., Ollington J.F., McConnell D.J.;				
RT	"Nucleotide sequence of the 5' region of the Bacillus licheniformis				
RT	alpha-amylase gene: comparison with the B. amyloliquefaciens gene."				
RL	J. Bacteriol.	158:369-372(1984).			
RN	[5]				
RP	SEQUENCE OF 1-29 FROM N.A.				
RX	MEDLINE=89213924; PubMed=2540150;				
RA	Laoide B.M., Chambliss G.H., McConnell D.J.;				
RT	"Bacillus licheniformis alpha-amylase gene, amyl, is subject to				
RT	promoter-independent catabolite repression in Bacillus subtilis."				
RL	J. Bacteriol.	171:2435-2442(1989).			
RN	[6]				
RP	SEQUENCE OF 30-47.				
RX	MEDLINE=82098050; PubMed=6172418;				
RA	Kuhn H., Fietzek P.P., Lampen J.O.;				
RT	"N-terminal amino acid sequence of Bacillus licheniformis				
RT	alpha-amylase: comparison with Bacillus amyloliquefaciens and				
RT	Bacillus subtilis enzymes."				
RL	J. Bacteriol.	149:372-373(1982).			
RN	[7]				
RP	MAPPING OF SUBSTRATE-BINDING SITE.				
RX	MEDLINE=21992788; PubMed=11997021;				
RA	Kandra L., Gyemant G., Remenyik J., Hovanszki G., Liptak A.;				
RT	"Action pattern and subsite mapping of Bacillus licheniformis				
RT	alpha-amylase (BLA) with modified maltooligosaccharide substrates."				
RL	FEBS Lett.	518:79-82(2002).			
RN	[8]				
RP	MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.				
RC	STRAIN=ATCC 6598;				
RX	MEDLINE=90368748; PubMed=2394736;				
RA	Declerck N., Joyet P., Gaillardin C., Masson J.M.;				
RT	"Use of amber suppressors to investigate the thermostability of				
RT	Bacillus licheniformis alpha-amylase. Amino acid replacements at 6				
RT	histidine residues reveal a critical position at His-133."				
RL	J. Biol. Chem.	265:15481-15488(1990).			
RN	[9]				
RP	MUTAGENESIS OF ALA-238.				
RC	STRAIN=ATCC 6598;				
RX	MEDLINE=96367070; PubMed=8771184;				
RA	Declerck N., Joyet P., Trosset J.Y., Garnier J., Gaillardin C.;				
RT	"Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:				
RT	multiple amino acid replacements and molecular modelling."				
RL	Protein Eng.	8:1029-1037(1995).			
RN	[10]				
RP	MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201;				
RP	ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLN-300;				
RP	AND GLU-365.				
RC	STRAIN=ATCC 6598;				
RX	MEDLINE=20425100; PubMed=10966804;				
RA	Declerck N., Machius M., Wiegand G., Huber R., Gaillardin C.;				
RT	"Probing structural determinants specifying high thermostability in				
RT	Bacillus licheniformis alpha-amylase."				
RL	J. Mol. Biol.	301:1041-1057(2000).			
RN	[11]				
RP	MUTAGENESIS OF GLN-293 AND ASN-294.				
RC	STRAIN=ATCC 6598;				


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Db 159 DRNOEISGTVQIQAWTKDFPFGNGTYSFSPKRWYHFDGVDWDESRKL-SRIYKFRGIGK 217
Qy 186 GWDEWEDVTENGNDYLYADIMDMHPEVNNELNMGVYNTLTGLDGRFIDAVKHKIKYSP 245
Db 218 AWDWEVDVTENGNDYLYADIMDMHPEVNNELNMGVYNTLTGLDGRFIDAVKHKIKYSP 277
Qy 246 TRDWINHVRATGKNMFAEFKNDLGALENYLNKTNWHSVDFVPLHNLNASKSGG 305
Db 278 FPDWLSDRVSQTGKPLFTVGEYWSYDINKLHNTKMTNGTMSLFDAPLHKNKFTASKSGG 337
Qy 306 NYDMROIENGTVVQRHHPMAVTFVDNHDSDPERALSFVEWPKPLAYALTLTREQGYS 365
Db 338 TFDRLTMTLWKDQPTLAVTFVDNHDSDPERALSFVEWPKPLAYALTLTREQGYS 397
Qy 366 VFYGDYVIGTHGVPAKMSKIDPILKARQYAGRQNDYLDHNNIIGWTEGNTAHNSG 425
Db 398 VFYGDYVIGTHGVPAKMSKIDPILKARQYAGRQNDYLDHNNIIGWTEGNTAHNSG 457
Qy 426 LATIMSDGAGNKMVGRNKAQGVWTDITGNRAGVTINADGNGNFSVNGSVSIWV 483
Db 458 LAALITDGPCKGKMYVKGHAGKVFYDLTCNRSDDTITNSDGMGSEKVGNGSGSVWV 515

RESULT 4
ID AMY BACAM STANDARD; PRT; 514 AA.
AC P00692;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
OS Bacillus amyloliquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IH;
RX MEDLINE=83108808; PubMed=6185474;
RA Takkinen K., Pettersson R.F., Kalkkinen N., Palva I., Soederlund H.,
RA Kaeeriaeinen L.;
RT "Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens
RT deduced from the nucleotide sequence of the cloned gene.";
RL J. Biol. Chem. 258:1007-1013(1983).
RN [2]
RP SEQUENCE OF 32-222.
RX MEDLINE=80241725; PubMed=6156671;
RA Chung H.S., Friedberg P.;
RT "Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-
RT amylase.";
RL Biochem. J. 185:387-395(1980).
RN [3]
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE=82051296; PubMed=6170539;
RA Palva I., Pettersson R.F., Kalkkinen N., Lehtoavaara P., Sarvas M.,
RA Soederlund H., Takkinen K., Kaeeriaeinen L.;
RT "Nucleotide sequence of the promoter and NH2-terminal signal peptide
RT region of the alpha-amylase gene from Bacillus amyloliquefaciens.";
RL Gene 15:43-51(1981).
RN [4]
RP SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE=88137952; PubMed=2830166;
RA Ruchonen L., Hackman P., Lehtoavaara P., Knowles J.K.C., Karaenen S.;
RT "Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by
RT its own signal peptide from Saccharomyces cerevisiae host cells.";
RL Gene 59:161-170(1987).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.
RX MEDLINE=20384196; PubMed=10924103;
RA Brzozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase."
```

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QY 183 DGKWDHEVDTEGNYDLYMADIMDHPEVNVNLRNKGWVWYTYTLGLDGFRIIDAVKHK 242
Db 209 EGKAWDVESSGNGYDLYMADYDHPDVAETTKWGIWYANELSDGFRIDAAKHK 268
QY 243 YSFTRDWNHVRSATGKMPAVAFWKNLGAENLYNKTNNHNSVFDVPLHYNLNASK 302
Db 269 FSLRDLVQVQATGEMFTVAEYQNNACKLJENYLNKTSFNQSVDFDVLPHFNLQASS 328
QY 303 SGGNYDRQIFNGTVQORHPHVAITFVDNHDSPQEEALESFVEEWFKPLAYALTLTREG 362
Db 329 QGGYDMLRLDGTVSRHPEKATFVENHDTQPGQSLESTVQTFKPLAYALTLTREG 388
QY 363 YPSVFYGDYGIPTHG-----VPAMKSKIDIPLEAKOKYAYGRQNDYLDHNNHIGWTREG 417
Db 389 YPOVFYGDYMG--TKGTSRPEKSLKDNIEILKARKEYAYGPOHDYIDHPVIGWTREG 446
QY 418 NTAHPNSGLATIMSDGAGGNKMWFGVGRKAGOVWTDITGNRAGVTTNADGWNFSVNGG 477
Db 447 DSSAAKSGLAALITDGGPGSKRMYAGLNKAGETWYDITGNRSDFVTKGSDGWFHVNNDG 506
QY 478 SVSIWVKNK 485
Db 507 SVSIYVQK 514

RESULT 5
AMY2_SALTY
ID _AMY2_SALTY STANDARD; PRT; 494 AA.
AC P26613;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amyase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYA OR STM1963
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=SW1103;
RX MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amyase, AmyA.";
RL J. Bacteriol. 174:6644-6652(1992).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=Lt2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT Lt2.";
RL Nature 413:852-856(2001).
[3]
RN SEQUENCE OF 1-6 FROM N.A.
RC STRAIN=SW1103;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes.";
RL J. Gen. Microbiol. 138:1051-1065(1992).
[4]
RN SEQUENCE OF 476-494 FROM N.A.
RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIIB, including a

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RT large non-coding region.";
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -I- SUBUNIT: Monomer (By similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
-----
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CC or send an email to license@isb-sib.ch).
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CC
CC ENBL; L01643; AAA27110.1; -.
CC ENBL; A8008787; AAL20875.1; -.
CC ENBL; M85241; AAA27079.1; -.
CC ENBL; L13280; AAA71970.1; -.
CC PIR; B45738; B45738.
CC HSSP; P06278; 1VJS.
CC StyGene; SGI0011; amyA.
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alpha_amy1_cat.
CC Pfam; PF00128; alpha-amyase; 1.
CC SMART; SM00642; Aamy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
CC Complete proteome.
CC ACT_SITE 235 235 BY SIMILARITY.
CC ACT_SITE 265 265 BY SIMILARITY.
CC ACT_SITE 332 332 BY SIMILARITY.
CC METAL 104 104 CALCIUM (BY SIMILARITY).
CC METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
CC SIMILARITY).
CC
CC CONFLICT 462 462 L -> S (IN REF. 1).
CC SEQUENCE 494 AA; 56522 MW; 5C1E862FEDD5E47C CRC64;
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Query Match 40.8%; Score 1105; DB 1; Length 494;
Best Local Similarity 44.1%; Pred. No. 5.1e-67;
Matches 217; Conservative 77; Mismatches 180; Indels 18; Gaps 6;

QY 6 NCTMQLQYFEWYLPNDGNHNRNLRSDASNLKDKXGISAVMTPPAWKASQD-DVYGAYDIY 64
Db 3 NPTLLQYFHWYYPDGGKLSWSELAERADGLNDIGINWVLPACKGASGGYSGYDYDLF 62
QY 65 DLGEFNQKGTIRTKYGTNRNLOQAANVALKSNQIQYGVGVMMHKGADATMVAVEVNP 124
Db 63 DLGEFDQKGTIATKYGDKRQLLTALDAKKNIAVLDDVVVNNHKGADKERRIRQVRNQ 122
QY 125 NNRNDEVSGEYTIKAWTKFPPRGNGTHSNKRWYHFDGVDDQSRKLNRIYKFRGD- 183
Db 123 DRTQIDNNIIECEGWTRYTFPARAGYSNFIWDTHCFSGIDHINPD-EDGIFKIVNDY 181
QY 184 -GKGWDWEYDTEGNYDLYMADIMDHPEVNVNLRNKGWVWYTYTLGLDGFRIIDAVKHK 242
Db 182 TGDGNDQVDDMGNFYLMGENIDFRNHAVTEIKYWARWMEQTHCDGFLDAVKHIP 241
QY 243 YSFTRDWNHVRSATGKMPAVAFWKNLGAENLYNKTNNHNSVFDVPLHYNLNASK 302
Db 242 AMFYKEWIEHVOAVAPKPLFIVAETWSHEVDKLTQYIDQVQDKTLMFLDAPLQMKFEASR 301
QY 303 SGGNYDRQIFNGTVQORHPHVAITFVDNHDSPQEEALESFVEEWFKPLAYALTLTREG 362
Db 302 QGAETDMRHIFFTGLVEADPFHVTLVANHDTPQLEAPVEPWFKPLAYALILLRENG 361
QY 363 YPSVFYGDYGIPTH-----GVPAMKSKIDIPLEAKOKYAYGRQNDYLDHNNHII 411
Db 362 VPSVFYDLYGASVEDSGENGETCRVDMPTV-NQLDRLILARQRFAGHIGTLFFDHPNCTI 420
QY 412 GWTREGTAHPNSGLATIMSDGAGGNKMWFGVGRKAGOVWTDITGNRAGVTTNADGWN 471

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Db 421 AFSRSGTEENP--GCVVVLSNGDDGKTKLLGDNVANKTWKTRDFLGNRDEYVVTNDQGEAT 478
Qy 472 FSVNGGVSIVW 483
Db 479 FFCNAGSVSVW 490

RESULT 6
ID AMY2_ECOLI STANDARD; PRT; 495 AA.
AC P26612; P78072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYA OR B1927.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=JALL;
RX MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA."
RL J. Bacteriol. 174:6644-6652(1992).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayaishi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitagawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampaio G., Seki Y., Sivasubramanian S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-Kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map."
RL DNA Res. 3:379-392(1996).
RN [4]
RN SEQUENCE OF 1-5 FROM N.A.
RC STRAIN=JALL;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes."
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [5]
RN SEQUENCE OF 475-495 FROM N.A.
RC STRAIN=JALL;
RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIIb, including a
RT large non-coding region."
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).

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CC -1- SURCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L01642; AAA23810.1; --
CC EMBL; AE000285; AAC74994.1; --
CC EMBL; D90833; BAA15755.1; --
CC EMBL; M85240; -- NOT ANNOTATED_CDS.
CC EMBL; L13279; AAA82575.1; --
CC PIR; D64956; AA5738.
CC HSP; P06278; 1VJS.
CC EcoGene; EG11387; amyA.
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alpha_amy1_cat.
CC Pfam; PF00128; alpha-amylase; 1.
CC SMART; SM00642; Amy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
CC Complete proteome.
CC ACT_SITE 235 235 BY SIMILARITY.
CC ACT_SITE 265 265 BY SIMILARITY.
CC ACT_SITE 332 332 BY SIMILARITY.
CC METAL 104 104 CALCIUM (BY SIMILARITY).
CC METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
CC SIMILARITY).
CC CONFLICT 19 20 KL -> SS (IN REF. 1).
CC CONFLICT 109 109 A -> V (IN REF. 1).
CC CONFLICT 149 149 Q -> E (IN REF. 1).
CC CONFLICT 234 234 L -> I (IN REF. 1).
CC SEQUENCE 495 AA; 56639 MW; 26AF6797DDA54D6 CRC64;
Qy Query Match 39.7%; Score 1075; DB 1; Length 495;
Db Best Local Similarity 43.7%; Pred. No. 5.3e-65;
Qy Matches 215; Conservative 76; Mismatches 183; Indels 18; Gaps 6;
Qy 6 NGTMMQYFEWYLNNDGNHNNLRSDANLKDKGISAVWIIPAMKGSQN-DVGVGVDLY 64
Db 3 NPTLLQCFHWYPEGGKLPDLAERADGDFNDIGINMVLPPAYKGGSGVGVSYDLF 62
Qy 65 DLGEFNOKGIRTKYGRNQLQAAVNAKSGNGIQVYGDVVMNHKGGADATMVRVAVNP 124
Db 63 DLGEFDQKSGIPYKDGKAQLLAIDALKRNDIAVLDDVVVNHKGGADEKEAIRVQVNA 122
Qy 125 NNRNQVSGEYTIETAMTKPFGGRNTHSNFKRWYHFDGVWDQSKLNRIYKFGD- 183
Db 123 DDRQTIDEIIECEGWTRYTFPARAGQYSQFIWDFKCFSGIDHNPED-EDGIFKIVNDY 181
Qy 184 -GKGWDEVDTEGNYDLYADIDMDHPVVELRNWGVYNTLTGLDGFRTDAVGHK 242
Db 182 TGEWMDQDDDELGNFDYLMGENIDFRNHAFTBEIKYWARVWMEQTCQDGFRLDAVHIP 241
Qy 243 YSFTRDWINHVRSATGKMTFAVAFKNDLGATENLKNKNHNSVDFDVLHYNLYNASK 302
Db 242 AWFYKEWIEHVQVAPKPLFIVAEYWSHEVDKLTQYIDQVEGKTMLEFADLQMKFHEASR 301
Qy 303 SGGNYDMRQIFNGTVQVRHPMHAFTVDNHDSPPEALESFVEWFKPLAYALTLTREQ 362
Db 302 MGRDYDMTQIFTGTLEADPFHATVTLVANHDTQPLQALEAPVEWFKPLAYALTLENG 361
Qy 363 YPSVFYDYGIPTHGV-----PAMSKIDIPLEARQKYACRQNDYLDHNNII 411
Db 362 VPSVFYDLYGAHYEDVGGDQYTPIDMPIIB-QLDELIILARQRFARHGVQTLFPDHPNCI 420
Qy 412 GWTREGNTAHPSGLATIMSDGAGGNKMFVGRNKGQVMTDITGNRAGVTVINADGWN 471
Db 421 AFSRSGTDEFP--GCVVVNSNGDDGKTKLLGDNVANKTWKTRDFLGNRDEYVVTNDQGEAT 478

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QY 472 ESVNGGVSITWV 483
Db 479 FFCNGGVSVMV 490

RESULT 7
AMYB PAEPO STANDARD; PRT; 1196 AA.
AC F21543;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Beta/alpha-amylase precursor [includes: Beta-amylase (EC 3.2.1.2);
DE Alpha-amylase (EC 3.2.1.1)].
OS Paenibacillus polymyxa (Bacillus polymyxa).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=1406;
RN [1]
RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=87165765; PubMed=2435707;
RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "Cloning and nucleotide sequence of the gene coding for enzymatically
RT active fragments of the Bacillus polymyxa beta-amylase.";
RL J. Bacteriol. 169:1564-1570(1987).
RN [2]
RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=89123046; PubMed=2464578;
RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "A single gene directs synthesis of a precursor protein with beta-
RT and alpha-amylase activities in Bacillus polymyxa.";
RL J. Bacteriol. 171:375-382(1989).
RN [3]
RP SEQUENCE OF 1-776 FROM N.A.
RC STRAIN=ATCC 8523;
RX MEDLINE=87231094; PubMed=2438660;
RA Rhodes C., Strasser J., Friedberg F.;
RT "Sequence of an active fragment of B. polymyxa beta amylase.";
RL Nucleic Acids Res. 15:3934-3934(1987).
RN [4]
RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
RX MEDLINE=91215008; PubMed=1827035;
RA Uozumi N., Matsuda T., Tsukagoshi N., Uda S.;
RT "Structural and functional roles of cysteine residues of Bacillus
RT polymyxa beta-amylase.";
RL Biochemistry 30:4594-4599(1991).
CC -!- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 KDa ALPHA-AMYLASE AFTER
CC SECRETION.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
CC polysaccharides so as to remove successive maltose units from the
CC non-reducing ends of the chains.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: In the N-terminal section; belongs to family 14 of
CC glycosyl hydrolases.
CC -!- SIMILARITY: In the C-terminal section; belongs to family 13 of
CC glycosyl hydrolases.
CC
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CC
CC -----
CC EMBL; M15817; AAA85446.1; -.
CC EMBL; Y00150; CAA68344.1; -.

DR PIR; A29130; A29130.
DR HSP; P36924; 189Z.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006048; Alpha_amyl_C.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR005085; CBM_25.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR001554; Glyco_hydro_14.
DR Pfam; PF00128; alpha-amylase_1_14.
DR Pfam; PF02806; alpha-amylase_1_14.
DR Pfam; PF03423; CBM_25; 2.
DR Pfam; PF01373; Glyco_hydro_14; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR PRINTS; PR00750; BETAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
DR PROSITE; PS00506; BETA_AMYLASE_1; 1.
DR PROSITE; PS00679; BETA_AMYLASE_2; 1.
DR KW Multifunctional enzyme; Hydrolase; Glycosidase; Signal;
KW Polysaccharide degradation; Repeat.
FT SIGNAL 1 35
FT CHAIN 36 1196 BETA/ALPHA-AMYLASE.
FT DOMAIN 36 454 BETA-AMYLASE.
FT REPEAT 455 558
FT REPEAT 565 668
FT DOMAIN 669 1196 ALPHA-AMYLASE.
FT DISULFID 118 126
FT ACT_SITE 198 198
FT ACT_SITE 394 394
FT MUTAGEN 118 118
FT MUTAGEN 126 126
FT MUTAGEN 358 358
FT CONFLICT 1 1
FT CONFLICT 67 67
FT CONFLICT 100 100
FT CONFLICT 154 154
FT CONFLICT 177 177
FT CONFLICT 227 228
FT CONFLICT 330 330
FT CONFLICT 425 425
FT CONFLICT 493 493
FT CONFLICT 532 532
FT CONFLICT 559 559
FT CONFLICT 665 665
FT CONFLICT 681 681
FT CONFLICT 696 696
FT CONFLICT 725 728
FT CONFLICT 736 736
FT CONFLICT 741 741
FT CONFLICT 758 758
SQ SEQUENCE 1196 AA; 130893 MW; A41EA6B70F257064 CRC64;
Query Match 11.8%; Score 320; DB 1; Length 1196;
Best Local Similarity 23.3%; Fred. No. 6.5e-14;
Matches 121; Conservative 71; Mismatches 189; Indels 138; Gaps 24;
QY 1 HHNGTNGTMMQVFFENYLPNDGNHNRSLSDASNLKDGISAVWTPPAWKGSQNDV-CYG 59
Db 766 NYGFNSNNSDQKWH-----GGDQGIINKLDYIKNGMFTAIWITPTVMQKSEYAHGYH 821
QY 60 AYDLYDLGEFNQKGTIRTKYKTRNLQQAVALNALKSNGIQVYGVVMMHKGADATEMVRA 119
Db 822 TYDFY-----AVDGHGLTMDKLQELVRKAHDKNIAMVMDVVVNHGT----- 862
QY 120 VEVNPNNEQSVSGEYITEATWKEDF-PGRGNTHSNF-KRWYHFDGVDWDQSKLNRI 177
Db 863 -----DFQPGNGFAKAPFDKADWYHHNGDITDGDYNSNNQ- 897
QY 178 YKFRGDKGMDWEVDTEGNYDLYMADIDMDHPEVNVNLRNMGVWVTNTLGLDGFIDA 237
Db 898 -----WKI--ENG--DVAGLDLHNENFATNELKCNWKLLNETGIDGLDIT 942
QY 238 VKHIKYSFTRDWINHVSATCKMFAVEFWKNDLGAIEVNLKTNKNNHSVDFVPLHNL 297

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Db 943 VKHVPKFLKDF-----DQAANTFTWGEIHFHGPAYVGDY---TRYLDAALDFPMYTTI 993
Qy 298 YNASKSGNDYDMRQIFNGTVVQRHPMAVT---FVDNHDSPQBEALSFV----- 344
Db 994 KDV--FGHQDSMRKIDRYSDRYRDAQINGVIDNHD-----VKRFLNDASGKPGAN 1045
Qy 345 -BEWFK-PLAYALTLTREQGVPSVFGYGIPIHGVPAKMSKIDPILERQKAYGRON 402
Db 1046 YDKWPQLKAALGFLLT-SRGIPITTYQTEQYSGGDDPA-----NRENMFNANH 1094
Qy 403 DYLDHNNIIGWTREGTAHNSGLATIMSDGAGNKKM-----FVGRNKAG-----Q 449
Db 1095 DLYQYIAKLIVYRN-----HP-----ALQNSQREKWKVDDSFYSFQSKNGDEAIVFINN 1145
Qy 450 VWTDTIT---GN---RAGTIVTINADGWNFSVNGSVSI 481
Db 1146 SWNSQTFITGNFNLNGTRLTNQLSNDVSQVINGNSITV 1184

RESULT 8
AMVA_VIGMU
ID _AMVA_VIGMU STANDARD; PRT; 421 AA.
AC P17859;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AM1.1.
OS Vigna mungo (Rice bean) (black gram).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3915;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RX MEDLINE=90332425; PubMed=2377468;
RA Yamauchi D., Minamikawa T.;
RT "Nucleotide sequence of cDNA for alpha-amylase from cotyledons of
germinating Vigna mungo seeds.";
RL Nucleic Acids Res. 18:4250-4250(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94120017; PubMed=8290640;
RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
RT "Nucleotide sequence of the alpha-amylase gene from Vigna mungo.";
RL Plant Physiol. 103:1459-1459(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL; X53049; CAA37217.1; -
CC EMBL; X73301; CAA51734.1; -
CC PIR; S10514; S10514.
CC HSSP; P04063; IAVA.
CC InterPro; IPR006589; Alp_amyl_cat_sub.
CC InterPro; IPR006047; Alpha_amyl_cat.
CC Pfam; PF00128; alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SM00642; Amy; 1.

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KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal.
FT CHAIN 1 23 PROBABLE.
FT ACT_SITE 24 421 ALPHA-AMYLASE.
FT ACT_SITE 201 421 BY SIMILARITY.
FT ACT_SITE 309 309 BY SIMILARITY.
FT METAL 113 113 CALCIUM 1 (BY SIMILARITY).
FT METAL 130 130 CALCIUM 2 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).
FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
FT METAL 149 149 CALCIUM 3 (BY SIMILARITY).
FT METAL 160 160 CALCIUM 3 (BY SIMILARITY).
FT METAL 168 168 CALCIUM 3 (BY SIMILARITY).
FT METAL 170 170 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DB4656 CRC64;

Query Match 10.5%; Score 283.5; DB 1; Length 421;
Best Local Similarity 26.0%; Pred. No. 5.4e-12;
Matches 101; Conservative 57; Mismatches 139; Indels 91; Gaps 18;

Qy 9 MMQYFEWYLPNDGNHNRLESNASNLKDGISAVWIPPAWKASQNDVGYGAYDLYDLGE 68
Db 26 LFOGFNWESSKGGWYNSLKNIPDLANAGITHVWLPSPQSVSPE--GYLPGRLYDL- 82
Qy 69 FNQGTIRTKYGRNOLQAAVNAKNGIOVYGVVNNHKGADATEMVRVAEVPNNRN 128
Db 83 -----ASKYGSKNELKSLIAAFHEKGIKCLADIVNHR-----TAER 119
Qy 129 QEVSGEYIEAWTKDFPPGNGNTHSNFKRWYHFDGVDMDQSKLNRIYKFGDGKGD 188
Db 120 KDGRIYCI-----FEG-GTPDSR-----QDWGPS-----PICRDDTAYSD 154
Qy 189 WEVDTEG-NYDLYMADIDMDH--FEVYNELRNWGVYNTLTGLDGFRTDAVKHIKYSF 245
Db 155 GTGNNDSEGEDY----AAPDIDLNPQVQRELSENNWNLKTEIFGDFGWRDFVGVYAPSI 210
Qy 246 TRDWINHVRSATGKNMFVAFAEFW-----KNDLGAENLYNKTNNHNSVFD 290
Db 211 SKYMEQT-----KPDFAVGEKWDSTSYGQDGKPNYQDSHRGALVNWVESAGAITAFD 265
Qy 291 VPLHYNLYNASKSGNVDMEQIF--NGT-----VVQRHPMAHTFVDNHDSPQBEALSF-V 344
Db 266 FTTK-GILQAAVQG---ELWRLIDPNKPGPKMGVKEPENAATFIDNHDSTGRLWPFPS 321
Qy 345 EEWFKPLAYALTITREQGVPSVFGDY 372
Db 322 DKVQGYAYILT---HPGTSIFDYHFF 346

RESULT 9
AMT4_PSESA
ID AMT4_PSESA STANDARD; PRT; 551 AA.
AC P22963;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glucan 1,4-alpha-maltotetrahydrolase precursor (EC 3.2.1.60) (G4-
amylase) (Maltotetraose-forming amylase) (Exo-maltotetraohydrolase)
DE (Maltotetraose-forming exo-amylase).
GN MTA.
OS Pseudomonas saccharophila.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae.
OX NCBI_TaxID=304;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=IAM 1504;
RX MEDLINE=90005970; PubMed=2676600;
RA Zhou J., Baba T., Takano T., Kobayashi S., Arai Y.;
RT "Nucleotide sequence of the maltotetraohydrolase gene from
Pseudomonas saccharophila.";

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FT	ACT_SITE	214	214	FT	HELIX	354	358
FT	ACT_SITE	240	240	FT	TURN	359	359
FT	ACT_SITE	315	315	FT	HELIX	363	376
FT	METAL	22	22	FT	TURN	377	377
FT	METAL	23	23	FT	TURN	380	381
FT	METAL	34	34	FT	STRAND	383	387
FT	METAL	37	37	FT	STRAND	393	398
FT	METAL	38	38	FT	STRAND	403	408
FT	METAL	137	137	FT	HELIX	415	417
FT	METAL	172	172	FT	TURN	418	418
FT	METAL	175	175	FT	STRAND	424	429
FT	METAL	183	183	FT	TURN	430	433
FT	METAL	218	218	FT	STRAND	434	438
FT	DISULFID	161	171	SQ	SEQUENCE	548	AA; 59876 MW; 2887217B3379158F CRC64;
FT	DISULFID	237	272		Query Match	9.9%;	Score 267; DB 1; Length 548;
FT	CONFLICT	286	302		Best Local Similarity	23.1%;	Pred. No. 9.3e-11;
FT					Matches 122; Conservative	69;	Mismatches 166; Indels 172; Gaps 26;
FT	TURN	28	29	QY	2	HNGTNGTMMQYFEWYL----	PNDGNHNRLRSDASNLKDGISAVWIPPAWKGASQNDVG 57
FT	TURN	34	35	Db	33	YHGGDEIILQGHVNVVREAPND--	WYNILRQQAATIAADGFSAIWMPVPRDFSSWSDG 90
FT	STRAND	40	42	QY	58	--YDAYDLYDLGEPKQKTIKTYGTRNQLQAAVNALKSGIOVYGDVYVNNHKGADATE	115
FT	TURN	46	47	Db	91	SKSGGGEGYFVHDFNKG----	RYGSDAQLRQAASALGGAGVKLYDVVVPNH----- 138
FT	HELIX	48	51	QY	116	MVRAVEVNPNNRNOEVSGEYTTIATKTFDPFGRGNTHSNPKMRWYHFDGVDWDQSRKLN	175
FT	TURN	53	55	Db	139	-----MNRGYDPKEI-----	NLPA----- 152
FT	TURN	56	62	QY	176	RIYKFRGDKGMDWEVD--TENGYN-----	DYLMYADIMD--HPEVNVNELRNWGVWYT 225
FT	TURN	63	63	Db	153	-----GQGF--WRNDCADPGNPNDCCDGRFIGGDADLNTGHPQVYGMFRDEFTNLR	203
FT	TURN	64	69	QY	226	NTLGLDGFPRIDAVKHIKYSTRDWINHVRSACTKNMFAFAEFKNDLGALE----	NYLNK 281
FT	TURN	70	71	Db	204	SOYGAGGFRDFVR-----GYAPERVNSWMTSDADNSFCVGELWK--	GPSEYPNWDWRNT 256
FT	STRAND	74	77	QY	282	TWNH-----SVFDPVPLHYNLNASKSGGNYDMRQIPNGTVPORHPHVAITFVD	330
FT	STRAND	87	89	Db	257	ASWQIIKQWSDRACKCFVDFALKERKQNGSIA-----	DMKHGLNGNPDPRREVAITFVD 312
FT	TURN	90	91	QY	331	NHDSQPEALESFVEEW-----FKPLAYALTLTREQGYPSVF-----	YGDYYGIPTH 377
FT	TURN	92	94	Db	313	NHDTGYSQNGQGOHHWALQDGLIRQAYAVILT--SPGTVPVYVMSHMYDWCYGF-----	365
FT	STRAND	108	108	QY	378	GVPAMKSKIDPILKARQKAYGRONDYLDHNNIIGTREGNTAHPNSGLATIMSDGAGGN	437
FT	STRAND	109	110	Db	366	-----IRQLIQVR--RAAGVRADSAISFH-----	SGYSGLVATVSGSQ 401
FT	STRAND	111	111	QY	438	KWMFVGRNKAGQVWTDITGNRAGTVTINADGWNFS----	VNGGSYSIW 482
FT	STRAND	113	126	Db	402	QTLVVALN-----SDL--GNPGQVAS-----	GSFSEAVNASNGQVRVW 437
FT	STRAND	127	127				
FT	STRAND	129	134				
FT	STRAND	138	138				
FT	TURN	141	142				
FT	TURN	152	153				
FT	TURN	157	157				
FT	TURN	158	160				
FT	TURN	169	169				
FT	TURN	170	171				
FT	TURN	172	172				
FT	TURN	178	179				
FT	TURN	181	182				
FT	TURN	183	184				
FT	TURN	186	187				
FT	TURN	189	205				
FT	TURN	208	213				
FT	TURN	216	218				
FT	TURN	221	231				
FT	TURN	233	234				
FT	TURN	236	239				
FT	TURN	245	247				
FT	TURN	250	251				
FT	TURN	253	256				
FT	TURN	259	270				
FT	TURN	271	271				
FT	TURN	274	275				
FT	TURN	277	285				
FT	TURN	288	293				
FT	TURN	295	297				
FT	TURN	301	304				
FT	TURN	305	306				
FT	TURN	307	309				
FT	TURN	314	316				
FT	TURN	322	324				
FT	TURN	333	335				
FT	TURN	336	345				
FT	TURN	349	353				

RESULT 12

AMX3 HORVU

ID AMX3 HORVU STANDARD; PRT; 368 AA.

AC P04747;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-

DE glucan glucanohydrolase) (Clone PHV19) (Fragment).

GN AMY1.3.

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

OC Triticeae; Hordeum.

OX NCBI_TaxID=4513;

RN [1]

RP SEQUENCE FROM N.A.

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CC -----
CC EMBL; M59351; AAA33895.1; -
CC DR EMBL; M24287; AAA33886.1; -
CC DR PIR; S12625; S12625.
CC DR HSSP; P04063; IAVA.
CC DR Gramene; P27933; -
CC DR InterPro; IPR006589; Alp_amyl_cat_sub.
CC DR InterPro; IPR006047; Alpha_amyl_cat.
CC DR InterPro; IPR006046; Glyco_hydro_13.
CC DR Pfam; PF00128; alpha-amylase; 1.
CC DR PRINTS; PR00110; ALPHAAMYLASE.
CC DR SMART; SM00642; Amy; 1.
CC DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 435 ALPHA-AMYLASE ISOZYME 3D.
FT ACT_SITE 203 203 BY SIMILARITY.
FT ACT_SITE 311 311 BY SIMILARITY.
FT METAL 116 116 CALCIUM 1 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 136 136 CALCIUM 2 (BY SIMILARITY).
FT METAL 138 138 CALCIUM 2 (BY SIMILARITY).
FT METAL 141 141 CALCIUM 2 (BY SIMILARITY).
FT METAL 151 151 CALCIUM 3 (BY SIMILARITY).
FT METAL 162 162 CALCIUM 3 (BY SIMILARITY).
FT METAL 167 167 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 170 170 SIMILARITY).
FT METAL 172 172 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 173 74 CALCIUM 1 AND 3 (BY SIMILARITY).
FT CONFLICT 137 137 PQ -> R (IN REF. 2).
FT CONFLICT 137 137 P -> R (IN REF. 2).
SQ SEQUENCE 435 AA; 47911 MW; 1BBDBA195BA0D6E CRC64;

Query Match 9.7%; Score 263.5; DB 1; Length 435;
Best Local Similarity 25.0%; Pred. No. 1.2e-10;
Matches 99; Conservative 52; Mismatches 144; Indels 101; Gaps 19;

QY 2 HNGTNGTMMQYFW-YLPDNGNHNRLRSDASNLKKGISAVIIPPAWKAGSQNDVGYGA 60
DB 21 NSGQAQVLFQGFNWSKQGGWYNMLKGQVDDIAKAGVTHVLPSPSHSVAPO--GYMP 78
QY 61 YDLVDFGEFQKGTIRTKYTRNQLQAVALNKSNGIQVYGVVNMHKGCGADATMVRAV 120
DB 79 GRLYDLD-----ASKYGTAAELSLIAAFHGKGVQCVADVVIH-----RCA 120
QY 121 EVNPNNRNQVSGEYTTIEAWTKFDPGRGNTHSNFKRWYHFGVDW-----DOSRKL 173
DB 121 E-----KKDARGVYCV-----FE-----GGTP-----DRLDWGPGMICSDDTQYS 155
QY 174 NNRIYKFRGDKGWDWEVDTEGNYDLYMTADIMDH--PEVYNELBNWGVWYNTIGLD 231
DB 156 DGTGHRDTGEGF-----AAPDIDLNPVRQVELDNLNLKSDVGFD 198
QY 232 GERIDAVKHIKYSTRDWINHRSATCKMFAVAEFWKN-----DLGAIE-- 276
DB 199 GWRDLFANGYSTDIAGYVSCRKG-----FVAETIWNLSYNGDGGKPAANQOGRQLV 253
QY 277 NYLNTKTNWNSVDFVPLHYNLNASKSGGNYDMRQIFNGT---VQRHPHMAVTFVDNHD 333
DB 254 MWNAVGGPAMTFDTTK-GLLQAGVQGLWRLRD-GNGKAPGMIGWLPEKAVTFVDNHD 311
QY 334 SQPEALESP-VSEWFKPLAYALTLTREQYPSVFY 368
DB 312 TGSQTKLWPPFPDKVMQGYAYILT---HPGVPCIFY 344

RESULT 14
AMY2_HORVU
ID _AMY2_HORVU
AC P04063;
```

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DT 01-NOV-1986 (Rel. 03, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase type B isozyme precursor (PC 3.2.1.1) (1,4-alpha-D-
DE Glucan glucanohydrolase) (AMY2-2) (High pI alpha-amylase).
GN AMY1.2.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RN SEQUENCE FROM N.A.
RA Rahmatullah R.J., Huang J.K., Clark K.L., Reeck G.R.,
RA Chandra G.R., Muthukrishnan S.;
RT "Nucleotide and predicted amino acid sequences of two different genes
RT for high-pI alpha-amylases from barley.";
RL Plant Mol. Biol. 12:119-121 (1989).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=85131184; PubMed=3871776;
RA Rogers J.C.;
RT "Two barley alpha-amylase gene families are regulated differently in
RT aleurone cells.";
RL J. Biol. Chem. 260:3731-3738 (1985).
RN [3]
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=94254083; PubMed=8196040;
RA Kadziola A., Abe J.-I., Svensson B., Haser R.;
RT "Crystal and molecular structure of barley alpha-amylase.";
RL J. Mol. Biol. 239:104-121 (1994).
RN [4]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH BASI.
RC STRAIN=cv. Menuet;
RX MEDLINE=98298441; PubMed=9634702;
RA Vallee F., Kadziola A., Bourne Y., Juy M., Rodenburg K.W.,
RA Svensson B., Haser R.;
RT "Barley alpha-amylase bound to its endogenous protein inhibitor BASI:
RT crystal structure of the complex at 1.9-A resolution.";
RL Structure 6:649-659 (1998).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- DEVELOPMENTAL STAGE: Production of alpha-amylase is hormonally
CC regulated. Germinating embryos produce the hormone gibberellic
CC acid, which within 10 hours stimulates the aleurone cells covering
CC the endosperm of the seed to produce alpha-amylase. The enzyme
CC then degrades the starch within the endosperm for use by the
CC developing plant embryo.
CC -1- INDUCTION: Type B isozyme mRNA is undetectable in unstimulated
CC cells and increases a hundred-fold after stimulation with
CC gibberellic acid.
CC -1- MISCELLANEOUS: There are at least 4 types of alpha-amylase in
CC barley.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
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CC -----
CC EMBL; X15226; CAA33298.1; -
CC DR EMBL; K02637; AAA38790.1; -
CC DR PIR; A31960; ALBHB.
CC DR PDB; 1AMY; 13-MAY-95.
CC DR PDB; 1AVA; 16-MAR-99.
CC DR PDB; 1BG9; 15-JUN-99.
CC DR InterPro; IPR006589; Alp_amyl_cat_sub.
CC DR InterPro; IPR006047; Alpha_amyl_cat.
```

DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SMO0642; Amy; 1.
 KW Germination; Carbohydrate metabolism; Hydrolase; Glycosidase; Seed;
 KW Calcium-binding; Signal; Multigene family; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 427
 FT ACT_SITE 203 203
 FT ACT_SITE 228 228
 FT ACT_SITE 313 313
 FT METAL 115 115
 FT METAL 132 132
 FT METAL 135 135
 FT METAL 137 137
 FT METAL 141 141
 FT METAL 151 151
 FT METAL 162 162
 FT METAL 165 165
 FT METAL 166 166
 FT METAL 167 167
 FT METAL 170 170
 FT METAL 172 172
 FT METAL 173 173
 FT CONFLICT 134 134
 FT CONFLICT 195 197
 FT CONFLICT 425 425
 FT STRAND 27 29
 FT TURN 33 34
 FT TURN 35 37
 FT TURN 39 40
 FT TURN 42 47
 FT TURN 48 49
 FT TURN 50 56
 FT TURN 57 57
 FT STRAND 60 63
 FT STRAND 69 69
 FT TURN 72 73
 FT STRAND 77 77
 FT TURN 80 81
 FT TURN 84 85
 FT TURN 87 88
 FT TURN 91 104
 FT TURN 105 105
 FT STRAND 107 112
 FT STRAND 116 116
 FT STRAND 121 122
 FT TURN 124 125
 FT STRAND 128 130
 FT TURN 139 140
 FT STRAND 144 146
 FT TURN 147 147
 FT STRAND 149 150
 FT TURN 152 154
 FT STRAND 165 165
 FT TURN 168 169
 FT STRAND 172 173
 FT TURN 175 176
 FT HELIX 178 193
 FT TURN 194 195
 FT STRAND 199 202
 FT TURN 203 204
 FT HELIX 205 207
 FT HELIX 210 220
 FT STRAND 224 227
 FT STRAND 235 235
 FT TURN 237 238
 FT STRAND 241 241
 FT HELIX 246 260
 FT TURN 261 262
 FT STRAND 265 268
 FT TURN 270 279
 FT HELIX 280 287
 FT HELIX 284 287

ALPHA-AMYLASE TYPE B ISOZYME.

CALCIUM 1.
 CALCIUM 2.
 CALCIUM 2.
 CALCIUM 2.
 CALCIUM 2.
 CALCIUM 3.
 CALCIUM 3.
 CALCIUM 3 (VIA CARBONYL OXYGEN).
 CALCIUM 1.
 CALCIUM 1 (VIA CARBONYL OXYGEN).
 CALCIUM 3 (VIA CARBONYL OXYGEN).
 CALCIUM 1 AND 3.
 G -> D (IN REF. 1).
 IGF -> HRL (IN REF. 2).
 E -> Q (IN REF. 1).

Query Match 9.7%; Score 262; DB 1; Length 427;
 Best Local Similarity 24.3%; Pred. No. 1.5e-10;
 Matches 102; Conservative 59; Mismatches 149; Indels 110; Gaps 19;
 QY 9 MMQYFEW-YLPNDGNHNRLRSASNLDKDGISAVWIPPAWKASQNDVGYGAYDLYDLG 67
 DB 27 LFGQFNWESWKHNGWYFLMGKVDIAAAGITHWLPASQSVAEQ--GYMPGRLYDL 84
 QY 68 EFNQKGTIRTKYGRNQLQAVALKSNQIQYGVDMVNHKGGADATWVAVENPNR 127
 DB 85 -----ASKYGNKAQLKSLIGALHGKVKAIADIVINHR-----TAE 120
 QY 128 NOEVSGETTIEAWTKFPDPPGRGNTHSNFKRWYHFDG-----VDWDQSRKL--NNRIYKF 180
 DB 121 HKDGRGIYCI-----FEGTTPDARDUDWGPHEMTCRDRPY-- 154
 QY 181 RGDGKWDWEVDTEGNYDYLMDADIMDHPEVNVNLRNMGVYTNLTGLDGFRIIDAVKH 240
 DB 155 -ADGTG---NPDT---CADFGAAPDIDHLNLRVQKELVWLNWLKADIGFDGWFDFAKG 207
 QY 241 IKYSFTRDWINHVSATGKNWFAVEFW-----KNDLGAIENTYLNKTNNHVS--- 288
 DB 208 YSADVAKIYIDR-----SEPSFAVAEITWTSLAYGGDGKPNLNQDHRQELVNWYDKVGGK 262
 QY 289 -----FDVPLHYNLNASKSGGNYDMRQIFNGT-----VVQRHPMAHVTVDNHDQPE 337
 DB 263 GPATTFDFTTK--GILNVAVEGELWRLR-----GTDGKAPGMIGWPAKAVTFVDNHDG 317
 QY 338 EALESEF--VEWFKPLAYALTLTREQGYSPVFGYGYGIPHTGVPAMKSKIDPILAEARQKY 396
 DB 318 QHWPFPFSDRVMOQYAYILT---HPGTGTCFYDHFDDW-----GLKEIDRLVSVTRH 368

RESULT 15

AMYM_BACST
 ID AMYM_BACST STANDARD; PRT; 719 AA.
 AC P19531;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Maltogenic alpha-amylase precursor (EC 3.2.1.133) (Glucan 1,4-alpha-maltohydrolase).
 GN AMYM.
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]

SEQUENCE FROM N.A., AND SEQUENCE OF 34-45.
STRAIN=C599;
Diderichsen B., Christiansen L.;
"Cloning of a maltogenic alpha-amylase from Bacillus
stearothermophilus";
FEMS Microbiol. Lett. 56:53-60(1988).
[2]
REVIEWS, AND X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
MEDLINE=99315215; PubMed=10397084;
Dauter Z., Dauter M., Brozowski A.M., Christensen S., Borchert T.V.,
Beier L., Wilson K.S., Davies G.J.;
"X-ray structure of Novamyl, the five-domain 'maltogenic' alpha-
amylase from Bacillus stearothermophilus: maltose and acarbose
complexes at 1.7-A resolution";
Biochemistry 38:8395-8392(1999).
CC -|- FUNCTION: Converts starch into maltose.
CC -|- CATALYTIC ACTIVITY: Hydrolysis of (1->4)-alpha-D-glucosidic
linkages in polysaccharides so as to remove successive alpha-
maltose residues from the non-reducing ends of the chains.
CC -|- COFACTOR: Binds 3 calcium ions per subunit.
CC -|- SUBUNIT: Monomer.
CC -|- BIOTECHNOLOGY: Used in the food industry to prevent bread from
staling. Sold under the name Novamyl by Novozymes.
CC -|- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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or send an email to license@isb-sib.ch.
CC -----
DR EMBL; M36539; AAA22233.1; -;
DR PIR; S28784; S28784.
DR PDB; 1QHO; 31-MAY-00.
DR PDB; 1QHP; 31-MAY-00.
DR InterPro; IPR006048; Alpha_amyl_C.
DR InterPro; IPR006047; Alpha_amyl_Cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PF00128; alpha-amylase_1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PF00110; ALPHAAMYLASE.
DR ProDom; PD001568; CBD_4; 1.
DR SMART; SM00632; AmyC; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure
FT SIGNAL 1 33
FT CHAIN 34 719 MALTOGENIC ALPHA-AMYLASE.
FT ACT_SITE 261 261
FT ACT_SITE 265 265
FT ACT_SITE 289 289
FT ACT_SITE 362 362
FT METAL 54 54
FT METAL 56 56 CALCIUM 1. (VIA CARBONYL OXYGEN).
FT METAL 59 59 CALCIUM 1.
FT METAL 60 60 CALCIUM 1.
FT METAL 81 81 CALCIUM 1 (VIA CARBONYL OXYGEN).
FT METAL 83 83 CALCIUM 1.
FT METAL 109 109 CALCIUM 2.
FT METAL 110 110 CALCIUM 2 (VIA CARBONYL OXYGEN).
FT METAL 112 112 CALCIUM 2.
FT METAL 134 134 CALCIUM 2.
FT METAL 135 135 CALCIUM 2.
FT METAL 164 164 CALCIUM 3.
FT METAL 217 217 CALCIUM 3 (VIA CARBONYL OXYGEN).
FT METAL 231 231 CALCIUM 3.
FT METAL 265 265 CALCIUM 3 (VIA CARBONYL OXYGEN).
FT METAL 109 109 D -> N (IN REF. 1).
FT CONFLICT 109 109

FT	CONFLICT	254	256	MISSING (IN REF. 1).
FT	CONFLICT	371	371	S -> SK (IN REF. 1).
FT	CONFLICT	379	391	ALAFILTSRGTPS -> RLFSLSLRGVRPP (IN REF. 1).
SQ	SEQUENCE	719	AA; 78675	MW; B40B61AD964F7D89 CRC64;

Query Match 9.6%; Score 259; DB 1; Length 719;
Best Local Similarity 22.3%; Pred. No. 4.4e-10;
Matches 122; Conservative 73; Mismatches 202; Indels 150; Gaps 25;

QY	5	TNGTWMQYFEWYLPND-----GNHNRRLSDASNLKDKGISAVWIPPAWKG-----ASQ	53
DB	58	TNNNAKSYGLYDPYKSKWMWGGDLEGVQRKLPYLKQLGVTTWLSVLDNLDTLACT	117
QY	54	NDVGYGAYDLYDLGEBFNQKGTIRTKYGRNQALQAAVNALKSNGIQVYGVVNMHKGADA	113
DB	118	DMTGVHGYWRD---FKQ---IEEHFGNWTTFDLVNDAHQNGIKIVIVDFVFNHSPFKA	171
QY	114	TEMVRAVEVNNRNQOVSGETTIEAWTKFDPFGNGNTHSNFKRWYHFDGVDWDSRKL	173
DB	172	NDSTFA-EGGALYNNGTYMGNY-----FDDATKGYFHHN-----	204
QY	174	NNRIYKFRGDGKWD-----WEVDTENGVDYLMYADIDMDHPVNVNELRWGVWYWT	227
DB	205	-----GDISNWDDEYEAQWKNFTDPAGFS---LADLSQENGTAQYLTAAVQLV-A	252
QY	228	LGLDGFRIIDAVKHIKYSFTRDWINHVRSATGKMFPAVEFWKNDLGAIEYLNKTNW-NH	286
DB	253	HGADGLRIDAVKHNSGFSKSLADKLYQK--KDIFLVGEWYGGDPT-ANHLEKVRVANN	309
QY	287	S---VPDVELHYNLN--ASKSGNYDMRQIPNGTVVQ-RHPMHAFTVDNHDSDQPEAL	340
DB	310	SGVNVLDLNTVIRNVFGTFTQTMVLDLNMVNQNGEYKKNLTFTDNDHMSRFLSV	369
QY	341	ESFVEEWFKPLAYALTITREQYPSVFG-----DYYGIPTHG-VPAMKSKIDPIL	390
DB	370	NSNKANLHQALAFILT---SRGTPSIYYTEQYMGAGNDPY---NRGMPAFDTTTTAFK	423
QY	391	EA-----RQKYAYGRQ--NDYLDHNNIIGWTRGNTAHPS	424
DB	424	EVTSLAGLRNNAAIQYGTTFQRIWNNVDYIYERKEFNDV---LVAINRNTQSSYSIS	479
QY	425	GLATIMSDGA-----GKNKMFVGRNKAQGVWTDITGNRAGTVTINADGNGNFSVN	475
DB	480	GLQTALPNGSYADYLSGLLGN-----GISVSNGSVASFTLA	516
QY	476	GGSVSTW	482
DB	517	PGAVSVW	523

Search completed: October 7, 2004, 00:13:25
Job time : 10.5063 secs

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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 58.5516 Seconds
(without alignments)
2340.424 Million cell updates/sec

Title: US-09-925-576C-12
Perfect score: 2708
Sequence: 1 HHNGTGTMMQYFEWYLPND.....ADGWNFSVNGSVSIWVK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2708	100.0	485	3	AY97812 Bacillus
2	2708	100.0	485	4	AAB29260 Bacillus
3	2708	100.0	485	4	AAB29261 Bacillus
4	2708	100.0	485	5	ABB06938 Bacillus
5	2708	100.0	485	5	AAU12154 Bacillus
6	2708	100.0	485	5	AAB47855 Bacillus
7	2708	100.0	485	5	ABM00046 AA560 SEQ
8	2675	98.8	480	4	ABM00046
9	2613	96.5	485	2	AAW12956 Alpha-amy
10	2613	96.5	485	2	AAW15420 Termamyl
11	2613	96.5	485	2	AY07386 Wild type
12	2613	96.5	485	3	AY99607 Bacillus
13	2613	96.5	485	5	ABB06939 Bacillus
14	2613	96.5	485	5	AAU12155 Bacillus
15	2613	96.5	485	5	AAB47856 Bacillus
16	2613	96.5	485	5	ABB76592 Termamyl
17	2596	95.9	516	5	ABB08773 Bacillus
18	2475.5	91.4	519	4	AAE09762 Bacillus
19	2475.5	91.4	519	4	AAE09763 Bacillus
20	2475.5	91.2	519	4	AAE09767 Bacillus
21	2469.5	91.2	519	4	AAE09764 Bacillus
22	2438	90.0	485	2	AAW12110 Alpha-amy
23	2437	90.0	485	2	AAW1836 Bacillus
24	2437	90.0	485	2	AAW31500 Bacillus
25	2437	90.0	485	2	AAW48261 Bacillus

ALIGNMENTS

RESULT 1
AY97812
ID AY97812 standard; protein; 485 AA.
XX
AC AY97812;
XX
DT 12-SEP-2003 (revised)
DT 21-AUG-2000 (first entry)
XX
DE Bacillus alkaline alpha-amyase AA560.
XX
KW Alkaline alpha-amyase; AA560; immunogenicity; allergenicity;
KW industrial product; pharmaceutical; hypoallergenic.
XX
OS Bacillus sp; 'DSM12649'.
XX
PN WC200022103-Al.
XX
PD 20-APR-2000.
XX
PF 12-OCT-1999; 99WO-DK000542.
XX
PR 13-OCT-1998; 98DK-00001301.
PR 04-OCT-1999; 99DK-00001418.
XX
(NOVO) NOVO-NORDISK AS.
XX
PI Olsen AA, Von Der Osten C, Andersen KV, Ernst S, Roggen EL;
XX
DR WPI; 2000-329163/28.
XX
N-PSDB; AAA30783.
XX
PT New modified polypeptides having an attached polymer for reducing immune
PT responses, useful in e.g. detergents, cleaning products, skin care
PT products, food or feed products, textile products or pharmaceuticals.
XX
PS Example 4; Page 102-105; 108pp; English.
XX
CC The invention relates to proteins with reduced immunogenicity, having one
CC or more modified amino acids, where the alpha-carbon atoms of the amino
CC acids are located less than 15 Angstroms from a ligand bound to the
CC protein. The modification may entail substitution of the endogenous
CC residue for a non-endogenous residue and/or attachment of polymeric
CC molecules such as carbohydrates or branched polyethylene glycols to the
CC amino acid residues. The residue to be modified is identified from the 3-
CC dimensional structure of the protein determined, for example, by X-ray
CC crystallography or NMR. A wide variety of enzymes may be modified
CC according to the invention, including proteases (especially subtilisins),

26 2437 90.0 485 2 AAY15422 Termamyl-
27 2437 90.0 485 2 AAY15416 Bacillus
28 2437 90.0 485 2 AAY07382 Wild type
29 2437 90.0 485 3 AAY99609 Bacillus
30 2437 90.0 485 3 AAY99603 Bacillus
31 2437 90.0 485 5 ABB06934 Bacillus
32 2437 90.0 485 5 AAU12150 Bacillus
33 2437 90.0 485 5 AAB47851 Bacillus
34 2437 90.0 485 5 ABB76587 Termamyl-
35 2437 90.0 485 6 ABB99481 Amino aci
36 2437 90.0 834 4 AAB30701 A Bacillu
37 2431 89.8 485 2 AAW12144 Alpha-amy
38 2431 89.8 485 2 AAW12109 Alpha-amy
39 2430 89.7 485 5 ABB76643 Termamyl-
40 2429 89.7 485 2 AAW31499 Bacillus
41 2429 89.7 485 2 AAW48260 Bacillus
42 2429 89.7 485 2 AAY15421 Termamyl-
43 2429 89.7 485 2 AAY15415 Bacillus
44 2429 89.7 485 2 AAY25150 Bacillus
45 2429 89.7 485 2 AAY07391 Wild type

CC carbohydrates (such as amylase), isomerases, transferases and
CC oxidoreductases. The modified proteins of the invention may be used for
CC reducing the allergenicity of industrial products (i.e., those which are
CC not intended to enter the circulatory system. The proteins may be used in
CC cleaning agents (such as laundry products, dish-washing products or hard
CC surface cleaning products), skin-care products, textile treatment
CC products (e.g., bleaching agents) and food products. The modified
CC polypeptides can also be used for reducing the immunogenicity of
CC pharmaceuticals. The modified proteins have reduced immunogenicity or
CC allergenicity while maintaining a high percentage of activity. The
CC present sequence represents an alkaline alpha-amylase, AA560, from
CC Bacillus DSM 12649, which may be modified according to the invention.
CC (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2708; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.7e-218;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKKGISAVWI PPAWKGASQNDVGYGA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKKGISAVWI PPAWKGASQNDVGYGA 60
QY 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAAVNALKSNGIQYVGYDVVMNHKGGADATEMVRV 120
DB 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAAVNALKSNGIQYVGYDVVMNHKGGADATEMVRV 120
QY 121 EYVNNRNQVSGEYTIETAWTKFDPGRGNTHSNFKRWYTHFGVDWDQSRKLNRIYKF 180
DB 121 EYVNNRNQVSGEYTIETAWTKFDPGRGNTHSNFKRWYTHFGVDWDQSRKLNRIYKF 180
QY 181 RGDGKGWDEVDTEGNGYDLYMADIDMDHPEVVMNLRNWGVYNTLTGLDGRIDAVKH 240
DB 181 RGDGKGWDEVDTEGNGYDLYMADIDMDHPEVVMNLRNWGVYNTLTGLDGRIDAVKH 240
QY 241 IKYSFTRDWINHVRSAFGKMFVAEFWKNLKGAIENLYLNKTNWHSVFDVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAFGKMFVAEFWKNLKGAIENLYLNKTNWHSVFDVPLHYNLYNA 300
QY 301 SKSGGNYDMRQIFNGTVVQHPMHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
DB 301 SKSGGNYDMRQIFNGTVVQHPMHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMSKIDPILAEARQKAYGRQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMSKIDPILAEARQKAYGRQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTINADGNGNFSVNGGSYS 480
DB 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTINADGNGNFSVNGGSYS 480
QY 481 IWYNK 485
DB 481 IWYNK 485

RESULT 2
AAB29260
ID AAB29260 standard; protein; 485 AA.
XX
AC AAB29260;
XX
XX
DT 07-FEB-2001 (first entry)
DE Bacillus sp. alpha-amylase #1.
XX
KW Alpha-amylase; laundry; detergent; textile desizing;
KW sweetener production; ethanol production; brewing; paper production.
XX
OS Bacillus sp.
XX
PN WO2000060060-A2.

XX 12-OCT-2000.
XX 28-MAR-2000; 2000WO-DK000149.
XX 31-MAR-1999; 99DK-00000439.
XX 13-APR-1999; 99DK-00000490.
XX 13-APR-1999; 99US-00290734.
XX (NOVO) NOVO NORDISK AS.
XX
XX Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
PI Bisgard-Frantzen H, Svendsen A, Andersen C;
XX
XX WPI: 2001-006814/01.
DR N-PSDB; AAC63114.
XX
XX New polypeptides having alpha-amylase activity and nucleic acids encoding
PT the enzymes, useful as a detergent or a dishwash detergent composition,
PT for textile desizing, for liquefaction of starch, or for ethanol
PT production.
XX
PS Claim 3; Page 106-108; 116pp; English.
XX
CC The present invention relates to proteins having alpha-amylase activity
CC and their coding sequences. These proteins are useful in a number of
CC industrial applications, including detergents, hard surface cleaning
CC compositions, in compositions for desizing textiles, fabrics and
CC garments, in the production of pulp and paper, in beer-making and
CC brewing, and in starch conversion processes such as sweetener and ethanol
CC production
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2708; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.7e-218;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKKGISAVWI PPAWKGASQNDVGYGA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKKGISAVWI PPAWKGASQNDVGYGA 60
QY 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAAVNALKSNGIQYVGYDVVMNHKGGADATEMVRV 120
DB 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAAVNALKSNGIQYVGYDVVMNHKGGADATEMVRV 120
QY 121 EYVNNRNQVSGEYTIETAWTKFDPGRGNTHSNFKRWYTHFGVDWDQSRKLNRIYKF 180
DB 121 EYVNNRNQVSGEYTIETAWTKFDPGRGNTHSNFKRWYTHFGVDWDQSRKLNRIYKF 180
QY 181 RGDGKGWDEVDTEGNGYDLYMADIDMDHPEVVMNLRNWGVYNTLTGLDGRIDAVKH 240
DB 181 RGDGKGWDEVDTEGNGYDLYMADIDMDHPEVVMNLRNWGVYNTLTGLDGRIDAVKH 240
QY 241 IKYSFTRDWINHVRSAFGKMFVAEFWKNLKGAIENLYLNKTNWHSVFDVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAFGKMFVAEFWKNLKGAIENLYLNKTNWHSVFDVPLHYNLYNA 300
QY 301 SKSGGNYDMRQIFNGTVVQHPMHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
DB 301 SKSGGNYDMRQIFNGTVVQHPMHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMSKIDPILAEARQKAYGRQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMSKIDPILAEARQKAYGRQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTINADGNGNFSVNGGSYS 480
DB 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTINADGNGNFSVNGGSYS 480
QY 481 IWYNK 485
DB 481 IWYNK 485

RESULT 3
 AAB29261
 ID AAB29261 standard; protein; 485 AA.
 XX
 AC AAB29261;
 XX
 DT 07-FEB-2001 (first entry)
 XX
 DE Bacillus sp. alpha-amylase #2.
 XX
 KW Alpha-amylase; laundry; detergent; textile desizing;
 KW sweetener production; ethanol production; brewing; paper production.
 XX
 OS Bacillus sp.
 XX
 FN WO200060060-A2.
 XX
 PD 12-OCT-2000.
 XX
 PF 28-MAR-2000; 2000WO-DK000149.
 XX
 PR 31-MAR-1999; 99DK-00000439.
 PR 13-APR-1999; 99DK-00000490.
 PR 13-APR-1999; 99US-00290734.
 XX
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
 PI Biegard-Frantzen H, Svendsen A, Andersen C;
 XX
 DR WPI; 2001-006814/01.
 DR N-PSDB; AAC63115.
 XX
 PT New polypeptides having alpha-amylase activity and nucleic acids encoding
 PT the enzymes, useful as a detergent or a dishwash detergent composition,
 PT for textile desizing, for liquefaction of starch, or for ethanol
 PT production.
 XX
 PS Claim 3; Page 111-112; 116pp; English.
 XX
 CC The present invention relates to proteins having alpha-amylase activity
 CC and their coding sequences. These proteins are useful in a number of
 CC industrial applications, including detergents, hard surface cleaning
 CC compositions, in compositions for desizing textiles, fabrics and
 CC garments, in the production of pulp and paper, in beer-making and
 CC brewing, and in starch conversion processes such as sweetener and ethanol
 CC production
 XX
 SQ Sequence 485 AA;
 Query Match 100.0%; Score 2708; DB 4; Length 485;
 Best Local Similarity 100.0%; Pred. No. 3.7e-218;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVGGA 60
 DB 1 HHNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVGGA 60
 QY 61 YDLVDLGEFNQKGTIRTKYGRNQLQAANLKSNGIQYGVGVVNMHKGADATEMVRV 120
 DB 61 YDLVDLGEFNQKGTIRTKYGRNQLQAANLKSNGIQYGVGVVNMHKGADATEMVRV 120
 QY 121 EVNPNRNRQESVGYTTIETAWTKFPDPCGRNTHSNFKRWYHFDGVDWQSKLNRIYKF 180
 DB 121 EVNPNRNRQESVGYTTIETAWTKFPDPCGRNTHSNFKRWYHFDGVDWQSKLNRIYKF 180
 QY 181 RGDGKGWDWEVDTEGNGYDLYMYADIDMDHPEVNVNELNRWGWYTTLTGLDGFRIIDAVKH 240
 DB 181 RGDGKGWDWEVDTEGNGYDLYMYADIDMDHPEVNVNELNRWGWYTTLTGLDGFRIIDAVKH 240
 QY 241 IKYSFTRDWINHRSATGKNMFAVEFWKNDLGAIENTNKNWHSVDFVPLHLYNA 300

Db 241 IKYSFTRDWINHRSATGKNMFAVEFWKNDLGAIENTNKNWHSVDFVPLHLYNA 300
 QY 301 SKSGENYDMROI FNGTIVVQHPMAVTFVDNHDSDPEALESFVEEWPKPLAYALTRE 360
 Db 301 SKSGENYDMROI FNGTIVVQHPMAVTFVDNHDSDPEALESFVEEWPKPLAYALTRE 360
 QY 361 QGYPSEVFGDYGIPTHTGVPAMKSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
 Db 361 QGYPSEVFGDYGIPTHTGVPAMKSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
 QY 421 HPNSGLATIMSDGAGGNKMMFVGKNGAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
 Db 421 HPNSGLATIMSDGAGGNKMMFVGKNGAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
 QY 481 IWVWK 485
 Db 481 IWVWK 485
 RESULT 4
 ABB06938
 ID ABB06938 standard; protein; 485 AA.
 XX
 AC ABB06938;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE Bacillus termamyl-like alpha-amylase protein SEQ ID NO:12.
 XX
 KW Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 KW washing; sweetener; ethanol; starch.
 XX
 OS Bacillus sp.
 XX
 FN WO200166712-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-DK000144.
 XX
 PR 08-MAR-2000; 2000DK-00000376.
 PR 15-MAR-2000; 2000US-0189857P.
 PR 23-FEB-2001; 2001DK-00000303.
 PR 26-FEB-2001; 2001US-0271382P.
 XX
 FA (NOVO) NOVOZYMES AS.
 XX
 PI Andersen C, Borchert TV, Nielsen BR;
 DR WPI; 2002-239612/29.
 DR N-PSDB; ABL50569.
 XX
 PT Novel variant of parent termamyl-like alpha-amylase useful as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 1; Page 148-149; 153pp; English.
 XX

The present invention describes a variant of a parent termamyl-like alpha
 -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 positions of a group of 31 possible amino acid positions. The alteration
 in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
 Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
 Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
 Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
 washing and/or dishwashing, textile desizing, and starch liquefaction.
 (I) is useful as a component in hard surface cleaning detergent
 composition, and for producing sweeteners and ethanol from starch. (I)
 has altered solubility, preferably increased solubility, in particular
 under washing, dish washing or hard surface cleaning conditions. The
 present sequence represents a Bacillus termamyl-like alpha-amylase which


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AC AAB47855;
XX
XX 02-APR-2002 (first entry)
XX
XX DE Bacillus alpha amylase AA560.
XX
XX KW Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;
XX KW starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
XX KW bakery; cereal bar; ice cream; coffee whitener; salad dressing;
XX KW cured meat; fermented meat; spice.
XX
XX OS Bacillus sp.
XX
XX XX WO200196537-A2.
XX
XX XX 20-DEC-2001.
XX
XX XX 13-JUN-2001; 2001WO-DK000404.
XX
XX XX 14-JUN-2000; 2000DK-00000917.
XX
XX XX 20-JUN-2000; 2000US-0212852P.
XX
XX XX (NOVO ) NOVOZYMES AS.
XX
XX XX Nielsen BR, Weibye M;
XX
XX XX WPI; 2002-098064/13.
XX
XX XX N-PSDB; AAI72216.
XX
XX XX New modified alpha-amylase derived from the genus Bacillus and/or is a
XX PT Termamyl-like alpha-amylase, which has been pre-oxidized for producing
XX PT maltodextrin or glucose syrup.
XX
XX XX Claim 5; Page 43-44; 47pp; English.
XX
XX XX The sequences given in AAB47850-56 show modified alpha-amylases derived
XX CC from the genus Bacillus. These alpha amylases are Termamyl- like alpha-
XX CC amylase and they have been pre-oxidized. The alpha amylase is useful for
XX CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
XX CC oxidized alpha-amylase until a product with a DE between 5-45 has been
XX CC provided and/or until a product with a molecular weight of between 5-30
XX CC kDa has been provided. The product comprises a maltodextrin with a DE of
XX CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The
XX CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
XX CC where the glucose syrup is useful as an ingredient in food, feed or
XX CC pharmaceuticals. Glucose syrup is useful in confectionery such as
XX CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
XX CC dairy and ice cream such as coffee whiteners, conventional foods such as
XX CC salad dressings, and food ingredients and preparations such as cured
XX CC meat, fermented meat, spices and seasoning encapsulated flavours
XX
XX SQ Sequence 485 AA;

Query Match 100.0%; Score 2708; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.7e-218;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSASNLKDKGISAVWTTPPAWKASQNDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSASNLKDKGISAVWTTPPAWKASQNDVGYGA 60

QY 61 YDLYDLGEFNOKGRTIRKYGRNLOQAANVNAKNSGIGQYGVGVNHNKGGADATEMVRV 120
DB 61 YDLYDLGEFNOKGRTIRKYGRNLOQAANVNAKNSGIGQYGVGVNHNKGGADATEMVRV 120

QY 121 EVNPNRNRQVSGEYTTIATWKTFDPGKGNTHSNFKRWYHYFDGVDWQSRKLNRIYKF 180
DB 121 EVNPNRNRQVSGEYTTIATWKTFDPGKGNTHSNFKRWYHYFDGVDWQSRKLNRIYKF 180

QY 181 RGDGKGWDEVDTENGHYDILMYADIDMDHPVNVNLRNKGWVWTTNLGLDGRIDAVKH 240
DB 181 RGDGKGWDEVDTENGHYDILMYADIDMDHPVNVNLRNKGWVWTTNLGLDGRIDAVKH 240

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QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWQNDLGALENYLNKTNHNSVDFVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWQNDLGALENYLNKTNHNSVDFVPLHYNLYNA 300

QY 301 SKSGNVDMRQIFNGTIVQRHPMAVTFVDNHDQPEEALLESFVEEFKPLAYALTITRE 360
DB 301 SKSGNVDMRQIFNGTIVQRHPMAVTFVDNHDQPEEALLESFVEEFKPLAYALTITRE 360

QY 361 QGYPSPVFGDYVGIPTHGVPAMKSKIDPILAEAROKYAYGRONDYLDHNNIIGWTRGNNTA 420
DB 361 QGYPSPVFGDYVGIPTHGVPAMKSKIDPILAEAROKYAYGRONDYLDHNNIIGWTRGNNTA 420

QY 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTGTITNADGWGNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTGTITNADGWGNFSVNGGSVS 480

QY 481 IWNK 485
DB 481 IWNK 485

RESULT 7
AAB76591
ID AAB76591 standard; protein; 485 AA.
XX
XX AC ABE76591;
XX
XX DT 19-AUG-2002 (first entry)
XX
XX DE Termamyl-like-alpha-amylase #6.
XX
XX KW Termamyl; alpha amylase; starch liquefaction; ethanol production;
XX KW textile desizing; detergent; enzyme.
XX
XX OS Bacillus sp.
XX
XX XX WO200210355-A2.
XX
XX PD 07-FEB-2002.
XX
XX PF 12-JUL-2001; 2001WO-DK000488.
XX
XX PR 01-AUG-2000; 2000DK-00001160.
XX PR 12-SEP-2000; 2000DK-00001354.
XX PR 10-NOV-2000; 2000DK-00001687.
XX PR 26-APR-2001; 2001DK-00000655.
XX
XX XX (NOVO ) NOVOZYMES AS.
XX
XX XX Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;
XX
XX DR WPI; 2002-280633/32.
XX
XX DR N-PSDB; ABL96212.
XX
XX PT Variant of parent Termamyl-like alpha amylase, useful in detergent
XX PT compositions, for starch liquefaction, ethanol production, washing and/or
XX PT dish washing, and textile desizing.
XX
XX PS Claim 8; Page 75-76; 90pp; English.
XX
XX CC This invention relates to variants of a parent Termamyl-like alpha-
XX CC amylases. These are used for starch liquefaction, ethanol production,
XX CC detergent, and textile desizing. The amylases have altered stability,
XX CC particularly at high temperatures from 70-120plusoc and low pH in the
XX CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
XX CC amylase
XX
XX SQ Sequence 485 AA;

Query Match 100.0%; Score 2708; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.7e-218;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


XX DE Bacillus Termamyl-like alpha-amylase.
 XX KW Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
 XX KW saccharification; muten; mutant; enzyme stability; hybrid.
 XX OS Bacillus sp.
 XX PN WO200029560-A1.
 XX PD 25-MAY-2000.
 XX PF 16-NOV-1999; 99WO-DK000628.
 XX PR 16-NOV-1998; 98DK-00001495.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;
 XX DR WPI; 2000-387777/33.
 XX PT Variant of parent termamyl-like alpha amylase useful for washing, textile
 PT desizing and starch liquefaction, comprising alterations in one or more
 PT solvent exposed amino acid residues.
 XX PS Claim 8; Page 61-62; 80pp; English.
 XX CC The present sequence is a parent alpha-amylase from which mutants with
 CC increased stability at acidic pH, low calcium concentration and high
 CC temperatures have been derived. The sequence encoding this protein was
 CC isolated from a Bacillus genomic DNA library. A variant may contain
 CC mutations in one or more solvent exposed amino acid residues to increase
 CC the overall hydrophobicity of the enzyme or the overall number of methyl
 CC groups in the side chains of exposed residues may be increased. The
 CC mutations can be incorporated by site-directed mutagenesis or by random
 CC mutagenesis. As a result of their increased stability, the variants are
 CC suitable for the industrial processing of starch, i.e. starch
 CC liquefaction and saccharification. They may also be useful for washing,
 CC dishwashing and textile desizing. Hybrid alpha-amylases comprising
 CC partial amino acid sequences derived from two or more alpha-amylases have
 CC also been created in order to increase enzyme stability
 XX SQ Sequence 485 AA;

Query Match 96.5%; Score 2613; DB 3; Length 485;
 Best Local Similarity 95.5%; Pred. No. 3.4e-210;
 Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKIGISAVMTIPPAWKASQNDVGYGA 60
 DB 1 HHNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKIGISAVMTIPPAWKASQNDVGYGA 60

QY 61 YDLYDLGEFNGKGTIRTKYGRNQLQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVRVAV 120
 DB 61 YDLYDLGEFNGKGTIRTKYGRNQLQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVRVAV 120

QY 121 EVNPNRNQVSGEYTEATWKTFDFPGRGNTNHNKRWYHFDGVDWDQSKLNNRIYKF 180
 DB 121 EVNPNRNQVSGEYTEATWKTFDFPGRGNTNHNKRWYHFDGVDWDQSKLNNRIYKF 180

QY 181 RDPGKGWDWEVDTENGYDYLMTADIMDHPVNNELRNKGVWYNTLGLDGRFIDAVKH 240
 DB 181 RGHGKAWDWEVDTENGYDYLMTADIMDHPVNNELRNKGVWYNTLGLDGRFIDAVKH 240

QY 241 IKTSFTEDWLNHVRSAATGKNFAVAEPEWKNLDGAIENLYNKTNNHNSVDFVPLHYNLYNA 300
 DB 241 IKTSFTEDWLNHVRSAATGKNFAVAEPEWKNLDGAIENLYNKTNNHNSVDFVPLHYNLYNA 300

QY 301 SKSGGNYDMRQIFNGTVVQRHPHMAVTFVDNHDSDQPEALESFVEWFKPLAYALTITRE 360
 DB 301 SKSGGNYDMRQIFNGTVVQRHPHMAVTFVDNHDSDQPEALESFVEWFKPLAYALTITRE 360

QY 361 QGYPSVFYGDYIGIPTHGVPAKMSKIDPILFAROKYAGRONDYLDHNNIIGWTREGNTA 420
 DB 361 QGYPSVFYGDYIGIPTHGVPAKMSKIDPILFAROKYAGRONDYLDHNNIIGWTREGNTA 420

QY 421 HPNSGLATIMSDGAGGKMKMFVGNKAGQVWTDITGNRAGTFTTNADGWGNSFVNGGVS 480
 DB 421 HPNSGLATIMSDGAGGKMKMFVGNKAGQVWTDITGNRAGTFTTNADGWGNSFVNGGVS 480

QY 481 IWNK 485
 DB 481 IWNK 485

RESULT 13
 ABB06939
 ID ABB06939 standard; protein; 485 AA.
 XX ABB06939;
 AC ABB06939;
 XX 19-JUN-2002 (first entry)
 DT
 XX DE Bacillus termamyl-like alpha-amylase protein SEQ ID NO:13.
 XX KW Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 KW washing; sweetener; ethanol; starch.
 XX OS Bacillus sp.
 XX WO200166712-A2.
 PD 13-SEP-2001.
 XX PF 07-MAR-2001; 2001WO-DK000144.
 XX PR 08-MAR-2000; 2000DK-00000376.
 PR 15-MAR-2000; 2000US-0189857P.
 PR 23-FEB-2001; 2001DK-00000303.
 PR 26-FEB-2001; 2001US-0271362P.
 XX (NOVO) NOVOZYMES AS.
 XX Andersen C, Borchert TV, Nielsen BR;
 WPI; 2002-239612/29.

Novel variant of parent termamyl-like alpha-amylase useful as a component
 in washing and dishwashing compositions, for textile desizing, for starch
 liquefaction, and for producing sweeteners and ethanol from starch.

Claim 8; Page 150-151; 153pp; English.

The present invention describes a variant of a parent termamyl-like alpha
 -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 positions of a group of 31 possible amino acid positions. The alteration
 in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
 Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
 Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
 Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
 washing and/or dishwashing, textile desizing, and starch liquefaction.
 (I) is useful as a component in hard surface cleaning detergent
 composition, and for producing sweeteners and ethanol from starch. (I)
 has altered solubility, preferably increased solubility, in particular
 under washing, dish washing or hard surface cleaning conditions. The
 present sequence represents a Bacillus termamyl-like alpha-amylase which
 is used in the exemplification of the present invention

Sequence 485 AA;

Query Match 96.5%; Score 2613; DB 5; Length 485;
 Best Local Similarity 95.5%; Pred. No. 3.4e-210;
 Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKAGSQNDVGCA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKAGSQNDVGCA 60
QY 61 YLDYDLGEFNGKGTITRTKYGTNRQLAAVNAKLSNGIQVYGVVNMHKGADATEMVRV 120
DB 61 YLDYDLGEFNGKGTITRTKYGTNRQLAAVNAKLSNGIQVYGVVNMHKGADATEMVRV 120
QY 121 EVNPNRNRQEVSGEYTIETAWTKFDPFGNGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
DB 121 EVNPNRNRQEVSGEYTIETAWTKFDPFGNGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
QY 181 RGDGKAWDEVDTENGNYDLYMADIDMDHPEVNVNLRNKGWYVNTLGLDGRIDAVKH 240
DB 181 RGDGKAWDEVDTENGNYDLYMADIDMDHPEVNVNLRNKGWYVNTLGLDGRIDAVKH 240
QY 241 IKYSFTTRDWINHVRSATGKNMFVAEFAFWKNDLGAIENTYLQKTNNHNSVDFVPLHYNLYNA 300
DB 241 IKYSFTTRDWINHVRSATGKNMFVAEFAFWKNDLGAIENTYLQKTNNHNSVDFVPLHYNLYNA 300
QY 301 SKSGGNYDMRQIFNGTVVQRHPHVAFTFVDNHDSDQPEEALSFVEEWFKPLAYALTRE 360
DB 301 SKSGGNYDMRQIFNGTVVQRHPHVAFTFVDNHDSDQPEEALSFVEEWFKPLAYALTRE 360
QY 361 QGYPSVFYGYGIPTHGVPAMKSKIDPILFARQKAYGRNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGYGIPTHGVPAMKSKIDPILFARQKAYGRNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGKWMFVGRNKGAGQVWTDITGNRAGTGTITNADGNGFNSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGKWMFVGRNKGAGQVWTDITGNRAGTGTITNADGNGFNSVNGGSVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485
RESULT 15
AAU12155
ID AAU12155 standard; protein; 485 AA.
AC AAU12155;
XX 09-APR-2002 (first entry)
DE Bacillus TERMAMYL-like alpha-amylase 707.
XX TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;
KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
KW amylopectin; limit dextrin; NOVAMYL; 707.
XX Bacillus sp.
XX WO200188107-A2.
XX 22-NOV-2001.
XX 10-MAY-2001; 2001WO-DK000323.
XX 12-MAY-2000; 2000DK-00000779.
XX (NOVO) NOVOZYMES AS.
XX Svendsen A, Jorgensen CT, Nielsen BR;
XX WPI; 2002-106123/14.
XX New variant of parent Termamyl-like alpha-amylase for use as a component
XX in washing and dishwashing compositions, for textile desizing, for starch
XX liquefaction, and for producing sweeteners and ethanolols from starch.
XX Claim 5; Page 81-83; 84pp; English.

CC The invention relates to a variant of parent TERMAMYL-like alpha- amylase
CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
CC or at position 234, where the variant has alpha-amylase activity and each
CC position corresponds to a position of a parent Termamyl-like alpha-
CC amylase sequence having a Bacillus licheniformis alpha-amylase sequence
CC of 483 amino acids, given in specification. The variant alpha- amylase, a
CC detergent additive comprising the variant or a detergent composition
CC comprising the variant, is useful for washing and/or dishwashing or
CC textile desizing. The alpha-amylase is useful for starch liquefaction or
CC ethanol production and as a component in a hard surface cleaning
CC detergent composition, and for producing sweeteners from starch. The
CC variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage
CC activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
CC branch linkage cleavage activity of amylopectin or a limit dextrin
CC prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a
CC natural variant of the TERMAMYL alpha-amylase, 707
XX
SQ Sequence 485 AA;
Query Match 96.5%; Score 2613; DB 5; Length 485;
Best Local Similarity 95.5%; Pred. No. 3.4e-210; Indels 0; Gaps 0;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKAGSQNDVGCA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKAGSQNDVGCA 60
QY 61 YLDYDLGEFNGKGTITRTKYGTNRQIAAVNALKSNQIQVYGVVNMHKGADATEMVRV 120
DB 61 YLDYDLGEFNGKGTITRTKYGTNRQIAAVNALKSNQIQVYGVVNMHKGADATEMVRV 120
QY 121 EVNPNRNRQEVSGEYTIETAWTKFDPFGNGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
DB 121 EVNPNRNRQEVSGEYTIETAWTKFDPFGNGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
QY 181 RGDGKAWDEVDTENGNYDLYMADIDMDHPEVNVNLRNKGWYVNTLGLDGRIDAVKH 240
DB 181 RGDGKAWDEVDTENGNYDLYMADIDMDHPEVNVNLRNKGWYVNTLGLDGRIDAVKH 240
QY 241 IKYSFTTRDWINHVRSATGKNMFVAEFAFWKNDLGAIENTYLQKTNNHNSVDFVPLHYNLYNA 300
DB 241 IKYSFTTRDWINHVRSATGKNMFVAEFAFWKNDLGAIENTYLQKTNNHNSVDFVPLHYNLYNA 300
QY 301 SKSGGNYDMRQIFNGTVVQRHPHVAFTFVDNHDSDQPEEALSFVEEWFKPLAYALTRE 360
DB 301 SKSGGNYDMRQIFNGTVVQRHPHVAFTFVDNHDSDQPEEALSFVEEWFKPLAYALTRE 360
QY 361 QGYPSVFYGYGIPTHGVPAMKSKIDPILFARQKAYGRNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGYGIPTHGVPAMKSKIDPILFARQKAYGRNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGKWMFVGRNKGAGQVWTDITGNRAGTGTITNADGNGFNSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGKWMFVGRNKGAGQVWTDITGNRAGTGTITNADGNGFNSVNGGSVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485
RESULT 15
AAU12155
ID AAB47856 standard; protein; 485 AA.
XX AAB47856;
XX AC AAB47856;
XX 02-APR-2002 (first entry)
XX Bacillus alpha amylase 707.
XX Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;
KW starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
KW bakery; cereal bar; ice cream; coffee whitener; salad dressing;

KB cured meat; fermented meat; spice.
OS Bacillus sp.
XX WO200196537-A2.
XX 20-DEC-2001.
XX 13-JUN-2001; 2001WO-DK000404.
XX 14-JUN-2000; 2000DK-00000917.
XX 20-JUN-2000; 2000US-0212852P.
XX (NOVO) NOVOZYMES AS.
XX
XX Nielsen BR, Weibye M;
XX WPI; 2002-098064/13.
XX
XX New modified alpha-amylase derived from the genus Bacillus and/or is a
XX Termamyl-like alpha-amylase, which has been pre-oxidized for producing
XX maltodextrin or glucose syrup.
XX
XX Claim 5; Page 44-46; 47pp; English.
XX
XX The sequences given in ABA47850-56 show modified alpha-amylases derived
XX from the genus Bacillus. These alpha amylases are Termamyl- like alpha-
XX amylase and they have been pre-oxidized. The alpha amylase is useful for
XX producing a maltodextrin or glucose syrup, by treating starch with a pre-
XX oxidized alpha-amylase until a product with a DE between 5-45 has been
XX provided and/or until a product with a molecular weight of between 5-30
XX kda has been provided. The product comprises a maltodextrin with a DE of
XX 18.5 and/or a maltodextrin with a molecular weight of 14-16 kda. The
XX alpha amylase is useful for producing a maltodextrin or glucose syrup,
XX where the glucose syrup is useful as an ingredient in food, feed or
XX pharmaceuticals. Glucose syrup is useful in confectionery such as
XX candies, beverages such as isotonic drinks, bakery such as cereal bars,
XX dairy and ice cream such as coffee whiteners, conventional foods such as
XX salad dressings, and food ingredients and preparations such as cured
XX meat, fermented meat, spices and seasoning encapsulated flavours
XX
XX Sequence 485 AA;

Search completed: October 7, 2004, 00:12:24
Job time : 60.5516 secs

Query Match 96.5%; Score 2613; DB 5; Length 485;
Best Local Similarity 95.5%; Pred. No. 3.4e-210;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGEFNQKGTIRTKYGRLOQAANVNLKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLYDLGEFNQKGTIRTKYGRLOQAANVNLKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNQEVSGEYITTEAWTKDFPCGRGNTHSNFKWRWYHFDGVDWQSRKLNRIYKF 180
DB 121 EVNPNRNQEVSGEYITTEAWTKDFPCGRGNTHSNFKWRWYHFDGVDWQSRKLNRIYKF 180
QY 181 RGDGKGDWEDVTENGNDYLYMADIDMDHPEVNVNLRNMGVWYNTLGLDGFRIADVKH 240
DB 181 RGDGKGDWEDVTENGNDYLYMADIDMDHPEVNVNLRNMGVWYNTLGLDGFRIADVKH 240
QY 241 IKYSFTEDWLNHRSATGKNFAVAEFWKNDLGAENYLNKTNWNSHVFDPVPLHNLNA 300
DB 241 IKYSFTEDWLNHRSATGKNFAVAEFWKNDLGAENYLNKTNWNSHVFDPVPLHNLNA 300
QY 301 SKSGGNDYMRQIFNGTVVQRPHAVTFVDNHDSDQPEEALSFVEEWFKPLAYALTRE 360
DB 301 SKSGGNDYMRQIFNGTVVQRPHAVTFVDNHDSDQPEEALSFVEEWFKPLAYALTRE 360
QY 361 QGYPSVFGDYGIPTHGVPAMSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFGDYGIPTHGVPAMSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420

Db 361 QGYPSVFGDYGIPTHGVPAMSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTWTINADGNGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTWTINADGNGNFSVNGGSVS 480
QY 481 IWVKN 485
Db 481 IWVKN 485

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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 ; Search time 14.886 Seconds
(without alignments)
3134.012 Million cell updates/sec

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Perfect score: 2708
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2613	96.5	518	1 A27705	alpha-amylase (EC
2	1887	69.7	512	1 ALBSL	alpha-amylase (EC
3	1870.5	69.1	549	1 A54541	alpha-amylase (EC
4	1863.5	68.8	549	1 A24549	alpha-amylase (EC
5	1859.5	68.7	549	1 A24436	alpha-amylase (EC
6	1847	68.2	514	1 ALBSN	alpha-amylase (EC
7	1813	66.9	548	1 ALBSF	alpha-amylase (EC
8	1363	50.3	493	2 S15713	alpha-amylase (EC
9	1298	47.9	484	2 G95160	alpha-amylase (imp
10	1296	47.9	484	2 F98026	alpha-amylase (EC
11	1282	47.3	492	2 A82079	alpha-amylase (imp
12	1148	42.4	491	2 C86781	alpha-amylase (imp
13	1114	41.1	506	2 G98247	cytoplasmic alpha-
14	1113	41.1	495	2 AD3038	alpha-amylase (imp
15	1107	40.9	494	1 B45738	alpha-amylase (EC
16	1098	40.5	494	2 AD0751	cytoplasmic alpha-
17	1085	40.1	495	2 B90962	cytoplasmic alpha-
18	1075	39.7	495	1 A45738	alpha-amylase (EC
19	1066	39.4	495	2 B85810	cytoplasmic alpha-
20	363.5	13.4	217	2 A19506	alpha-amylase (EC
21	320.5	11.8	482	2 S31478	alpha-amylase (EC
22	320	11.8	1196	2 A29130	beta-amylase (EC 3
23	283.5	10.5	421	2 S10514	alpha-amylase (EC
24	280	10.3	423	2 T09942	alpha-amylase (EC
25	280	10.3	504	2 A55861	alpha-amylase (EC
26	270.5	10.0	551	2 S05667	glucan 1,4-alpha-m
27	270	10.0	440	2 S14958	alpha-amylase (EC
28	263.5	9.7	435	2 S12625	alpha-amylase (EC
29	262.5	9.7	435	2 JC7137	alpha-amylase (EC

30 262 9.7 427 1 ALBHB
31 261.5 9.7 547 2 A32803
32 261 9.6 826 2 E96720
33 259 9.6 428 2 T05521
34 256.5 9.5 428 2 S10013
35 256.5 9.5 434 2 S12775
36 256.5 9.5 438 1 ALBH
37 254 9.4 429 1 JE0406
38 253 9.3 437 2 S14956
39 253 9.3 438 2 S14957
40 252.5 9.3 710 2 S63598
41 252.5 9.3 1449 2 T30552
42 250.5 9.3 413 1 ALWT3
43 248.5 9.2 437 2 S07040
44 247.5 9.1 713 1 ALBSXR
45 246.5 9.1 498 2 A48305

alpha-amylase (EC
glucan 1,4-alpha-m
probable alpha-amy
alpha-amylase (EC
alpha-amylase (EC
alpha-amylase (EC
alpha-amylase (EC
alpha-amylase (EC
alpha-amylase (EC
cyclomaltoextrin
glucosyltransferas
alpha-amylase (EC
alpha-amylase (EC
cyclomaltoextrin
alpha-amylase (EC

RESULT 1
A27705
alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C;Species: Bacillus sp.
C;Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A27705
R;Tsukamoto, A.; Kimura, K.; Iehii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A;Title: Nucleotide sequence of the maltohexaose-producing amylase gene from an alkalophil
A;Reference number: A27705; MUID:88162814; PMID:3258152
A;Accession: A27705
A;Molecule type: DNA
A;Residues: 1-518 <TSU>
A;Cross-references: GB:M1862; NID:G142496; PIDN:AAA22231.1; PID:G142497
A;Experimental source: chromosomal DNA of strain 707
A;Note: amino end of mature protein also determined
C;Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyliolofaciase type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-518/Product: alpha-amylase #status experimental <MAT>
F;236-369/Domain: alpha-amylase core homology <AMY>
F;139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted
F;269,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match 96.5%; Score 2613; DB 1; Length 518;
Best Local Similarity 95.5%; Pred. No. 2.3e-174;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDXGISAIVLPPPAWKASQNDVGGA 60
Db 34 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKSGITAVLPPPAWKASQNDVGGA 93
Qy 61 YDLYLDFEFNQKQGITRTKYGTNRNLQAANLKSNGIQVYGDVVMNHKGGADATEMVRV 120
Db 94 YDLYLDFEFNQKQGITRTKYGTNRNLQAANLKSNGIQVYGDVVMNHKGGADATEMVRV 153
Qy 121 EVNPNRNQEVSGEYTTTEAWTKFDPGNGNTHSNFKRWTHFGDQVDQSKLNRIYKF 180
Db 154 EVNPNRNQEVSGEYTTTEAWTRFDPGNGNTHSNFKRWTHFGDQVDQSKLNRIYKF 213
Qy 181 RGDCGKGDWEVDTEGNGVDYLMYADIDMDHPEVNVNELNMGVWYNTLTGLDGFRIIDAVKH 240
Db 214 RGHKAMDWEVDTEGNGVDYLMYADIDMDHPEVNVNELNMGVWYNTLTGLDGFRIIDAVKH 273
Qy 241 IKYSFTRDWINHVRSATGKNMFAVEFWKNDLGAIEYLNKTNWNSHVSFVDFPLHYNLYNA 300
Db 274 IKYSFTRDWINHVRSATGKNMFAVEFWKNDLGAIEYLNKTNWNSHVSFVDFPLHYNLYNA 333

ALIGNMENTS

QY 301 SKGGNMDRQIFNGTIVVQRHPHVAITFVDNHDSDQEEALESFVEWFKPLAYALTITRE 360
 |||||
 Db 334 SKGGNMDRNIENGITVQRHPHVAITFVDNHDSDQEEALESFVEWFKPLAYALTITRE 393
 |||||
 QY 361 QGYPSVFYGYGYPGTHGVPAKSKIDPILFARQKAYGQNDYLDHNNIIGWTRRGNTA 420
 |||||
 Db 394 QGYPSVFYGYGYPGTHGVPAKSKIDPILFARQKAYGQNDYLDHNNIIGWTRRGNTA 453
 |||||
 QY 421 HPNSGLATMSDAGGKNGKMFVGRNKGQVWTDITGNRAGTIVTINADGNGFNSVNGSGVS 480
 |||||
 Db 454 HPNSGLATMSDAGGSKMFPVGRNKGQVWSDITGNRTGTIVTINADGNGFNSVNGSGVS 513
 |||||
 QY 481 IWVWK 485
 |||||
 Db 514 IWVWK 518
 |||||

RESULT 2
 ALBSL
 alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
 N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C;Species: Bacillus licheniformis
 C;Date: 30-Jun-1987 #sequence, revision 24-Apr-1998 #text_change 15-Sep-2000
 C;Accession: A91997; B24549; A91796; A21663; I39774; I39772; A26151; S53788; A00844
 R;Yuuki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Udaka, S.
 J. Biochem. 98, 1147-1156, 1985
 A;Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylase deduced from the DNA sequences.
 A;Reference number: A91997; MUID:86111694; PMID:2418011
 A;Accession: A91997
 A;Molecule type: DNA
 A;Residues: 1-162, 'R', 164-512 <YU>
 A;Cross-references: GB:X03236; NID:g39551; PIDN:CRA26981.1; PID:g39552
 A;Experimental source: ATCC 27811
 R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requa, R.
 J. Bacteriol. 166, 635-643, 1986
 A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus
 A;Reference number: A91817; MUID:86195857; PMID:3009417
 A;Accession: B24549
 A;Molecule type: DNA
 A;Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>
 A;Cross-references: GB:M13256; NID:g142510; PIDN:AAA22240.1; PID:g142511
 A;Experimental source: NCIB 8061
 R;Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.
 J. Bacteriol. 156, 369-372, 1984
 A;Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase gene
 A;Reference number: A91796; MUID:84185455; PMID:6609154
 A;Accession: A91796
 A;Molecule type: DNA
 A;Residues: 1-104 <STE>
 A;Cross-references: GB:K01984; NID:g142432; PIDN:AAA22193.1; PID:g142433
 R;Sibakov, M.; Palva, I.
 Eur. J. Biochem. 145, 567-572, 1984
 A;Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amylase gene
 A;Reference number: A21663; MUID:85076654; PMID:6334606
 A;Accession: A21663
 A;Molecule type: DNA
 A;Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 81-104 <LQ>
 A;Experimental source: chromosomal DNA of ATCC 14580
 A;Note: The authors translated the codon CGT for residue 48 as Gly and GAC for residue 61 as Glu.
 R;Laoid, B.M.; Chambliss, G.H.; McConnell, D.J.
 J. Bacteriol. 171, 2435-2442, 1989
 A;Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent regulation
 A;Reference number: I39773; MUID:89213924; PMID:2540150
 A;Accession: I39774
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-29 <LQ>
 A;Cross-references: GB:M26412; NID:g341477; PIDN:AAA22237.1; PID:g516590
 R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
 Gene 96, 37-41, 1990
 A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con

A;Reference number: I39772; MUID:91092499; PMID:2265757
 A;Accession: I39772
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-32, 'I' <OR>
 A;Cross-references: GB:M62637; NID:g142498; PIDN:AAA22232.1; PID:g142499
 R;Kuhn, H.; Pietzek, P.P.; Lampen, J.O.
 J. Bacteriol. 149, 372-373, 1982
 A;Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: comparison with the sequence of the N-terminal amino acid sequence of Bacillus subtilis
 A;Reference number: A26151; MUID:82098050; PMID:6172418
 A;Accession: A26151
 A;Molecule type: protein
 A;Residues: 30-37, 'B', 39-41, 'X', 43-47 <KU>
 R;Machius, M.; Wiegand, G.; Huber, R.
 J. Mol. Biol. 246, 545-559, 1995
 A;Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2.2 angstroms
 A;Reference number: S53788; MUID:95182462; PMID:7877175
 A;Accession: S53788
 A;Molecule type: protein
 A;Residues: 'D', 220-227 <MAC>
 A;Note: sequence represents amino end of an internal fragment created by a single enzymatic cleavage
 R;Machius, M.; Wiegand, G.; Huber, R.
 submitted to the Brookhaven Protein Data Bank, July 1995
 A;Reference number: A65206; PDB:1BPL
 A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210; 222-511
 A;Note: these structural studies suggest 163 is Leu rather than Arg
 R;Song, H.K.; Hwang, K.Y.; Chang, C.; Suh, S.W.
 submitted to the Brookhaven Protein Data Bank, October 1996
 A;Reference number: A68680; PDB:1VJS
 A;Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210; 222-511
 C;Genetics:
 A;Gene: amyL
 C;Function:
 A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A;Pathway: glycogen/starch degradation
 C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
 C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide hydrolase
 F;30-512/Product: signal sequence #status predicted <SIG>
 F;227-360/Domain: alpha-amylase core homology <MAT>
 F;133-229/Domain: alpha-amylase core homology <AMY>
 F;260,290,357/Active site: Asp, Glu, Asp #status experimental
 Query Match 69.7%; Score 1887; DB 1; Length 512;
 Best Local Similarity 68.0%; Pred. No. 8.1e-124;
 Matches 330; Conservative 69; Mismatches 76; Indels 10; Gaps 4;
 QY 6 NGTMOYFEWYLPNDGNHNRLSASNLDKGISAVWIPPAWKGSQNDVGYGAYDLYD 65
 |||||
 Db 33 NGTMOYFEWYLPNDGNHNRLSASNLDKGISAVWIPPAWKGSQNDVGYGAYDLYD 92
 |||||
 QY 66 LGBFNKGRTIRTKYGFNOLQAANALKNGIQVGVVNMHKGADATMVRVAEVPN 125
 |||||
 Db 93 LGBFHKGRTIRTKYGFNOLQAANALKNGIQVGVVNMHKGADATMVRVAEVPN 152
 |||||
 QY 126 NRNQVSGYTTIATWTKPFGPGNGTHSNFKRWYHFDGVMDQSKLNRIYKFRGDGK 185
 |||||
 Db 153 DRNRVISGEHLIKAWTHFFHFGPGSTYDFKWHYHFDGTDWDSRKL-NRIYKFQ--GK 209
 |||||
 QY 186 GWDWEVDTEGNDYIMYADIDMDHFEVNVNELRWGVTNTGLDGRIDAVKHICYSP 245
 |||||
 Db 210 AWDWEVSNENGNDYIMYADIDMDHFEVNVNELRWGVTNTGLDGRIDAVKHICYSP 269
 |||||
 QY 246 TRDWINHVSATGKNFAVAFKNDLGAENYLNKTNHNSVDFVPLHYNLNASKSGG 305
 |||||
 Db 270 LRDNVNHVREKTEKENTVAEYQNDLGAENYLNKTNHNSVDFVPLHYQFHAASQGG 329
 |||||
 QY 306 NYDMRQIFNGTIVVQRHPHVAITFVDNHDSDQEEALESFVEWFKPLAYALTITRE 365
 |||||
 Db 330 GYDMRKLNLSTVVSKEFLKAVTFVDNHDTPQGQSLSTVQTWFKPLAYAFILTR 389
 |||||
 QY 366 VFYGDYVGYPTHG-----VPAMKSKTDPILEAFQKAYGRQNDYLDHNNIIGWTR 420
 |||||

Db 390 VFYGMVG--TKGDSQREIPALKHKIEPILKARKQYAGQHDYDFDHHDIIVGWTREGDSS 447
Qy 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTITNADGWGNFVNGGSVS 480
Db 448 VANSGLAALITDGPGGAKRMVYGRQNAGETWHDITGNRSEPVWINSNCGEFGVHNGGSVS 507
Qy 481 IWNK 485
Db 508 IYQR 512

RESULT 3
A54541
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DN1792)
N:Alternate names: 1.4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus stearothermophilus
C:Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
C:Accession: A54541
R:Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEMS Microbiol. Lett. 77, 271-276, 1991
A:Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A:Reference number: A54541
A:Accession: A54541
A:Molecule type: DNA
A:Residues: 1-549 <JQR>
A:Cross-references: GB:X59476
A:Experimental source: chromosomal DNA of strain DN1792
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-549/Product: alpha-amylase #status predicted <MAT>
F:235-368/Domain: alpha-amylase core homology <AMY>
F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F:268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 69.1%; Score 1870.5; DB 1; Length 549;
Best Local Similarity 66.9%; Pred. No. 1.3e-122;
Matches 320; Conservative 74; Mismatches 83; Indels 1; Gaps 1;
Qy 6 NGTMMQYFEWYLPNDGNHNRSLRSDASNLKDKGISAVWIPAWKAGSONDVGYGAYDLYD 65
Db 39 NGTMMQYFEWYLPDGGTLWTWKVANEANLSSGLITALWLPAYKGRSDVGYGYDLYD 98
Qy 66 LGFENQKGTIRTKYGTNRNLQAAVNAKLSNGIQYGVDMVNMHKGADATEMVRVAVENPN 125
Db 99 LGFENQKGTVRTKYGTAKYQLQAAHAAGMQYADVDFHKGADTEWDAVEVNP 158
Qy 126 NRQEVSGEVTIEAWTKFDPFGNGTHSNFKRWYHFDGVDWDSRKLNNRIYKFRGDGK 185
Db 159 DRNQEISGTQIQIAWTKFDPEGRNTYSSPKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
Qy 186 GWDWEVDTENGYDLYMAYADIDMDHPVNLWNGVYNTTGLDGRIDAVKHKYSF 245
Db 218 AWDWEVDTENGYDLYMAYADIDMDHPVNLWNGVYNTTGLDGRIDAVKHKYSF 277
Qy 246 TRDWINHVRSGATGNMFAVAFWKNLGAENYLNKTNWNSHVFDPVPLHYNLNASKSGG 305
Db 278 FPDWLSVRSQTGKPLFTVGEIWSYDINKLHNYITKIDGTMSLTDAPLHNFYTSKSGG 337
Qy 306 NYDMRQIFNGTVQVRHMPHIAVTFVDNHDSPQEEALESFVEWFKFLAYALTLTREQQVPS 365
Db 338 AFDMLTMTNLMKDQPLAVTFVDNHDTEPGALQSWDPWFKFLAYALTLTREQGYPC 397
Qy 366 VFYGDYGIPTGHVPAWMSKIDPILKARQYAGQNDYLDHNNIIGWTRGNTAHNPSG 425
Db 398 VFYGDYGIPTGHVPAWMSKIDPILKARQYAGQNDYLDHNNIIGWTRGNTAHNPSG 457

Qy 426 LATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTITNADGWGNFVNGGSVSIVW 483
Db 458 LAALITDGPGGKWMYVYGRQNAGETWHDITGNRSDTITNADGWGEFKVNGGSVWV 515

RESULT 4
A24549
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)
N:Alternate names: 1.4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus stearothermophilus
C:Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C:Accession: A24549; I39501; I39770
R:Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamea, M.H.; Kindle, K.L.; Carmona, C.; Requadt,
J. Bacteriol. 166, 635-643, 1986
A:Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearother
A:Reference number: A91817; MUID:86195857; PMID:3009417
A:Accession: A24549
A:Molecule type: DNA
A:Residues: 1-549 <GRA>
A:Cross-references: GB:M13255; NID:g142512; PIDN:AAA22241.1; PID:g142513
A:Experimental source: genomic DNA of strain NZ-3
R:Sato, H.; Nishida, H.; Isono, K.
J. Bacteriol. 170, 1034-1040, 1988
A:Title: Evidence for movement of the alpha-amylase gene into two phylogenetically dista
A:Reference number: I39501; MUID:88139156; PMID:3257753
A:Accession: I39501
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 536-549 <RES>
A:Cross-references: GB:M29577; NID:g142476; PIDN:AAA22225.1; PID:g142478
A:Experimental source: strain DY-5
A:Accession: I39770
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 536-549 <RE2>
A:Cross-references: GB:M29578; NID:g142484; PIDN:AAA22228.1; PID:g142486
A:Experimental source: strain 799
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-549/Product: alpha-amylase #status predicted <MAT>
F:235-368/Domain: alpha-amylase core homology <AMY>
F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F:268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 68.8%; Score 1863.5; DB 1; Length 549;
Best Local Similarity 66.9%; Pred. No. 3.8e-122;
Matches 320; Conservative 73; Mismatches 84; Indels 1; Gaps 1;
Qy 6 NGTMMQYFEWYLPNDGNHNRSLRSDASNLKDKGISAVWIPAWKAGSONDVGYGAYDLYD 65
Db 39 NGTMMQYFEWYLPDGGTLWTWKVANEANLSSGLITALWLPAYKGRSDVGYGYDLYD 98
Qy 66 LGFENQKGTIRTKYGTNRNLQAAVNAKLSNGIQYGVDMVNMHKGADATEMVRVAVENPN 125
Db 99 LGFENQKGTVRTKYGTAKYQLQAAHAAGMQYADVDFHKGADTEWDAVEVNP 158
Qy 126 NRQEVSGEVTIEAWTKFDPFGNGTHSNFKRWYHFDGVDWDSRKLNNRIYKFRGDGK 185
Db 159 DRNQEISGTQIQIAWTKFDPEGRNTYSSPKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
Qy 186 GWDWEVDTENGYDLYMAYADIDMDHPVNLWNGVYNTTGLDGRIDAVKHKYSF 245
Db 218 AWDWEVDTENGYDLYMAYADIDMDHPVNLWNGVYNTTGLDGRIDAVKHKYSF 277
Qy 246 TRDWINHVRSGATGNMFAVAFWKNLGAENYLNKTNWNSHVFDPVPLHYNLNASKSGG 305

Db 278 FPDWLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFTYASKSGG 337

QY 306 NYDMROIFNGTVQVRHPMAHTVFDVNDHDSQPEALESFVEEWPFPKPLAYALTITREOGYPS 365

Db 338 AFDMSTLMMNTLMKQDPTLATVFDVNDHDEPGQALQSWDPWPKPLAYAFILTRQEGYPC 397

QY 366 VFYGDYIGTPTGVHPAMKSKIDPILBARQKYAQRQNDYLDHNNIIGWTRGNHTAHNPSG 425

Db 398 VFYGDYIGTPTGVHPAMKSKIDPILBARQKYAQRQNDYLDHNNIIGWTRGNHTAHNPSG 457

QY 426 LATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTTINADGWNFSVNGSVSIWV 483

Db 458 LAALITDGGGKMWYVKGQAGKVFYDLTGNRSDTVTINSDDGGEFKVNGGSVWV 515

RESULT 5

A24436

alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C/Species: Bacillus stearothermophilus

C/Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999

C/Accession: A24436; I39777

R/Nakajima, R.; Imanaka, T.; Aiba, S.

J. Bacteriol. 163, 401-406, 1985

A/Reference number: A24436; MUID:85234394; PMID:3924897

A/Accession: A24436

A/Molecule type: DNA

A/Residues: 1-549 <NA>

A/Cross-references: GB:M11450

A/Experimental source: plasmid pAT5

A/Note: amino end of the mature protein also determined

R/Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.

Gene 96, 37-41, 1990

A/Title: In vivo genetic engineering: homologous recombination as a tool for plasmid construction

A/Reference number: I39772; MUID:91092499; PMID:2465757

A/Accession: I39777

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-45 <RES>

A/Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515

A/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the chromosome

C/Genetics:

A/Gene: amyS

A/Genome: plasmid

A/Start codon: GTG

C/Function:

A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A/Pathway: glycogen/starch degradation

C/Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide

F/1-34/Domain: signal sequence #status predicted <SIG>

F/35-549/Product: alpha-amylase #status experimental <MAT>

F/235-368/Domain: alpha-amylase core homology <AMY>

F/139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted

F/268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 68.7%; Score 1859.5; DB 1; Length 549;

Best Local Similarity 66.7%; Pred. No. 7.3e-122;

Matches 319; Conservative 73; Mismatches 85; Indels 1; Gaps 1;

QY 6 NGTMMQVFEWYLPNDGNHNNRLSDASNLKDGISAVWIPPAWKASQNDVGVGYDLYD 65

Db 39 NGTMMQVFEWYLPDDGTLTWTKVANEANLSSGLTALWLPYAKGTSRSDVGVGYDLYD 98

QY 66 LGFBNQKGTTRTKYGTNRNQQAVALKSGIYQVGDVWVNHKGADATMTWPAVEVNP 125

Db 99 LGFBNQKGAVRTKYGTAKQYLAQIAHAAGMQVYADVDFHKGADGTWVDVAVEVNS 158

QY 126 NRNOQVSGEYTTIRAWTKFDPFGNGTHSNFKRWYHFDGVDVQSKLNLRNRYKFRGDGK 185

Db 159 DRNQEISGTTQIQWTKFDPFGNGTYSSFNKRWYHFDGVDVNDSEKLL-SRIYKFRGIGK 217

QY 186 GWDWEVDTENGYDLYMYADIDMDHPVNVNLRNWGWYNTLTGLDGFRIADVVKHICYSP 245

Db 218 ANDWEVDTENGYDLYMYADIDMDHPVNVNLRNWGWYNTLTGLDGFRIADVVKHICYSP 277

QY 246 TRDWNHVSATGKNMFAVAEFPKNDLGAENYLNKNTNNHNSVDFVPLHNLNASKSGG 305

Db 278 FPDWLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFTYASKSGG 337

QY 306 NYDMROIFNGTVQVRHPMAHTVFDVNDHDSQPEALESFVEEWPFPKPLAYALTITREOGYPS 365

Db 338 AFDMSTLMMNTLMKQDPTLATVFDVNDHDEPGQALQSWDPWPKPLAYAFILTRQEGYPC 397

QY 366 VFYGDYIGTPTGVHPAMKSKIDPILBARQKYAQRQNDYLDHNNIIGWTRGNHTAHNPSG 425

Db 398 VFYGDYIGTPTGVHPAMKSKIDPILBARQKYAQRQNDYLDHNNIIGWTRGNHTAHNPSG 457

QY 426 LATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTTINADGWNFSVNGGSVSIWV 483

Db 458 LAALITDGGGKMWYVKGQAGKVFYDLTGNRSDTVTINSDDGGEFKVNGGSVWV 515

RESULT 6

ALSN

alpha-amylase (EC 3.2.1.1) precursor - Bacillus amylioliquefaciens

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C/Species: Bacillus amylioliquefaciens

C/Date: 30-Nov-1980 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999

C/Accession: A92389; A90307; I39756; I39763; A00843

R/Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L.

J. Biol. Chem. 258, 1007-1013, 1983

A/Title: Amino acid sequence of alpha-amylase from Bacillus amylioliquefaciens deduced from cDNA

A/Reference number: A92389; MUID:83108808; PMID:6185474

A/Contents: pUB110

A/Accession: A92389

A/Molecule type: DNA

A/Residues: 1-514 <NA>

A/Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA2215

R/Chung, H.S.; Friedberg, F.

Biochem. J. 185, 387-395, 1980

A/Title: Sequence of the N-terminal half of Bacillus amylioliquefaciens alpha-amylase.

A/Reference number: A90307; MUID:80241725; PMID:6156671

A/Accession: A90307

A/Molecule type: protein

A/Residues: 32-53, 'I', 55-63, 'L', 65-78, 'D', 80-83, 'S', 85-222 <CHU>

R/Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;

Gene 15, 43-51, 1981

A/Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of the alpha-amylase gene

A/Reference number: I39756; MUID:82051296; PMID:6170539

A/Accession: I39756

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-96 <RES>

A/Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298

R/Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karaenen, S.

Gene 59, 161-170, 1987

A/Title: Efficient secretion of Bacillus amylioliquefaciens alpha-amylase cells by its own signal peptide

A/Reference number: I39763; MUID:88137952; PMID:2830166

A/Accession: I39763

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-39 <RES>

A/Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431

C/Function:

A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A/Pathway: glycogen/starch degradation

C/Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F/1-31/Domain: signal sequence #status predicted <SIG>

F/32-514/Product: alpha-amylase #status predicted <MPT>

F/229-362/Domain: alpha-amylase core homology <AMY>

F/133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted

F/262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match 68.2%; Score 1847; DB 1; Length 514;


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QY 6 NGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVGAYDLYD 65
Db 4 NHTMMQYFEWHLAADGDHWRKLAEMAPELKAGKIDVTWVPPVTKAVSAEDTGYYDLYD 63
QY 66 LGFEFNQKGTIRTKYGRNLOQAANVNAKLSNGIQVYGDVVMNHKGGADATMVRVAVENPN 125
Db 64 LGFEFDQKGTIRTKYGTQKELIEAIEACQKNGIAVYVDLVNMHKAAGADETEVFKEVIEDPN 123
QY 126 NRNOQVSGEYTIETAWTKFDPGGRGNTHSNFKRWYHFDGVDQSKLNRIYKFRGDGK 185
Db 124 DRTKEISEPPEIEBGTWTKFTPPGGRDQYSSFKWNSHFNGTDFD-AREERTGVIAGENK 182
QY 186 GWDWEVDTENGNYDLYMAYADIDMDHPEVNVNLRNMGVWYNTLTGLDGFPRIDAVKHLYKF 245
Db 183 KWNENVDDEGNVDYLMFANIDYHNDVREMDKWLIDTLQCGGFLDAIKLHNHF 242
QY 246 TRDWINHVRSAATGNMFAVAEFMKNLGAENLYNKTNWNHVSFVDPVPLHYNLYNASKSG 305
Db 243 IKFEFAAEMIRKRGQDFYIVGFEFWSNLDACREFLDTVDYQIDLFVSLHYKLHEASLGR 302
QY 306 NYDMROI FNGTVVQRHPMAHVTVDNHDQPEBALESFVEEWPFKPLAYALTLTREOGYPS 365
Db 303 DFLSKIFDPTLVQTHETHAVTFVDNHDQPEBALESFVEEWPFKPLAYALTLLRRDGPV 362
QY 366 VFYGDYGI----PTHGVPAMKSKIDPILAEARKQYAYGRQNDYLDHNNIIGWTREGNTAH 421
Db 363 VFYGDYGI GGPFPVUG---KKEILDILLSARCKAYGQEDYFDHANTIGWVRGVEI 419
QY 422 PNSGLATIMSDGAGGNKMMFVGRNKAQGVWTDITGNRAGTVTINADGWGNFVNGSGSVI 481
Db 420 EGSQCAVWISNGDGEKRMFIGHSHRAGEVWVDLTKSCDDQITTEEDGWATFHVCGGGSV 479
QY 482 W 482
Db 480 W 480

RESULT 9
G95160
alpha-amylase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: G95160
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95160
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-484 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75480.1; PID:g14972868; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
C:Gene: SPI382
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 47.9%; Score 1298; DB 2; Length 484;
Best Local Similarity 50.6%; Pred. No. 7.8e-83;
Matches 243; Conservative 69; Mismatches 162; Indels 6; Gaps 4;

QY 6 NGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVGAYDLYD 65
Db 3 NOTLMOYFEWYLPDGHQWHLAENAPHLAHLGISHVWMPAPKATNEKDVGVGYDLPD 62
QY 66 LGFEFNQKGTIRTKYGRNLOQAANVNAKLSNGIQVYGDVVMNHKGGADATMVRVAVENPN 125
Db 63 LGFEFNQKGTIRTKYGFEDYLOAIQALKAGQIQPMADVVLNHNKAAADHREAFQVIEDPV 122
QY 126 NRNOQVSGEYTIETAWTKFDPGGRGNTHSNFKRWYHFDGVDQSKLNRIYKFRGDGK 185
Db 124 DRTKEISEPPEIEBGTWTKFTPPGGRDQYSSFKWNSHFNGTDFD-AREERTGVIAGENK 182
QY 186 GWDWE--VDTENGNYDLYMAYADIDMDHPEVNVNLRNMGVWYNTLTGLDGFPRIDAVKHLY 243
Db 182 GWANEELVDNENGNYDLYMAYADLPKHPVEIQNIYDWDADWFMETTGAGFRDLDAVKHIDS 241
QY 244 SFTRDWINHVRSAATGNMFAVAEFMKNLGAENLYNKTNWNHVSFVDPVPLHYNLYNASKS 303
Db 242 FFMRFNIRDMKKGIDGDFYVGFGEFWSNLDACREFLDTVDYQIDLFVSLHYKLHEASLGR 301
QY 304 GGNVDMROI FNGTVVQRHPMAHVTVDNHDQPEBALESFVEEWPFKPLAYALTLTREOGY 363
Db 303 DFLSKIFDPTLVQTHETHAVTFVDNHDQPEBALESFVEEWPFKPLAYALTLLRRDGPV 362
QY 482 W 482
Db 480 W 480
```

```
Db 123 DRTVGLGEPFTINGWTSFTFDGRQDTYNGFHHWYHFTGTDYDAKRS-KSGIYLIQGDNK 181
QY 186 GWDWE--VDTENGNYDLYMAYADIDMDHPEVNVNLRNMGVWYNTLTGLDGFPRIDAVKHLY 243
Db 182 GWANEELVDNENGNYDLYMAYADLPKHPVEIQNIYDWDADWFMETTGAGFRDLDAVKHIDS 241
QY 244 SFTRDWINHVRSAATGNMFAVAEFMKNLGAENLYNKTNWNHVSFVDPVPLHYNLYNASKS 303
Db 242 FFMRFNIRDMKKGIDGDFYVGFGEFWSNLDACREFLDTVDYQIDLFVSLHYKLHEASLGR 301
QY 304 GGNVDMROI FNGTVVQRHPMAHVTVDNHDQPEBALESFVEEWPFKPLAYALTLTREOGY 363
Db 302 GANYDLRGIFTDSLVELPKAVTFVDNHDQPEBALESFVEEWPFKPLAYALTLLRRDQGL 361
QY 364 PSVFYGDYGI--PTHGVPAMKSKIDPILAEARKQYAYGRQNDYLDHNNIIGWTREGNTAH 422
Db 362 PCVFYGDYGI GGPFPVUG---KKEILDILLSARCKAYGQEDYFDHANTIGWVRG--AEN 419
QY 422 PNSGLATIMSDGAGGNKMMFVGRNKAQGVWTDITGNRAGTVTINADGWGNFVNGSGSVI 482
Db 420 QSPIAVLISNDQENSKSMFVGEWNTQTFVDLGNHQGVTDIDERGQGFVPSARSVW 479

RESULT 10
F98026
alpha-amylase (BC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: F98026
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:1154234
A:Accession: F98026
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-484 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAL00043.1; PID:g15458876; GSPDB:GN00174
C:Genetics:
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase

Query Match 47.9%; Score 1296; DB 2; Length 484;
Best Local Similarity 50.4%; Pred. No. 1.1e-82;
Matches 242; Conservative 71; Mismatches 161; Indels 6; Gaps 4;

QY 6 NGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVGAYDLYD 65
Db 3 NOTLMOYFEWYLPDGHQWHLAENAPHLAHLGISHVWMPAPKATNEKDVGVGYDLPD 62
QY 66 LGFEFNQKGTIRTKYGRNLOQAANVNAKLSNGIQVYGDVVMNHKGGADATMVRVAVENPN 125
Db 63 LGFEFNQKGTIRTKYGFEDYLOAIQALKAGQIQPMADVVLNHNKAAADHREAFQVIEDPV 122
QY 126 NRNOQVSGEYTIETAWTKFDPGGRGNTHSNFKRWYHFDGVDQSKLNRIYKFRGDGK 185
Db 123 DRTVGLGEPFTINGWTSFTFDGRQDTYNGFHHWYHFTGTDYDAKRS-KSGIYLIQGDNK 181
QY 186 GWDWE--VDTENGNYDLYMAYADIDMDHPEVNVNLRNMGVWYNTLTGLDGFPRIDAVKHLY 243
Db 182 GWANEELVDNENGNYDLYMAYADLPKHPVEIQNIYDWDADWFMETTGAGFRDLDAVKHIDS 241
QY 244 SFTRDWINHVRSAATGNMFAVAEFMKNLGAENLYNKTNWNHVSFVDPVPLHYNLYNASKS 303
Db 242 FFMRFNIRDMKKGIDGDFYVGFGEFWSNLDACREFLDTVDYQIDLFVSLHYKLHEASLGR 301
QY 304 GGNVDMROI FNGTVVQRHPMAHVTVDNHDQPEBALESFVEEWPFKPLAYALTLTREOGY 363
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Db 302 GANYDLRGIFDLSVLKPKDQKAVTFVNDHDTQRCQALESTVEWFKPAAYALILLRQDGL 361
Qy 364 PSVFYGYDYGIP-THGVPAKMSKIDPILAEARQKAYGRQNDYLDHNNIIGTWREGNTAHP 422
Db 362 PCVFYGYDYGISGQYAADPKIILDRLLAIRKDLAYGEONDYDFHANCIGWVRSG--AEN 419
Qy 423 NSGLATTMSDAGGNKMFVGRNKAQGWTDITGNRAGTGTINADGNFVNGSGSVIW 482
Db 420 QSPIAVLISNDQENSKSMFVGQEWNTQTFVDLLSGHQGVTDIEGYGQFPVSARSVW 479
RESULT 11
AH2079
alpha-amylase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH2079
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
C;Accession: AH2079
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-492 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA073889.1; PID:g17131281; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr2190
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
Query Match 47.3%; Score 1282; DB 2; Length 492;
Best Local Similarity 49.8%; Pred. No. 1e-81;
Matches 244; Conservative 78; Mismatches 152; Indels 16; Gaps 5;
Qy 6 NGTMQYFEWYLPNDGNHNRSLDASNLKDKGISAVMIPPAWKG-ASQNDVGYGAYDLY 64
Db 5 NGTMQYFHWYIPNDGNLWSKVASAPELADAGFTAMWLPAYKGFAGSFDVGVGVDLF 64
Qy 65 DLGFNQKGTIRTKYGTNRNLQQAVALKNGIQVGVDMHKGADATEMVRAVEVNP 124
Db 65 DLGFNQKGTIRTKYGTNRNLQQAVALKNGIQVGVDMHKGADATEMVRAVEVNP 124
Qy 125 NNRNQVSGEYTTAEATKFPDGRGNTHSNFKRWYHFDGVDMQSRKLNRIYKRGDG 184
Db 125 DRLNPKGGLQDITKTYTHYFPGQKYSNFEWHWHFDDAVDYNEYS-GRSTVYLLG 183
Qy 185 KGWDWEYDTNGNYDLYADIDMDHPEVNVNLRNNGVWYNTLTGLDGFRIADAVKHYS 244
Db 184 KNFDYVALEKGNFAYLWGCDDLPQNEWVRGEVYMGKCLDTTKVDGFRIDAIKHISTW 243
Qy 245 FTDRWNHVSATGKMFVAEFAWDLGAIENYLNKTNHNSVDFVPLHNLNASKSG 304
Db 244 FPEWDALERHAKDLFMVGEYVNDINTLLWYDVAVRGKMSVDFVPLHNFHQASKG 303
Qy 305 GNYDMROIENGTVVQRHPHMAVTFVDNHDSDPEALESFVEEWFKPLAYALTLTREOGYP 364
Db 304 GNYDMROIENGTVVQRHPHMAVTFVDNHDSDPEALESFVEEWFKPLAYALTLTREOGYP 363
Qy 365 SVFYGYGIPFTHG-----VPAMSKIDPILAEARQKAYGRQNDYLDHNNIIGW 413
Db 364 CVFHADYGAIEYEDWGDGNGRNYIFMPSHRWIDKLLYARKYAYGQYNYLDHNNIIGW 423
Qy 414 TRENTAHPNSGLATIMSDGAGNKMFGVGRNKAQGWTDITGNRAGTGTINADGNFVS 473
Db 424 TRLGDADHP-QGMVAVIMSDGSEGIKMWEGV--KPTNKFIDLTEHKEAVYTNWNGWGEFR 480
Qy 474 VNGSSVSIW 483
Db 481 CLGGSVSVW 490

RESULT 12

C86781

alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C;Accession: C86781

R;Bolojin, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich,
Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: C86781

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-491 <STO>

A;Cross-references: GB:AE005176; PID:g12724224; PIDN:AAK05349.1; GSPDB:GN00146

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: amyL

C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 42.4%; Score 1148; DB 2; Length 491;
Best Local Similarity 43.2%; Pred. No. 2.2e-72;
Matches 207; Conservative 96; Mismatches 172; Indels 4; Gaps 3;
Qy 8 TMMQYFEWYLPNDGNHNRSLDASNLKDKGISAVMIPPAWKAS-QNDVGYGAYDLYDL 66
Db 3 TILQAPFEWYLPDSQHWNNIKENIPDLGLGFSGLWLPASKAASGVEDVGYGYDLYDL 62
Qy 67 GFNQKGTIRTKYGTNRNLQQAVALKNGIQVGVDMHKGADATEMVRAVEVNP 126
Db 63 GFNQKGTIRTKYGTNRNLQQAVALKNGIQVGVDMHKGADATEMVRAVEVNP 122
Qy 127 NNRNQVSGEYTTAEATKFPDGRGNTHSNFKRWYHFDGVDMQSRKLNRIYKRGDGK 186
Db 123 HLNNIENKTYEVTFTFFRQKQYDNIYIWNHFTGIDYDE-RKQEEILEF--SGHE 179
Qy 187 WDWEVDTPNGNYDLYADIDMDHPEVNVNLRNNGVWYNTLTGLDGFRIADAVKHYSFT 246
Db 180 WDWEVDTPNGNYDLYADIDMDHPEVNVNLRNNGVWYNTLTGLDGFRIADAVKHYSFT 239
Qy 247 RDWNVHVSATGKMFVAEFAWDLGAIENYLNKTNHNSVDFVPLHNLNASKSGN 306
Db 240 DKWLEQRAKQLDRKLFVGEYVSDDLGKLYLEQSSDRILQLEFVPLHFNKKEASSTNGE 299
Qy 307 YDMROIENGTVVQRHPHMAVTFVDNHDSDPEALESFVEEWFKPLAYALTLTREOGYP 366
Db 300 FDMRTULFDTLTASQPELSVTFVDNHDSDPEALESFVEEWFKPLAYALTLTREOGYP 359
Qy 367 FYGDIYGIPTGHVPAMSKIDPILAEARQKAYGRQNDYLDHNNIIGTWREGNTAHPNSGL 426
Db 360 FWDGLYGIPTGHVPAMSKIDPILAEARQKAYGRQNDYLDHNNIIGTWREGNTAHPNSGL 419
Qy 427 ATTMDSGAGNKMFGVGRNKAQGWTDITGNRAGTGTINADGNFVNGSGSVIWNK 485
Db 420 SCILTNKNGSKYMIIDKAVAGKYIDLFRHPIPTLDQNGGAEFVNDGSGSVVWVDK 478
RESULT 13

C98247

cytoplasmic alpha-amylase (1,4-alpha-d-glucan glucanohydrolase) [imported] - Agrobacteriu

C;Species: Agrobacterium tumefaciens

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002

C;Accession: G98247

R;Goodner, B.; Hinkley, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: G98247

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-506 <KUR>

A;Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:g15159379; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L_1863

A;Map position: linear chromosome
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 41.1%; Score 1114; DB 2; Length 506;
Best Local Similarity 44.9%; Pred. No. 5.4e-70;
Matches 222; Conservative 79; Mismatches 177; Indels 16; Gaps 6;

QY 3 NGTGTMMQYFEWYLPNDGNHNRSLSDASNLKDGISAVWIPPAWKASQN-DVGYGAY 61
DB 11 NMAGRLLQFFHYYPDGKLVSEVAEAKESLAKMGITDVLPPAYKGAAGYSVGYDIT 70

QY 62 DLYDLGEFNQGTIRTKYGRNOLQAVALNKSNGIQVYGVVNMHKGADATMVRV 121
DB 71 DLFDLGEFQKGVATKYGDRAALEHAGTKLKGIRVTHDVVNLHMGADAKEKVRVR 130

QY 122 VNPNNRQEVSGEYTTIEAWTKFDPGRGNTHSNFKRWYHFDGVDWDSRKLNN--RIYK 179
DB 131 VNPDDRTDIDDEFPALAYTRFTFPGRNKGKSKFIWDLKCFSGVDHIEBPTDGI 190

QY 180 FRDGGKGMDEVTENGNDYLMYADIDMDHPVNLNKGWVYNTLGLDGRIDAVK 239
DB 191 EYGDGE-WNEVDQENGNDYLMYADIDMDHPVNLNKGWVYNTLGLDGRIDAVK 249

QY 240 HIKYSFTRDWINHVSATGKMFVAFWKNLKGALENYLNKTNMNSHVSFVPLHYNLN 299
DB 250 HIPAWFRDWMHRETVDPDLFVVAEYHHPDLKSLYELVDKQLMFLDVALHHSFD 309

QY 300 ASKSGGNDYRQIFNGTVQRPMPHVAFTFVDNHSQPEEALESFVBEWFKPLAYALT 359
DB 310 ASKQGGDFMRSIFDGLSVSAVDPHVAITLVDNHTQPLQSLAPVFPFKPLAYAIL 369

QY 360 EQYPSVYGYG--IPTHGVPAKSKID-----PILEARQKAYGRQNDYLDH 409
DB 370 EGVPCVFPDLGTSYTDGNDGNEYKIDIPAEICLPKLEARSFANGPQTDIFDDAS 429

QY 410 IIGWTRGNTAHNSGLATIMSAGKGMFVGRNKGAGVQVTDITGNRAGTIVINAD 469
DB 430 CIAFIRHGTADAP--GCVVMSNGEPGEKQADLGPERSAGSVWRDFLGHRHEHTL 487

QY 470 GNFSVNGSGSVIWW 483
DB 488 GTPTNGSGSVVWV 501

RESULT 14
AD3038
alpha-amylase amYA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AD3038
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-495 <KUR>

A;Cross-references: GB:AE008689; PIDN:AAK44722.1; PID:g17742354; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)

C;Genetics:
A;Map position: linear chromosome

C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 41.1%; Score 1113; DB 2; Length 495;

Best Local Similarity 45.2%; Pred. No. 6.2e-70;
Matches 221; Conservative 79; Mismatches 173; Indels 16; Gaps 6;

QY 8 TMMQYFEWYLPNDGNHNRSLSDASNLKDGISAVWIPPAWKASQN-DVGYGAYDYL 66
DB 5 TLLQFFHYYPDGKLVSEVAEAKESLAKMGITDVLPPAYKGAAGYSVGYDITDYL 64

QY 67 GFNQGTIRTKYGRNOLQAVALNKSNGIQVYGVVNMHKGADATMVRVAVENPN 126
DB 65 GFQDQKGVATKYGDRAALEHAGTKLKGIRVTHDVVNLHMGADAKEKVRVRVNP 124

QY 127 RNOEVSGEYTTIEAWTKFDPGRGNTHSNFKRWYHFDGVDWDSRKLNN--RIYK 184
DB 125 RTDIDDEFPALAYTRFTFPGRNKGKSKFIWDLKCFSGVDHIEBPTDGI 184

QY 185 KGMDEVTENGNDYLMYADIDMDHPVNLNKGWVYNTLGLDGRIDAVKH 244
DB 185 E-WNEVDQENGNDYLMYADIDMDHPVNLNKGWVYNTLGLDGRIDAVKH 243

QY 245 FTRDWINHVSATGKMFVAFWKNLKGALENYLNKTNMNSHVSFVPLHYNLN 304
DB 244 FRDWMHRETVDPDLFVVAEYHHPDLKSLYELVDKQLMFLDVALHHSFD 303

QY 305 GNYDMRQIFNGTVQRPMPHVAFTFVDNHSQPEEALESFVBEWFKPLAYALT 364
DB 304 GDFMRSIFDGLSVSAVDPHVAITLVDNHTQPLQSLAPVFPFKPLAYAIL 363

QY 365 SVFYGYG--IPTHGVPAKSKID-----PILEARQKAYGRQNDYLDH 414
DB 364 CVFYDLPGLGTSYTDGNDGNEYKIDIPAEICLPKLEARSFANGPQTDIFDDAS 423

QY 415 REGNTAHNSGLATIMSAGKGMFVGRNKGAGVQVTDITGNRAGTIVINAD 474
DB 424 RHGTADAP--GCVVMSNGEPGEKQADLGPERSAGSVWRDFLGHRHEHTL 481

QY 475 NGSGSVIWW 483
DB 482 NGSGSVVWV 490

RESULT 15
B45738
alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Salmonella typhimurium

C;Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: B45738

R;Paha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 174, 6644-6652, 1992

A;Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.
A;Reference number: A45738; MUID:9301517; PMID:1400215

A;Accession: B45738
A;Molecule type: DNA

A;Residues: 1-494 <RAH>
A;Cross-references: GB:L01643; NID:g154043; PIDN:AAA27110.1; PID:g154045

C;Genetics:
A;Gene: amyA

C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

C;Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
F;202-335/Domain: alpha-amylase core homology <AMI>

F;239,265,332/Active site: His, Glu, Asp #status predicted
Query Match 40.9%; Score 1107; DB 1; Length 494;

Best Local Similarity 44.1%; Pred. No. 1.6e-69;
Matches 217; Conservative 78; Mismatches 179; Indels 18; Gaps 6;

QY 6 NGTMMQYFEWYLPNDGNHNRSLSDASNLKDGISAVWIPPAWKASQN-DVGYGAYDYL 64
DB 3 NPTLQYFHWYYPDGKLVSEVAEAKESLAKMGITDVLPPAYKGAAGYSVGYDITDYL 62

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.501 Seconds
(without alignments)
3290.816 Million cell updates/sec

Title: US-09-925-576C-12
Perfect score: 2708
Sequence: 1 HHNGTNGTMQYFEWYLPND.....ADGWNFSVGGSVSIWNK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2409	89.0	516	2	O82839
2	1942	71.7	533	2	Q9AQ54
3	1934	71.4	513	16	O81Y14
4	1926	71.1	513	16	O81A54
5	1889.5	69.8	613	2	O59222
6	1874	69.2	519	2	O9RQ78
7	1872.5	69.1	549	2	O31193
8	1867.5	69.0	521	2	P71034
9	1867.5	69.0	549	2	O9KW76
10	1813.5	67.0	501	2	O93148
11	1576.5	58.2	507	16	O87HG6
12	1363	50.3	493	2	O03657
13	1336	49.3	481	16	O89Y11
14	1307.5	48.3	486	16	O8DT08
15	1307.5	48.3	488	16	O8E0M2
16	1300.5	48.0	488	16	O8E696

17	1298	47.9	484	16	Q97049
18	1296	47.9	484	16	O8DFC8
19	1282	47.3	492	16	O8YU21
20	1279.5	47.2	486	2	O68875
21	1262.5	46.5	484	2	O50583
22	1260.5	46.5	485	2	O53786
23	1148	42.4	491	16	O9C859
24	1114	41.1	506	16	O8U916
25	1098	40.5	494	16	O8Z5S5
26	1085	40.1	495	16	O8XBB6
27	1080	39.9	495	16	O8FGL8
28	1073	39.6	495	16	O7UAB0
29	1071	39.5	495	16	O83R40
30	1048.5	38.7	529	3	O877B1
31	494.5	18.3	461	1	O33476
32	494.5	18.3	461	1	O8NKR4
33	475.5	17.6	461	1	O8NKR5
34	467	17.2	469	1	O50200
35	462.5	17.1	460	1	O9P9L0
36	462.5	17.1	460	1	O08452
37	462.5	17.1	473	17	O8U3I9
38	459	16.9	432	14	O8JZK3
39	444	16.4	457	1	O93647
40	320.5	11.8	482	2	O60051
41	284.5	10.5	421	10	O7X9T1
42	280	10.3	423	10	O42678
43	280	10.3	504	1	O60224
44	279	10.3	416	10	O8LJ06
45	278	10.3	424	10	O8LP27

ALIGNMENTS

RESULT 1

O82839	PRELIMINARY;	PRT;	516 AA.
ID	O82839		
AC	O82839;		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Amylase.		
OS	Bacillus sp.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1409;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=KSM-1378;		
RX	MEDLINE=98342096; PubMed=9675143;		
RA	Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T., Ozaki K., Ito S.;		
RA	"Improved thermostability of a Bacillus alpha-amylase by deletion of an arginine-glycine residue is caused by enhanced calcium binding.";		
RL	Biochem. Biophys. Res. Commun. 248:372-377(1998).		
DR	EMBL; AB008763; BAA32431.1; -		
DR	HSSP; P06278; 1VJS.		
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	InterPro; IPR006047; Alpha_amyl_cat.		
DR	InterPro; IPR006589; Alp_amyl_cat_sub.		
DR	InterPro; IPR006046; Glyco_hydro_13.		
DR	Pfam; PF001128; alpha-amylase; 1.		
DR	PRINTS; PR00110; ALPHAMYLASE.		
DR	SMART; SM00642; Amy; 1.		
SO	SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;		
Query Match			
Best Local Similarity 86.0%; Score 2409; DB 2; Length 516;			
Matches 417; Conservative 37; Mismatches 31; Indels 0; Gaps 0;			
Qy	1 HHNGTNGTMQYFEWYLPNDGNHNRILRSASNLKDGISAVWTPPAWKASQNDVGYGA		
Db	32 HHNGTNGTMQYFEWYLPNDGNHNRILRSDAANLKSIGITAVWTPPAWKGTSONDVGYGA		

Q97q49	streptococc
Q8dpc8	streptococc
Q8yuz1	anabaena sp
O68875	streptococc
O50583	streptococc
Q53786	streptococc
Q9cgs9	lactococcus
Q8u916	agrobacteri
Q8z5s5	salmonella
O8xb6	escherichia
O8fgl8	escherichia
Q7uab0	shigella fl
Q83r40	shigella fl
Q877b1	aspergillus
O33476	pyrococcus
Q8nkr4	thermococcu
O8nkr5	thermococcu
O50200	thermococcu
Q9p9l0	pyrococcus
O08452	pyrococcus
Q8u3i9	pyrococcus
O8jzk3	uncultured
O93647	thermococcu
Q60051	thermoactin
Q7x9t1	phaseolus a
Q42678	cuscuta ref
Q60224	natronococc
O8lj06	musa acumin
Q8lp27	pharbitis n

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QY 61 YDLYDLGEFNOKGTRIRTKYTRNLOQAANVAKLSNGIQVYGDVVMNHKGGADATEMVRVAV 120
DB 92 YDLYDLGEFNOKGTRIRTKYTRNLOQAANVAKLSNGIQVYGDVVMNHKGGADATEMVRVAV 151
QY 121 EVNPNRNQSVSGEYTIETAWTKDFDFGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKFP 180
DB 152 EVNPNRNQSVSGEYTIETAWTKDFDFGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKFP 211
QY 181 RGCGKWDWEVDTEGNGYDLYADIDMDHPEVNNELRWGVTYNTLGLDGRIDAVKH 240
DB 212 RGCGKWDWEVDTEGNGYDLYADIDMDHPEVNNELRWGVTYNTLGLDGRIDAVKH 271
QY 241 IKYSFTDWTNHNVSATGKMFVAFWPKNDLGAENLYLNKTNWHSFVDFPLHYNLXNA 300
DB 272 IKYSFTDWTNHNVSATGKMFVAFWPKNDLGAENLYLNKTNWHSFVDFPLHYNLXNA 331
QY 301 SKSGGNYDMRQIFNGTVVQHPHMAVTFVDNHDSPQEEALESFVEWFKPLAYALTLTRE 360
DB 332 SKSGGNYDMRQIFNGTVVQHPHMAVTFVDNHDSPQEEALESFVEWFKPLAYALTLTRE 391
QY 361 QGYPSVFGYDYGIPTHGVPMKSKIDPILAEARKYAGRONDYLDHNNIIGWTRGNTA 420
DB 392 QGYPSVFGYDYGIPTHGVPMKSKIDPILAEARKYAGRONDYLDHNNIIGWTRGNTA 451
QY 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTTINADGWNFGVNGSVS 480
DB 452 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTTINADGWNFGVNGSVS 511
QY 481 IWYNK 485
DB 512 VWVKQ 516
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RESULT 2
Q9AQ54
ID Q9AQ54 PRELIMINARY; PRT; 533 AA.
AC Q9AQ54;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP KSM B-404.
RT "Cloning of maltopentaose-producing amylase from Bacillus megaterium
Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220440; AAK00598.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

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Query Match 71.7%; Score 1942; DB 2; Length 533;  
Best Local Similarity 69.6%; Pred. No. 1.1e-113;  
Matches 336; Conservative 57; Mismatches 86; Indels 4; Gaps 2;  
QY 6 NGTMQVFEWYLPNDGNHNNRLSDASNLKDKGISAVWIPPAWKASQNDVGYGAYDLYD 65  
DB 52 NGTMQVFEWYLPNDGNHNNRLSDASNLKDKGISAVWIPPAWKATQNDVGYGAYDLYD 111  
QY 66 LGDFNOKGTRIRTKYTRNLOQAANVAKLSNGIQVYGDVVMNHKGGADATEMVRVAVNPN 125  
DB 112 LGDFNOKGTRIRTKYTRNLOQAANVAKLSNGIQVYGDVVMNHKGGADATEMVRVAVNPN 171
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QY 126 NRNOEVSGETTIEAWTKDFDFGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKFRGDGK 185  
DB 172 NRNOEVSGETTIEAWTKDFDFGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKFRGIGK 230  
QY 186 GMDWEVDTEGNGYDLYADIDMDHPEVNNELRWGVTYNTLGLDGRIDAVKHKYP 245  
DB 231 GMDWEVDTEGNGYDLYADIDMDHPEVNNELRWGVTYNTLGLDGRIDAVKHKYP 290  
QY 246 TRDWNHNVSATGKMFVAFWPKNDLGAENLYLNKTNWHSFVDFPLHYNLXNA 305  
DB 291 TRDWNHNVSATGKMFVAFWPKNDLGAENLYLNKTNWHSFVDFPLHYNLXNA 350  
QY 306 NYDMRQIFNGTVVQHPHMAVTFVDNHDSPQEEALESFVEWFKPLAYALTLTRE 365  
DB 351 NYDMRQIFNGTVVQHPHMAVTFVDNHDSPQEEALESFVEWFKPLAYALTLTRE 410  
QY 366 VFYGDYGI---PTHGVPMKSKIDPILAEARKYAGRONDYLDHNNIIGWTRGNTAHP 422  
DB 411 VFYGDYGI---PTHGVPMKSKIDPILAEARKYAGRONDYLDHNNIIGWTRGNTAHP 470  
QY 423 NSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTTINADGWNFGVNGSVSIW 482  
DB 471 NSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTTINADGWNFGVNGSVSIW 530  
QY 483 VNK 485  
DB 531 VQR 533
```

RESULT 3
Q81YJ4
ID Q81YJ4 PRELIMINARY; PRT; 513 AA.
AC Q81YJ4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN AMYS OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaiter J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolisko A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
DR EMBL; AB017035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

```
Query Match 71.4%; Score 1934; DB 16; Length 513;  
Best Local Similarity 69.4%; Pred. No. 3.4e-113;  
Matches 335; Conservative 59; Mismatches 85; Indels 4; Gaps 2;
```

Qy 6 NGTMMQYFEWYLPNDGNHNRRLSDAGNLKDGISAVWIPPAWKASQNDVGYGAYDLYD 65
Db 32 NGTLMQYFEWYAPSDRNHNRRLTDAENLAQKIGTSVWIPPAKGTQNDVGYGAYDLYD 91
Qy 66 LGFENQKGTIRTKYGTNRNOLQAAVNALKSGNGIYQYGVVNMHKGADATEMVRVAVENPN 125
Db 92 LGFENQKGTIRTKYGTNRNOLQAAVNALKSGNGIYQYGVVNMHKGADATEMVRVAVENPN 151
Qy 126 NRNOEVSGETIETAWTKFDPFGRGNTHSNFKRWYHFGDVGVDWDSRKLNNRIYKFRGDGK 185
Db 152 NRNOEVSGETIETAWTKFDPFGRGNTHSNFKRWYHFGDVGVDWDSRKLNNRIYKFRGDGK 210
Qy 186 GWDVEVDTEGNGYDYLMAVDIMDHPVNNELRWNGVYNTLGLDGFRIIDAVKHIXYSF 245
Db 211 AWDVEVSSENGYDYLMAVDIMDHPVNNELRWNGVYNTLGLDGFRIIDAVKHIXYSF 270
Qy 246 TRDWINHVSATGKMFVAFWQNDLGAENLNTKTNWHSVDFVPLHYNLYNASKSGG 305
Db 271 LRDMVNHVROQTGKEMFTVAEYQNDLQTLNNYLAKVYNSQSVFDPALHYNFHYASTGNG 330
Qy 306 NYDMRQIFNGTVVORHPMHAFTVDNHDSPQEEALESFVEWFKPLAYALTLTREQGYPS 365
Db 331 NYDMRNLGTVMQNHAPALAVTLVENHDSQPGSLESVSPWFKPLAYALTLTREQGYPS 390
Qy 366 VFYGDYVGI---PTHGVPAMKSKIDPILAEARQYAYGRQNDYLDHNNIIGTWREGNTAHP 422
Db 391 VFYGDYVGTGNSSEYEPALCKIDPILAEARQYAYGRQNDYLDHNNIIGTWREGNTAHP 450
Qy 423 NSGLATIMSDGAGKMKVGRNKGAGQVWTDITGNRAGTVTINADGNGFVNSGVSIV 482
Db 451 NSGLATILSDGPGGKMKVGRNKGAGQVWTDITGNRAGTVTINADGNGFVNSGVSIV 510
Qy 483 VNK 485
Db 511 VQ 513

RESULT 4

Q81AS4 ID Q81AS4 PRELIMINARY; PRT; 513 AA.
AC Q81AS4; 2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glucan 1,4-alpha-maltohexaoidase (EC 3.2.1.98).
GN BC3482.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP MEDLINE=22608415; PubMed=12721630;
RX Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.,
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis";
RL Nature 423:87-91(2003).
DR EMBL; AE017009; AAP10417.1; --
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR Pfam; PF00128; alpha-amyl_cat.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BF9F9F6 CRC64;

Query Match

71.1%; Score 1926; DB 16; Length 513;

Best Local Similarity 68.9%; Pred. No. 1.1e-112;
Matches 333; Conservative 58; Mismatches 88; Indels 4; Gaps 2;
Qy 6 NGTMMQYFEWYLPNDGNHNRRLSDAGNLKDGISAVWIPPAWKASQNDVGYGAYDLYD 65
Db 32 NGTLMQYFEWYAPSDRNHNRRLTDAENLAQKIGTSVWIPPAKGTQNDVGYGAYDLYD 91
Qy 66 LGFENQKGTIRTKYGTNRNOLQAAVNALKSGNGIYQYGVVNMHKGADATEMVRVAVENPN 125
Db 92 LGFENQKGTIRTKYGTNRNOLQAAVNALKSGNGIYQYGVVNMHKGADATEMVRVAVENPN 151
Qy 126 NRNOEVSGETIETAWTKFDPFGRGNTHSNFKRWYHFGDVGVDWDSRKLNNRIYKFRGDGK 185
Db 152 NRNOEVSGETIETAWTKFDPFGRGNTHSNFKRWYHFGDVGVDWDSRKLNNRIYKFRGDGK 210
Qy 186 GWDVEVDTEGNGYDYLMAVDIMDHPVNNELRWNGVYNTLGLDGFRIIDAVKHIXYSF 245
Db 211 AWDVEVSSENGYDYLMAVDIMDHPVNNELRWNGVYNTLGLDGFRIIDAVKHIXYSF 270
Qy 246 TRDWINHVSATGKMFVAFWQNDLGAENLNTKTNWHSVDFVPLHYNLYNASKSGG 305
Db 271 LRDMVNHVROQTGKEMFTVAEYQNDLQTLNNYLAKVYNSQSVFDPALHYNFHYASTGNG 330
Qy 306 NYDMRQIFNGTVVORHPMHAFTVDNHDSPQEEALESFVEWFKPLAYALTLTREQGYPS 365
Db 331 NYDMRNLGTVMQNHAPALAVTLVENHDSQPGSLESVSPWFKPLAYALTLTREQGYPS 390
Qy 366 VFYGDYVGI---PTHGVPAMKSKIDPILAEARQYAYGRQNDYLDHNNIIGTWREGNTAHP 422
Db 391 VFYGDYVGTGNSSEYEPALCKIDPILAEARQYAYGRQNDYLDHNNIIGTWREGNTAHP 450
Qy 423 NSGLATIMSDGAGKMKVGRNKGAGQVWTDITGNRAGTVTINADGNGFVNSGVSIV 482
Db 451 NSGLATILSDGPGGKMKVGRNKGAGQVWTDITGNRAGTVTINADGNGFVNSGVSIV 510
Qy 483 VNK 485
Db 511 VQ 513
RESULT 5
Q59222 ID Q59222 PRELIMINARY; PRT; 613 AA.
AC Q59222;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
GN AMY.
OS Bacillus sp. TS-23.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=38441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TS-23;
RA Lin L.-L., Chu W.S., Hsu W.H.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22045; AAA63900.1; --
DR HSP; P06278; IYGS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0008477; F:purine nucleosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR002044; CBD_4.
DR Pfam; PF00128; alpha-amylase; 13.
DR Pfam; PF00696; CBM_20; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR PRODOM; PD001569; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.

SQ	SEQUENCE	613 AA; 69537 MW; 14684A30FC2895E8 CRC64;			
	Query Match	69.8%; Score 1889.5; DB 2; Length 613;			
	Best Local Similarity	68.1%; Pred. No. 2.6e-110;			
	Matches	327; Conservative 64; Mismatches 88; Indels 1; Gaps 1;			
QY	6	NGTMMQYFEWYLPNDGNHNRRLRSASNLKDKGISAVWIPPAWKASQNDVGYGAYDLYD 65			
DB	36	NETMMQYFEWDLNDGTGLTWKXNEAANLSSGITALWLPAYKGTSGSDVGYGVYDLYD 95			
QY	66	LGEFNQGTIRTKYGRNQLQAANVALKSGNGIQYGVGVNMHKGADATWVRVAVENPN 125			
DB	96	LGEFNQGTIRTKYGRNQLQAANVALKSGNGIQYGVGVNMHKGADATWVRVAVENPN 155			
QY	126	NRNQEVSGEYTIKAWTKFDPGRGNTHSNFKRWYHFDGVDQSRKLNRIYKFRGDC 185			
DB	156	NRNQEVSGEYTIKAWTKFDPGRGNTHSNFKRWYHFDGVDQSRKLNRIYKFRGDC 214			
QY	186	GWDEVDTEGNDYDLMYADIDMDHPEVNMELRNWGVYNTLGLDGFRIIDAVKHIKY 245			
DB	215	AWDEVDTEGNDYDLMYADIDMDHPEVNMELRNWGVYNTLGLDGFRIIDAVKHIKY 274			
QY	246	TRDWINHVSATCKMFAVAFKNDLGATENYLNKTNHNSVDFVPLHYNLYNASKSG 305			
DB	275	FPDLTVRNQTKNLFVAGFNSYDVNKLHNYITKNGSMSLFDAPLHNNFYTASKSG 334			
QY	306	NYDMRQIFNGTVVQRHPMHAVTFVDNHDSEPEALESFVEEWFKPLAYALTLTREOGY 365			
DB	335	YFDMRYLLNLTMLKQDPSLATVLDVNDHDTQPGSLSQSWEPFPLAYAFILTRQGYPC 394			
QY	366	VYFGDYGIPTGHPVPMKSKIDPILARQKYAYGRQNDYLDHNIIGTWREGNTAHPSG 425			
DB	395	VYFGDYGIPTGHPVPMKSKIDPILARQKYAYGRQNDYLDHNIIGTWREGNTAHPSG 454			
QY	426	LATIMSDGAGNKMVFGRNKAQGVTDITGNRAGTNTINADGWNFSVNGSGSVIWNK 485			
DB	455	LAALITDGPCKGMYVKKHAGKVFYDLTGNRSDTNTINADGWNFSVNGSGSVIWNK 514			
RESULT 6					
ID	Q9RQ8	PRELIMINARY; PRT; 519 AA.			
AC	Q9RQ8				
DT	01-MAY-2000	(TrEMBLrel. 13, Created)			
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)			
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)			
DE	Raw starch digesting amylase precursor.				
OS	Cytophaga sp.				
OC	Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;				
OC	Flexibacteraceae; Cytophaga.				
OX	NCBI_TaxID=29535;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Jeang C.L., Chen L.S., Chen M.Y.;				
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF067653; AAF00567.1; --				
DR	HSSP; P06278; 1VJS.				
DR	GO; GO:0004556; P:alpha-amylase activity; IEA.				
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.				
DR	InterPro; IPR006047; Alpha_ami_cat.				
DR	InterPro; IPR006589; Alp_ami_cat_sub.				
DR	Pfam; PF00128; alpha-amylase; 1.				
DR	PRINTS; PR00110; ALPHAMYLASE.				
DR	SMART; SM00642; Amy; 1.				
KW	SIGNAL.				
FT	CHAIN				
SQ	SEQUENCE	519 AA; 58337 MW; 3B6B88A4DF98B163 CRC64;			
	Query Match	69.2%; Score 1874; DB 2; Length 519;			
	Best Local Similarity	67.1%; Pred. No. 2e-109;			
	Matches	325; Conservative 68; Mismatches 87; Indels 4; Gaps 2;			

QY	5	TNGTMMQYFEWYLPNDGNHNRRLRSASNLKDKGISAVWIPPAWKASQNDVGYGAYDLY 64			
DB	37	TNGTMMQYFEWYLPNDGNHNRRLRSASNLKDKGISAVWIPPAWKASQNDVGYGAYDLY 96			
QY	65	DLGEFNQGTIRTKYGRNQLQAANVALKSGNGIQYGVGVNMHKGADATWVRVAVENPN 124			
DB	97	DLGEFNQGTIRTKYGRNQLQAANVALKSGNGIQYGVGVNMHKGADATWVRVAVENPN 156			
QY	125	NRNQEVSGEYTIKAWTKFDPGRGNTHSNFKRWYHFDGVDQSRKLNRIYKFRGDC 184			
DB	157	NRNQEVSGEYTIKAWTKFDPGRGNTHSNFKRWYHFDGVDQSRKLNRIYKFRGDC 215			
QY	185	KGWDEVDTEGNDYDLMYADIDMDHPEVNMELRNWGVYNTLGLDGFRIIDAVKHIKY 244			
DB	216	KGWDEVDTEGNDYDLMYADIDMDHPEVNMELRNWGVYNTLGLDGFRIIDAVKHIKY 275			
QY	245	TRDWINHVSATCKMFAVAFKNDLGATENYLNKTNHNSVDFVPLHYNLYNASKSG 304			
DB	276	FLKDWVDNARATGKEMFTVGEYQNDLGALENNYLAQYVQSLDAPLHNNFYAASG 335			
QY	305	GNYDMRQIFNGTVVQRHPMHAVTFVDNHDSEPEALESFVEEWFKPLAYALTLTREOGY 364			
DB	336	GYDMRYLLNLTMLKQDPSLATVLDVNDHDTQPGSLSQSWEPFPLAYAFILTRQGYPC 395			
QY	365	VYFGDYGIPTGHPVPMKSKIDPILARQKYAYGRQNDYLDHNIIGTWREGNTAH 421			
DB	396	VYFGDYGIPTGHPVPMKSKIDPILARQKYAYGRQNDYLDHNIIGTWREGNTAH 455			
QY	422	PNSGLATIMSDGAGNKMVFGRNKAQGVTDITGNRAGTNTINADGWNFSVNGSGSVI 481			
DB	456	AKSGLATITDGPCKGMYVKKHAGKVFYDLTGNRSDTNTINADGWNFSVNGSGSVI 515			
QY	482	WYWK 485			
DB	516	WYWK 519			
RESULT 7					
ID	O31193	PRELIMINARY; PRT; 549 AA.			
AC	O31193				
DT	01-JAN-1998	(TrEMBLrel. 05, Created)			
DT	01-JAN-1998	(TrEMBLrel. 05, Last sequence update)			
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)			
DE	Alpha amylase.				
GN	AMI.				
OS	Bacillus stearothermophilus.				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.				
OX	NCBI_TaxID=1422;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 31195;				
RA	da Silva A.C.R., Fernandes B., Pueyo M.T.;				
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF032864; AAB86961.1; --				
DR	PIR; A54541; A54541.				
DR	HSSP; P06278; 1VJS.				
DR	GO; GO:0004556; P:alpha-amylase activity; IEA.				
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.				
DR	InterPro; IPR006047; Alpha_ami_cat.				
DR	InterPro; IPR006589; Alp_ami_cat_sub.				
DR	Pfam; PF00128; alpha-amylase; 1.				
DR	PRINTS; PR00110; ALPHAMYLASE.				
DR	SMART; SM00642; Amy; 1.				
SQ	SEQUENCE	549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;			
	Query Match	69.1%; Score 1872.5; DB 2; Length 549;			
	Best Local Similarity	67.2%; Pred. No. 2.6e-109;			
	Matches	321; Conservative 73; Mismatches 83; Indels 1; Gaps 1;			
QY	6	NGTMMQYFEWYLPNDGNHNRRLRSASNLKDKGISAVWIPPAWKASQNDVGYGAYDLYD 65			

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Db 39 NGTMMQYFEWYLPDDGTLWTWKVANEANLSSLGITALLWLPAYKGTSDSDVGYGYDLYD 98
Qy 66 LGFENQKGTIRTKYGTNRNQLQAANVNAKSNQIQVYGDVVMNHKGGADATEMVRVAVENPN 125
Db 99 LGFENQKGTIRTKYGTNRNQLQAANVNAKSNQIQVYGDVVMNHKGGADATEMVRVAVENPN 158
Qy 126 NRNEVSSEYTIETAWTKFDPFGRGNTHSNFKRWYTHFDGVWDQSRKLNRIYKPRGDGK 185
Db 159 DRNQEISGTQIQAWTKFDPFGRGNTHSNFKRWYTHFDGVWDQSRKLNRIYKPRGDGK 217
Qy 186 GWDNEVDTEGNYDLYMADIDMDHPEVNVNRLRWGVMYVNTLGLDGRIDAVKHKYSF 245
Db 218 AWDNEVDTEGNYDLYMADIDMDHPEVNVNRLRWGVMYVNTLGLDGRIDAVKHKYSF 277
Qy 246 TRDWINHVSATGKMFVAFWFKNDLGAENYLNKTNWNSVDFDPLHYNLYNASKSGG 305
Db 278 FPDWLSVRSQTGKPLFTVGYWSDYINKLHNYITKINGTMSLFDAPLHNFYTASKSGG 337
Qy 306 NYDMRQIFNGTVVORHPHIAVTFVDNHDSPQEALESFVEWFKPLAYALTITREQGYPS 365
Db 338 AFDMRTLTMTNLMKDQPTLAVTFVDNHDTEPQALQSWDPWFKPLAYALTITREQGYPC 397
Qy 366 VFYGDYGIPTGHPVPMKSKIDPILAEARQKAYAGRONDYLDHNIIGWTRGNTAHNPSG 425
Db 398 VFYGDYGIPOYNIPSLKSKIDPLIARRDYAYGTQHDYLDHSDIIGWTRGNTAHNPSG 457
Qy 426 LATIMSDGAGNKMFWGRNKGAGQVWTDITGNRAGTVTINADGNGFNSVNGSVSIW 483
Db 458 LAALITDGPCKGKMYVKGQKAGKVFYDLTGNRSDTITNSDGMGEFKVNGSVSVW 515

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RESULT 8

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P71034
ID P71034 PRELIMINARY; PRT; 521 AA.
AC O9KMY6;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE Alpha-amylase precursor.
OS Bacillus sp. MK 716.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=54116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MK 716.
RA Sidhu G.S., Chakrabarti T.;
RT "Molecular cloning and expression of the gene encoding for
thermostable alpha-amylase of a thermophilic bacterial isolate.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75445; AAB18785.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SIGNAL.
FT CHAIN 35 521 ALPHA-AMYLASE.
SQ SEQUENCE 521 AA; 59311 MW; 5612A88596D922E1 CRC64;

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Query Match 69.0%; Score 1867.5; DB 2; Length 521;
Best Local Similarity 66.9%; Pred. No. 5.1e-109;
Matches 320; Conservative 73; Mismatches 84; Indels 1; Gaps 1;

Qy 6 NGTMMQYFEWYLPDDGTLWTWKVANEANLSSLGITALLWLPAYKGTSDSDVGYGYDLYD 65
Db 39 NGTMMQYFEWYLPDDGTLWTWKVANEANLSSLGITALLWLPAYKGTSDSDVGYGYDLYD 98

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Qy 66 LGFENQKGTIRTKYGTNRNQLQAANVNAKSNQIQVYGDVVMNHKGGADATEMVRVAVENPN 125
Db 99 LGFENQKGTIRTKYGTNRNQLQAANVNAKSNQIQVYGDVVMNHKGGADATEMVRVAVENPN 158
Qy 126 NRNEVSSEYTIETAWTKFDPFGRGNTHSNFKRWYTHFDGVWDQSRKLNRIYKPRGDGK 185
Db 159 DRNQEISGTQIQAWTKFDPFGRGNTHSNFKRWYTHFDGVWDQSRKLNRIYKPRGDGK 217
Qy 186 GWDNEVDTEGNYDLYMADIDMDHPEVNVNRLRWGVMYVNTLGLDGRIDAVKHKYSF 245
Db 218 AWDNEVDTEGNYDLYMADIDMDHPEVNVNRLRWGVMYVNTLGLDGRIDAVKHKYSF 277
Qy 246 TRDWINHVSATGKMFVAFWFKNDLGAENYLNKTNWNSVDFDPLHYNLYNASKSGG 305
Db 278 FPDWLSVRSQTGKPLFTVGYWSDYINKLHNYITKINGTMSLFDAPLHNFYTASKSGG 337
Qy 306 NYDMRQIFNGTVVORHPHIAVTFVDNHDSPQEALESFVEWFKPLAYALTITREQGYPS 365
Db 338 AFDMRTLTMTNLMKDQPTLAVTFVDNHDTEPQALQSWDPWFKPLAYALTITREQGYPC 397
Qy 366 VFYGDYGIPTGHPVPMKSKIDPILAEARQKAYAGRONDYLDHNIIGWTRGNTAHNPSG 425
Db 398 VFYGDYGIPOYNIPSLKSKIDPLIARRDYAYGTQHDYLDHSDIIGWTRGNTAHNPSG 457
Qy 426 LATIMSDGAGNKMFWGRNKGAGQVWTDITGNRAGTVTINADGNGFNSVNGSVSIW 483
Db 458 LAALITDGPCKGKMYVKGQKAGKVFYDLTGNRSDTITNSDGMGEFKVNGSVSVW 515

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RESULT 9

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Q9KMY6
ID Q9KMY6 PRELIMINARY; PRT; 549 AA.
AC O9KMY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Alpha-amylase (RC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Beijer S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17557; CAB93517.1; -.
DR PIR; A54541; A54541.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco hydro I3.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR GlycoBase; Hydrolyase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3E66DF9120BCE CRC64;

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Query Match 69.0%; Score 1867.5; DB 2; Length 549;
Best Local Similarity 66.9%; Pred. No. 5.4e-109;
Matches 320; Conservative 73; Mismatches 84; Indels 1; Gaps 1;

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Qy 6 NGTMMQYFEWYLPDDGTLWTWKVANEANLSSLGITALLWLPAYKGTSDSDVGYGYDLYD 65
Db 39 NGTMMQYFEWYLPDDGTLWTWKVANEANLSSLGITALLWLPAYKGTSDSDVGYGYDLYD 98
Qy 66 LGFENQKGTIRTKYGTNRNQLQAANVNAKSNQIQVYGDVVMNHKGGADATEMVRVAVENPN 125
Db 99 LGFENQKGTIRTKYGTNRNQLQAANVNAKSNQIQVYGDVVMNHKGGADATEMVRVAVENPN 158
Qy 126 NRNEVSSEYTIETAWTKFDPFGRGNTHSNFKRWYTHFDGVWDQSRKLNRIYKPRGDGK 185

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Db	159	DRNQEISGTYIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESKL-SRIYKFRGIGK	217			
Qy	186	GHDEVDFTENGNDYLYAKYADIMDHDPVWNLERNWGVYVNTLTGLDGRIDAVKHKYSF	245			
Db	218	AWDEVDFTENGNDYLYAMYADLMDHDPVWTELKNWGWYVNTTNDGFRDLDAVHKHKSF	277			
Qy	246	TRDMINHYRSATGKNMFAVAEFWKNDLGAIENTYLNKTNWNHVSFVDFVPLHYNLYNASKSGG	305			
Db	278	FPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFTYASKSGG	337			
Qy	306	NYDMRQIFNGTVQWRHPMAVTFVDNHDSDPEBALSSFVEEFKPLAYALTUTREQGHP	365			
Db	338	AFDMETLMTNLMDKQDPTLAVTFVDNHDTPGQALOSWDPWPKPLAYAFILITREQGYPG	397			
Qy	366	VPEYGDYGIPTGHWGPAKMSKIDPLEARQKAYAGRQNDYLHDHNIIGWTREGNTAHPNSG	425			
Db	398	VEYGDYGIPTQNPISUKSKIDPLLIARRDAYGTQHDYLDHSDIIGWTREGVTEKPGSG	457			
Qy	426	LATIMSDGAGNKWIFVGRNKGAGQWTDITGNRAGVTVTINADGWGNSVNGSGSVIW	483			
Db	458	LAALITDGGSGKMWYGVKGQHAGKVFYDLTGNRSDVTITSDCWGEFKVNGSGSVWV	515			
RESULT 10						
Q93148 PRELIMINARY; PRT; 501 AA.						
ID	Q93148	AC	Q93148;			
DT	01-DEC-2001	DT	(TreMBLrel. 19, Created)			
DT	01-DEC-2001	DT	(TreMBLrel. 19, Last sequence update)			
DT	01-JUN-2003	DT	(TreMBLrel. 24, Last annotation update)			
DE	Amylase.					
GN	AMYK38.					
OS	Bacillus sp. KSM-K38.					
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.					
NCBI_Taxid=129736;						
ON	SEQUENCE FROM N.A.					
RP	STRAIN=KSM-K38;					
RC	Hayaishi Y.;					
RA	"Isolation of a new Bacillus alpha-amylase.";					
RT	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; AB051102; BAB71820.1; --	DR	EMBL; AB051102; BAB71820.1; --			
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.	DR	GO; GO:0004556; F:alpha-amylase activity; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.	DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR006047; Alpha amyl cat.	DR	InterPro; IPR006047; Alpha amyl cat.			
DR	Pfam; PF00128; alpha-amylase; 1.	DR	Pfam; PF00128; alpha-amylase; 1.			
SEQ	SEQUENCE 501 AA, 57485 MW, 1240P46739A5CC11 CRC64;					
Query Match 67.0%; Score 1813.5; DB 2; Length 501;						
Best Local Similarity 64.2%; Pred. No. 1.2e-105;						
Matches 310; Conservative 78; Mismatches 92; Indels 3; Gaps 2						
Qy	3	NGTGTGTMQYFSEWYLPNDGNHNRILRSPASNLKDKGISAVMIPPAAWKGASQNDVGYCAYD	62			
Db	22	DGLNGTMMQYIEWHLENQGHNRLLHDDAALSAGITAIWIPPAYKNSQADVGYGAYD	81			
Qy	63	LYDLGEFNGKGTIRTKYGTNRQLQAANVNAKNSGIVQYGVGVNHNKGGADATEMTRAVEV	122			
Db	82	LYDLGEFNGKGTVRTKYGTKAQLERAIGLSKSDINIVYGDVNMNKMGAFTFAVQAVQ	141			
Qy	123	NPNNRQEVSGYTTTEAWTKEDFPGRGNTHSNFKRWYHFDGVDWDESKLNNRIYKFRG	182			
Db	142	NPTNRWDITSAGYTTIDAWTGFDFSGRNNAYSDFKRWYHFDGVDWDESKLNNRIYKFRG	199			
Qy	183	DGKGQDWEVDTEGNDYLYAKYADIMDHDPVWNLERNWGVYVNTLTGLDGRIDAVKHK	242			
Db	200	NTNWNVRVDENGYDYLGSNIDFSPEVQDELKQWGSWFTDGLDGRIDAVKHK	258			
Qy	243	YSTRTDWINHRSATGKNMFAVAEFWKNDLGAIENTYLNKTNWNHVSFVDFVPLHYNLYNASK	302			
Db	259	FWYTSDWVRHQRNEADQDFVYGEYKQDVGALFYEDMMWMSLFDVNNYNNFYRASQ	318			


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Db 322 SGGYDMRQIWMGILMKDNPVAKAVTLVENHDTQPLQALESTVDMWFKFLAVAFILLREEG 381
Qy 363 YPSVFGDYGG-----IPTHGVPAKMSKIDPILFARQKAYAGRQNDYLDHNNIIGW 413
Db 382 YPSVYADYGAQYSDKGYNINMAKVP-----YIEBLVTLRKEYAYGKQNSYLDHWDVLGW 437
Qy 414 TREGNTAHPNSGLATIMSDGAGGNKWMFVGRNKAQGVWTDITGNRAGTVTINADGWNFS 473
Db 438 TREGDAEHPNS--MAVINSDGPGTKWMTYG--KPSRYVDKLGIIRTEEVWTDANGWARFP 494
Qy 474 VNGGSVSIWV 483
Db 495 VNGGSVSVWV 504

RESULT 12
Q03657 PRELIMINARY; PRT; 493 AA.
AC Q03657;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
GN AMYE.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RA Marcel T.;
RL Nucleic Acids Res. 0:0-0(0).
DR EMBL; X60779; CAA43194.1; -.
DR PIR; S15713; S15713.
DR HSP; P06278; 1VJS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; Glyco hydro_I3.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 493 AA; 56537 MW; FECCD2F805BB4694 CRC64;
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Query Match 50.3%; Score 1363; DB 2; Length 493;
Best Local Similarity 51.1%; Pred. No. 1.9e-77;
Matches 246; Conservative 78; Mismatches 149; Indels 8; Gaps 3;

Qy 6 NGTMMQYFEWYLPNDGNHNRSLDASNLKDKGISAVMIPPAMKASQNDVGYGAYDLYD 65
Db 4 NHTMMQYFEWHLAAGDGHKRLAEMAPELKAKGIDTVWVPVTKAVSAEDTGYGYDLYD 63

Qy 66 LGEPNQGTTRTKYGTNRQLOAAVNAKLSNGIQYGVGVNMHKGADATEMVRVAVNPN 125
Db 64 LGEPDQGTTRTKYGTNRQLOAAVNAKLSNGIQYGVGVNMHKGADATEMVRVAVNPN 123

Qy 126 NRQVSGEYTIKAWTKFDPFGNTHSNFKRWYHFDGVDMDSRKLNNRIYKFRGDGK 185
Db 124 DRYKIESEPEIEGWTFTFPGRGDQVSSFAKNSEHFNGLDFFD-ARBERTGVFRIAGENK 182

Qy 186 GWDVEVDTENGNDYLMYADIDMDHPEVNAELNRWGVYNTNLTGLDGRIDAVKHKYSF 245
Db 183 KWNENVDFGNDYLMFANIDYNHPDVRREMDGKWLIDTLCGGFRDLAKIHNEF 242

Qy 246 TRWINHVRATGKMFVAFKNDLGAENYLNKTNWHSVDFVPLHNLNASKSGG 305
Db 243 IKEFAEMIRKRGQDFYIVGEFNMNSLDACREFLDITVDYQIDLVDVSLHYKLHEASLGR 302

Qy 306 NYDMRQIFNGTVQVRHPMHAFTFVDNHDSPEREALESFVEWFKPLAYALTLTREQYPS 365
Db 303 DFLSKLIDFTLVQTHPTHAVTFVDNHDSPEREALESWIGWFKPSAYALTLLRQGYPV 362
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Qy 366 VFYGDYGI-----PTHGVPAKMSKIDPILFARQKAYAGRQNDYLDHNNIIGWREGNTAH 421
Db 363 VFYGDYGIIGGPEPVDG---KKEILDILLSARCNKAYGEQEDYDPHANTIGWVRGVBEI 419
Qy 422 PNSGLATIMSDGAGGNKWMFVGRNKAQGVWTDITGNRAGTVTINADGWNFSVNGGSVSI 481
Db 420 EGSCAVVISNGDDGCKRMFGEHRAGEVWVDLTKSCDDQITIBEDGWATPHVCGGGVSV 479
Qy 482 W 482
Db 480 W 480

RESULT 13
Q89YP1 PRELIMINARY; PRT; 481 AA.
AC Q89YP1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase precursor.
GN BT4690.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VPI-5482 / ATCC 29148;
RA MEDLINE=2250858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RA "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016946; AA079795.1; -.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EE1A CRC64;
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Query Match 49.3%; Score 1336; DB 16; Length 481;
Best Local Similarity 49.6%; Pred. No. 9e-76;
Matches 238; Conservative 90; Mismatches 150; Indels 2; Gaps 2;

Qy 6 NGTMMQYFEWYLPNDGNHNRSLDASNLKDKGISAVMIPPAMKASQNDVGYGAYDLYD 65
Db 3 NGVMMQYFEWHLNDGKLVKQIKEDALHLHDIGVTAWIIPYAKADEQDEGATYDLYD 62

Qy 66 LGEPNQGTTRTKYGTNRQLOAAVNAKLSNGIQYGVGVNMHKGADATEMVRVAVNPN 125
Db 63 LGEPDQGTTRTKYGTNRQLOAAVNAKLSNGIQYGVGVNMHKGADATEMVRVAVNPN 122

Qy 126 NRQVSGEYTIKAWTKFDPFGNTHSNFKRWYHFDGVDMDSRKLNNRIYKFRGDGK 185
Db 123 ERTKALGEPPEIQGTWGFSGHGRKDHSDPKWYHFSFGTGDQAQK-RSGVFOIQEGEK 181

Qy 186 GWDVEVDTENGNDYLMYADIDMDHPEVNAELNRWGVYNTNLTGLDGRIDAVKHKYSF 245
Db 182 AWSEGVDSNGYDFFLNCNDILDHPEVSELNRWGWVSNELNDGMRDLAKHMKDQF 241

Qy 246 TRWINHVRATGKMFVAFKNDLGAENYLNKTNWHSVDFVPLHNLNASKSGG 305
Db 242 VAQFLDAVRSERGNDFYAVGEYWNGLDALDAYIEAVGHKVNLFDFVPLHNMFOASQEGK 301

Qy 306 NYDMRQIFNGTVQVRHPMHAFTFVDNHDSPEREALESFVEWFKPLAYALTLTREQYPS 365
Db 302 DYDLRLDKLTVEHHPDLAVTIVDNDHTQGSLSNESNEDWFKPLAYALTLLMKEGYPC 361

Qy 366 VFYGDYGIPTHGVPAKMSKIDPILFARQKAYAGRQNDYLDHNNIIGWREGNTAHPNSG 425
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Db 362 LFYDGYGKIGKSPHTRI-IDILLDARRKYAYGDIQIEYFDHPSTGTGFTIRGDEEHNGSG 420
QY 426 LATIMSDGAGGNKWMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGSGSVSLWNK 485
Db 421 LVFLMSNDEAGSKIMSLGKHKGVWHEITGTSISEBITLDEEGNGEFSVESRLNLAWVVK 480

RESULT 14
Q8DT08 PRELIMINARY; PRT; 486 AA.
AC Q8DT08;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Intracellular alpha-amylase (EC 3.2.1.1).
GN AMYA OR SMU.1590.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.,
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT pathogen."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
DR EMBL: AE014990; AAN59233.1; -.
DR GO: GO:0004556; F:alpha-amylase activity; IEA.
DR GO: GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amyl_cat.
DR InterPro: IPR006589; Alp_amyl_cat_sub.
DR Pfam: PF00128; alpha-amylase; 1.
DR SMART: SM00642; Amy; 1.
DR Glycosidase; Hydrolase;
KW Complete proteome.
SQ SEQUENCE 486 AA; 56457 MW; EF482B92FB37C4D8 CRC64;

Query Match 48.3%; Score 1307.5; DB 16; Length 486;
Best Local Similarity 50.0%; Pred. No. 5.6e-74;
Matches 242; Conservative 72; Mismatches 165; Indels 5; Gaps 4;

QY 5 TNGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGYDLY 64
Db 2 TNETMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGYDLY 61

QY 65 DLGEFNQKGTIRTKYGTNRQLQAQVNAKSNGLQVYGVDMVNHKGGADATEMVRVAVNP 124
Db 62 DLGEFNQKGTIRTKYGTNRQLQAQVNAKSNGLQVYGVDMVNHKGGADATEMVRVAVNP 121

QY 125 NNRRQVSGBYTTBAWTKFDPGGRGNTHSNFKRWYHFDGVDWDSQRKLNRR--IYKFRG 184
Db 122 SNRQEKISEPYELEGWTFQFPGRQDNYSDFKWHYHFTGVDYDALHN-ENGIVMILGDN 180

QY 185 KGW--DWEVDTEGNGYDLYMADIMDPHPEVNELRNWGWYVNTGLDGFRIADVKHK 242
Db 181 KGWASQENIDQENGNYDLYMADIDFKHPEVQEHLDWVAMFLETSGVGGRFLDAIKHD 240

QY 243 YSFTRDWINHVSATGKNMFAVAFKNDLGAIEYNLKNKNWNHVSFDPVPLHYNLYNASK 302
Db 241 KTFMAQPIRYIREHLKADLYVFGYWKDSHFDITDYLHSVDLQPDLLIDVMLHSLFPAQ 300

QY 303 SGGNYDMRQIPNGTVQRRPHMAVTFVDNHDSPPEEALESFVSEWFKPLAYALTLTREQ 362
Db 301 KGSDFDLSTILDDSLMSKSHDPFAVTFVDNHDSPQSGQALESTVAEWFKPLAYGLILLRQEG 360

QY 363 YPSVYGYDYGIP--THGVPAWMSKIDPILKARQKAYGRQNDYLDHNNIIGWTEGNTAH 421
Db 361 IPCVYGYDYGIGFEFAQESFQTLVDKLLYTRQHVYGSQEDYFDYANCIGWTCIGDEEH 420
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QY 422 PNSGLATIMSDGAGGNKWMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGSGSVI 481
Db 421 PD-GVAVIISNGEANGKRMNMGEFNRNKFVDYLNANCTEVEVILDDQGWGDFPQVQASLSA 479

QY 482 WYWK 485
Db 480 WYWK 483

RESULT 15
Q8EOM2 PRELIMINARY; PRT; 488 AA.
AC Q8EOM2;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Alpha amylase family protein.
GN SAG0708.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margalit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Pinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae."
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
DR EMBL: AG014223; AAM99595.1; -.
DR TIGR: SAG0708; -.
DR GO: GO:0004556; F:alpha-amylase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amyl_cat.
DR InterPro: IPR006589; Alp_amyl_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS: PR00110; ALPHAAMYLASE.
DR SMART: SM00642; Amy; 1.
DR Complete proteome.
SQ SEQUENCE 488 AA; 56555 MW; 57249E354B2F053E CRC64;

Query Match 48.3%; Score 1307.5; DB 16; Length 488;
Best Local Similarity 49.6%; Pred. No. 5.6e-74;
Matches 241; Conservative 81; Mismatches 155; Indels 9; Gaps 5;

QY 5 TNGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGYDLY 64
Db 2 TNELMQAFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGYDLY 61

QY 65 DLGEFNQKGTIRTKYGTNRQLQAQVNAKSNGLQVYGVDMVNHKGGADATEMVRVAVNP 124
Db 62 DLGEFNQKGTIRTKYGTNRQLQAQVNAKSNGLQVYGVDMVNHKGGADATEMVRVAVNP 121

QY 125 NNRRQVSGBYTTBAWTKFDPGGRGNTHSNFKRWYHFDGVDWDSQRKLNRR--IYKFRG 182
Db 122 ENRQEAISEPYELEGWTFQFPGRQDNYSDFKWHYHFTGVDYDALHN-ENGIVMILG 178

QY 183 DKGW--DWEVDTEGNGYDLYMADIMDPHPEVNELRNWGWYVNTGLDGFRIADVKHK 240
Db 179 DNKGWADDDLLIDDENGNYDLYMADIDFKHPEVQEHLDWVAMFLETSGVGGRFLDAVKH 238

QY 241 IKYSFTDWINHVSATGKNMFAVAFKNDLGAIEYNLKNKNWNHVSFDPVPLHYNLYN 300
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:12:34 ; Search time 15.0278 Seconds
(without alignments)
1666.155 Million cell updates/sec

Title: US-09-925-576C-12

Perfect score: 2708
Sequence: 1 HHNGTGTMMQYFEWLPND.....ADGNGFSVNGSGSVIWNK 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2708	100.0	485	4	US-09-290-734-24 Sequence 24, Appl
2	2708	100.0	485	4	US-09-290-734-26 Sequence 26, Appl
3	2708	100.0	485	4	US-09-417-359A-5 Sequence 5, Appl
4	2708	100.0	485	4	US-09-545-586-24 Sequence 24, Appl
5	2708	100.0	485	4	US-09-545-586-26 Sequence 26, Appl
6	2613	96.5	485	3	US-08-600-656-7 Sequence 7, Appl
7	2613	96.5	485	3	US-09-170-670-6 Sequence 6, Appl
8	2613	96.5	485	3	US-09-193-068-6 Sequence 6, Appl
9	2613	96.5	485	3	US-09-183-412-6 Sequence 6, Appl
10	2613	96.5	485	3	US-09-354-191A-7 Sequence 7, Appl
11	2613	96.5	485	4	US-09-291-023A-13 Sequence 13, Appl
12	2613	96.5	485	4	US-09-290-734-6 Sequence 6, Appl
13	2613	96.5	485	4	US-09-381-687-5 Sequence 5, Appl
14	2613	96.5	485	4	US-09-545-586-6 Sequence 6, Appl
15	2613	96.5	485	4	US-09-540-715A-13 Sequence 13, Appl
16	2613	96.5	485	4	US-09-769-864-6 Sequence 6, Appl
17	2437	90.0	485	2	US-08-446-803-2 Sequence 2, Appl
18	2437	90.0	485	2	US-08-861-837-2 Sequence 2, Appl
19	2437	90.0	485	3	US-08-600-656-2 Sequence 2, Appl
20	2437	90.0	485	3	US-09-170-670-2 Sequence 2, Appl
21	2437	90.0	485	3	US-09-170-670-8 Sequence 8, Appl
22	2437	90.0	485	3	US-09-193-068-2 Sequence 2, Appl
23	2437	90.0	485	3	US-09-193-068-8 Sequence 8, Appl
24	2437	90.0	485	3	US-09-183-412-2 Sequence 2, Appl
25	2437	90.0	485	3	US-09-183-412-8 Sequence 8, Appl
26	2437	90.0	485	3	US-09-284-097-5 Sequence 5, Appl
27	2437	90.0	485	3	US-09-354-191A-2 Sequence 2, Appl

Sequence 2, Appl
Sequence 8, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 8, Appl
Sequence 1, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 7, Appl
Sequence 1, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-290-734-24
; Sequence 24, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgaard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-290-734-24

Query Match	100.0%;	Score 2708;	DB 4;	Length 485;
Best Local Similarity	100.0%;	Pred. No. 6.4e-225;	Mismatches 0;	Indels 0;
Matches	485;	Conservative 0;	Gaps 0;	
Qy	1	HHNGTGTMMQYFEWLPNDGNEHNRRLSDASNLKDKGISAVMIPPAWKASQNDVGGA	60	
Db	1	HHNGTGTMMQYFEWLPNDGNEHNRRLSDASNLKDKGISAVMIPPAWKASQNDVGGA	60	
Qy	61	YDLYLGEFNGKQGTIRTKYGTNRQLQAANVNLKSGIQVYGVVMMHKGADATEMVRV	120	
Db	61	YDLYLGEFNGKQGTIRTKYGTNRQLQAANVNLKSGIQVYGVVMMHKGADATEMVRV	120	
Qy	121	EVNPNNEQSVGEYTIKATKDFPCGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF	180	
Db	121	EVNPNNEQSVGEYTIKATKDFPCGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF	180	
Qy	181	RGDGKGDWEDVTENGNDYLMYADIMDHPVVNLRNMGVWYNTLGLDGFDAVKH	240	
Db	181	RGDGKGDWEDVTENGNDYLMYADIMDHPVVNLRNMGVWYNTLGLDGFDAVKH	240	
Qy	241	IKYSFTRDWINHVRSAFGKMFVAEFAEKNDLGAIEYLNKTNHNSVDFVPLHYNLYNA	300	
Db	241	IKYSFTRDWINHVRSAFGKMFVAEFAEKNDLGAIEYLNKTNHNSVDFVPLHYNLYNA	300	
Qy	301	SKGGNGDMQIQIFNGTIVQRPHEAVTFVDNHSQPEALESFVEEFKPLAYALTITRE	360	
Db	301	SKGGNGDMQIQIFNGTIVQRPHEAVTFVDNHSQPEALESFVEEFKPLAYALTITRE	360	

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Db 301 SKSGGNYDMRQIFENGTVVQRHPMHA VTFVDNHD SQPEALESFVEBFWKPLAYALTLTRE 360
QY 361 QGYPSVFGDYGIPTHGVPAMKSKIDPIL EARKQYAYGRNDYLDHNNIIGTREGNTA 420
Db 361 QGYPSVFGDYGIPTHGVPAMKSKIDPIL EARKQYAYGRNDYLDHNNIIGTREGNTA 420
QY 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
QY 481 IWYNK 485
Db 481 IWYNK 485

RESULT 2
US-09-290-734-26
; Sequence 26, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Prantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el - Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-290-734-26

Query Match 100.0%; Score 2708; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 6.4e-225;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWYLPNDGNHNNLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Db 1 HNGTGTMMQYFEWYLPNDGNHNNLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYLGEFNQKGTIRTKYGTNRQLQAAVNALKNSGIIQYGVYVMMHKGADATEMVRV 120
Db 61 YDLYLGEFNQKGTIRTKYGTNRQLQAAVNALKNSGIIQYGVYVMMHKGADATEMVRV 120
QY 61 YDLYLGEFNQKGTIRTKYGTNRQLQAAVNALKNSGIIQYGVYVMMHKGADATEMVRV 120
Db 61 YDLYLGEFNQKGTIRTKYGTNRQLQAAVNALKNSGIIQYGVYVMMHKGADATEMVRV 120
QY 121 EVNPNRNQEVSGEYTI EAWTKFDFPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTI EAWTKFDFPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF 180
QY 181 RGDGKWDHEVDTENGNDYLYMADIDMDHPEVNNELRNWGVYTYNTLGLDGRIDAVKH 240
Db 181 RGDGKWDHEVDTENGNDYLYMADIDMDHPEVNNELRNWGVYTYNTLGLDGRIDAVKH 240
QY 241 IKYSFTRDWINHVR SATGKNMFVAFBFWKNDLGA IENYLKNTNWNHSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVR SATGKNMFVAFBFWKNDLGA IENYLKNTNWNHSVFDVPLHYNLYNA 300
QY 241 IKYSFTRDWINHVR SATGKNMFVAFBFWKNDLGA IENYLKNTNWNHSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVR SATGKNMFVAFBFWKNDLGA IENYLKNTNWNHSVFDVPLHYNLYNA 300
QY 301 SKSGGNYDMRQIFENGTVVQRHPMHA VTFVDNHD SQPEALESFVEBFWKPLAYALTLTRE 360
Db 301 SKSGGNYDMRQIFENGTVVQRHPMHA VTFVDNHD SQPEALESFVEBFWKPLAYALTLTRE 360
QY 361 QGYPSVFGDYGIPTHGVPAMKSKIDPIL EARKQYAYGRNDYLDHNNIIGTREGNTA 420
Db 361 QGYPSVFGDYGIPTHGVPAMKSKIDPIL EARKQYAYGRNDYLDHNNIIGTREGNTA 420
QY 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
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Db 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
QY 481 IWYNK 485
Db 481 IWYNK 485

RESULT 3
US-09-417-359A-5
; Sequence 5, Application US/09417359A
; Patent No. 6461849
; GENERAL INFORMATION:
; APPLICANT: Olsen, Arne Agerlin
; APPLICANT: Osten, Claus von der
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Ernst, Steffen
; APPLICANT: Roggen, Erwin Iudo
; TITLE OF INVENTION: A Modified Polypeptide
; FILE REFERENCE: 5666.200-US
; CURRENT APPLICATION NUMBER: US/09/417,359A
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: PA 1998 01301
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PA 1999 01418
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/105,624
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/157,426
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-417-359A-5

Query Match 100.0%; Score 2708; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 6.4e-225;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWYLPNDGNHNNLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Db 1 HNGTGTMMQYFEWYLPNDGNHNNLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYLGEFNQKGTIRTKYGTNRQLQAAVNALKNSGIIQYGVYVMMHKGADATEMVRV 120
Db 61 YDLYLGEFNQKGTIRTKYGTNRQLQAAVNALKNSGIIQYGVYVMMHKGADATEMVRV 120
QY 121 EVNPNRNQEVSGEYTI EAWTKFDFPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTI EAWTKFDFPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF 180
QY 181 RGDGKWDHEVDTENGNDYLYMADIDMDHPEVNNELRNWGVYTYNTLGLDGRIDAVKH 240
Db 181 RGDGKWDHEVDTENGNDYLYMADIDMDHPEVNNELRNWGVYTYNTLGLDGRIDAVKH 240
QY 241 IKYSFTRDWINHVR SATGKNMFVAFBFWKNDLGA IENYLKNTNWNHSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVR SATGKNMFVAFBFWKNDLGA IENYLKNTNWNHSVFDVPLHYNLYNA 300
QY 301 SKSGGNYDMRQIFENGTVVQRHPMHA VTFVDNHD SQPEALESFVEBFWKPLAYALTLTRE 360
Db 301 SKSGGNYDMRQIFENGTVVQRHPMHA VTFVDNHD SQPEALESFVEBFWKPLAYALTLTRE 360
QY 361 QGYPSVFGDYGIPTHGVPAMKSKIDPIL EARKQYAYGRNDYLDHNNIIGTREGNTA 420
Db 361 QGYPSVFGDYGIPTHGVPAMKSKIDPIL EARKQYAYGRNDYLDHNNIIGTREGNTA 420
QY 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
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Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 4

US-09-545-586-24
; Sequence 24, Application US/09545586
; Patent No. 6528298
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6528298e1 -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/545.586
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US/09/290.734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-545-586-24

Query Match 100.0%; Score 2708; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 6.4e-225;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMOYFEWYLPNDGNHNRLRSDASNLKDGISAVWIPPAWKASQNDVGGA 60
Db 1 HHNGTGTMOYFEWYLPNDGNHNRLRSDASNLKDGISAVWIPPAWKASQNDVGGA 60
Qy 61 YDLVGLGEFKQGTIRTKYGRNQLQAAVNALKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLVGLGEFKQGTIRTKYGRNQLQAAVNALKNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTTIEAWTKFDPGGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTIEAWTKFDPGGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Qy 181 RGDGKGWDWEVDTEGNGYDYLMYADIDMDHPEVVNLRNMGVWYNTLGLDGFPRIDAVKH 240
Db 181 RGDGKGWDWEVDTEGNGYDYLMYADIDMDHPEVVNLRNMGVWYNTLGLDGFPRIDAVKH 240
Qy 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLNKTNWNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLNKTNWNSVDFVPLHYNLYNA 300
Qy 301 SKSGNDYMRQIFNGTVVQRHPMAVTFVDNHDQPEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGNDYMRQIFNGTVVQRHPMAVTFVDNHDQPEALESFVEEWFKPLAYALTITRE 360
Qy 361 QGYPSVFYDYGIPTHGVPAWMSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYDYGIPTHGVPAWMSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGNKMFVGNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 5

US-09-545-586-26
; Sequence 26, Application US/09545586
; Patent No. 6528298
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6528298e1 -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/545.586
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US/09/290.734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-545-586-26

Query Match 100.0%; Score 2708; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 6.4e-225;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMOYFEWYLPNDGNHNRLRSDASNLKDGISAVWIPPAWKASQNDVGGA 60
Db 1 HHNGTGTMOYFEWYLPNDGNHNRLRSDASNLKDGISAVWIPPAWKASQNDVGGA 60
Qy 61 YDLVGLGEFKQGTIRTKYGRNQLQAAVNALKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLVGLGEFKQGTIRTKYGRNQLQAAVNALKNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTTIEAWTKFDPGGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTIEAWTKFDPGGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Qy 181 RGDGKGWDWEVDTEGNGYDYLMYADIDMDHPEVVNLRNMGVWYNTLGLDGFPRIDAVKH 240
Db 181 RGDGKGWDWEVDTEGNGYDYLMYADIDMDHPEVVNLRNMGVWYNTLGLDGFPRIDAVKH 240
Qy 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLNKTNWNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLNKTNWNSVDFVPLHYNLYNA 300
Qy 301 SKSGNDYMRQIFNGTVVQRHPMAVTFVDNHDQPEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGNDYMRQIFNGTVVQRHPMAVTFVDNHDQPEALESFVEEWFKPLAYALTITRE 360
Qy 361 QGYPSVFYDYGIPTHGVPAWMSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYDYGIPTHGVPAWMSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGNKMFVGNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 6

US-08-600-656-7
; Sequence 7, Application US/08600656
; Patent No. 6093562
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan

APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60935620 No. 60935620disk of No. 60935620th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,656
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-600-656-7

Query Match	96.5%;	Score 2613;	DB 3;	Length 485;	
Best Local Similarity	95.5%;	Pred. No. 9.7e-217;			
Matches 463;	Conservative 13;	Mismatches 9;	Indels 0;	Gaps 0;	
QY	1	HHNGTNGTMMQYFEWYLPNDGNHWRRLRS	DASNLKDKGISAVMT	PPPAWKASQNDVG	YGA 60
DB	1	HHNGTNGTMMQYFEWYLPNDGNHWRRLNS	DASNLKSGITAVMI	PPPAWKASQNDVG	YGA 60
QY	61	YDLYDLGEFNGKGTIRTKYGRNQLQAAVN	ALSKNSGIQVYGDVVMNHKGGADAT	EMTVRAV	120
DB	61	YDLYDLGEFNGKGTIRTKYGRSOLQAAV	TSLKNGIQVYGDVVMNHKGGADAT	EMTVRAV	120
QY	121	EVNPNNEQVSGEYTTIEMTKPDPGCRN	THSNFKRWTHFDGVDQSKLNNRIYK	PF 180	
DB	121	EVNPNNNEQVETGTYTTEMTTRFDP	PGCRNTHSSFKRWTHFDGVDQSRRLN	NNRIYKPF 180	
QY	181	RGDGKGDWEVDTENGNYDILMYADI	DMDHPEVVNELRNMGVYTTNLGLD	GPRIDAVKH	240
DB	181	RGHGKADWEVDTENGNYDILMYADI	DMDHPEVVNELRNMGVYTTNLGLD	GPRIDAVKH	240
QY	241	IKYSFTRDWINHVSATGKNMFAVAE	FWKNDLGAENYLNKTNHNSVDFVPL	HYNLNYA 300	
DB	241	IKYSFTRDWINHVSATGKNMFAVAE	FWKNDLGAENYLNKTNHNSVDFVPL	HYNLNYA 300	
QY	301	SKSGGNYDMRQIPIFNGTVVQRHP	MAVTFVDNHDSQPBEALESFVBE	FWFKPLAYALT	TRE 360
DB	301	SKSGGNYDMENIPIFNGTVVQRHP	SHAVTFVDNHDSQPBEALESFVBE	FWFKPLAYALT	TRE 360
QY	361	QGYPSPVGYDYGIPTHGVPAMKSKI	PIPILEARQYAYGRONDYLDHNNI	IIGWTR	REGNTA 420
DB	361	QGYPSPVGYDYGIPTHGVPAMRSKI	PIPILEARQYAYGKONDYLDHNNI	IIGWTR	REGNTA 420
QY	421	HPNSGLATIMSDGAGGNKWFVGRN	KAGQVWTDITGNRAGVT	TINADCGWGNF	SVNGSVS 480
DB	421	HPNSGLATIMSDGAGGKNWFVGRN	KAGQVWSDITGNRTGVT	TINADCGWGNF	SVNGSVS 480
QY	481	IWNK 485			

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Db          481  IWNK  485

RESULT 7
US-09-170-670-6
; Sequence 6, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-170-670-6

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Query Match	96.5%;	Score 2613;	DB 3;	Length 485;		
Best Local Similarity	95.5%;	Pred. No. 9.7e-217;				
Matches 463;	Conservative	13;	Mismatches 9;	Indels 0; Gaps 0;		
Qy	1	HHNGTNGTMOYFEWYLPNDGNHNRLRS	DASNLKDKGISAVMTT	PPAAWKASQNDVGYGA 60		
Db	1	HHNGTNGTMOYFEWYLPNDGNHNRLNS	DASNLKSKGITAVMTT	PPAAWKASQNDVGYGA 60		
Qy	61	YDYLDLGEFQKGTIRTKYGRNQLQA	AVNALKSNGIQVYGDVVMNHKGGADAT	EMVRV 120		
Db	61	YDYLDLGEFQKGTIRTKYGRS	QLQAAVTSLKNNGIQVYGDVVMNHKGGADAT	EMVRV 120		
Qy	121	EVAPNNRNQEVSGEYTTIEAMTK	DFPGRGNTHSNFKRWYHFDGVDWDQSRKLN	RIYKF 180		
Db	121	EVAPNNRNQEVSGEYTTIEAWTR	DFPGRGNTHSGFKRWYHFDGVDWDQSRRLN	RIYKF 180		
Qy	181	RGDGKGWDWEVDTENGNYDYL	MYADIMDHPVVVNLNRN	GVWYNTNTLGLDGFRIDAVKH 240		
Db	181	RGHGKAWDEVDTENGNYDYL	MYADIMDHPVVVNLNRN	GVWYNTNTLGLDGFRIDAVKH 240		
Qy	241	IKYSFTTRDWINHVR	SATGKNMFAVAEPWKNDL	GAIENLYLNKTNHNSVDFVPLHNYLNA 300		
Db	241	IKYSFTTRDWINHVR	SATGKNMFAVAEPWKNDL	GAIENLYLQKTNHNSVDFVPLHNYLNA 300		
Qy	301	SKSGCNTDMRQIFNGT	VVQRP	HMVATTVFDNHNDSQPEALESFVEEWF	KPLAYALTLTRE 360	
Db	301	SKSGCNTDMRNI	FNGT	VVQRP	SHAVTVFDNHNDSQPEALESFVEEWF	KPLAYALTLTRE 360
Qy	361	QGVPSPVGYGYGTP	HGVPAMKSDIP	ILEARQKAYGRQNDYLDHNI	IIGWTR	REGNTA 420
Db	361	QGVPSPVGYGYGTP	HGVPAMKSDIP	ILEARQKAYGRQNDYLDHNI	IIGWTR	REGNTA 420
Qy	421	HPNSGLATIMSDGAG	GKNKMFVGR	NKAGQVWTDITGNRAGT	VTVTINADG	WGNFVSNGGSGVS 480
Db	421	HPNSGLATIMSDGAG	GKWMFVGR	NKAGQVWSDITGNRTGT	VTVTINADG	WGNFVSNGGSGVS 480
Qy	481	IWNK 485				
Db	481	IWNK 485				

RESULT 8
US-09-193-068-6
; Sequence 6, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:

; APPLICANT: Svendsen, Allan
; APPLICANT: Kjruliff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-193-068-6

Query Match 96.5%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217; Indels 0; Gaps 0;
Matches 463; Conservative 13; Mismatches 9;
Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRLRSASNLKDKGISAIVWIPPAWKASQNDVGGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Qy 61 YDLGELFQKQRTIKYGTNRNLOAAVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLGELFQKQRTIKYGTNRNLOAAVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQSVSGEYTTIEATKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
Db 121 EVNPNRNQSVSGEYTTIEATKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
Qy 181 RGCKGWDWEVDYENGNDYLMYADIDMDHPEVVMNLRNNGVWYTNLTGLDGFRIIDAVKH 240
Db 181 RGCKGWDWEVDYENGNDYLMYADIDMDHPEVVMNLRNNGVWYTNLTGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRASATGKNMFAVAEFKNDLGAENLYLNKNTNNHSHVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRASATGKNMFAVAEFKNDLGAENLYLNKNTNNHSHVDFVPLHYNLYNA 300
Qy 301 SKSGGNDMEQIENGTVVQRPHPHVAFTVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
Db 301 SKSGGNDMEQIENGTVVQRPHPHVAFTVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
Qy 361 QGYPSVFYGYGYPHPTGVPAMSKIDPILAEARKYAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYGYGYPHPTGVPAMSKIDPILAEARKYAYGRQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKNMFMVGRNKAGQVWTDITGNRAGTGTITINADGWGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGKNMFMVGRNKAGQVWTDITGNRAGTGTITINADGWGNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 9

US-09-183-412-6
; Sequence 6, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaeruliff, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662

; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-183-412-6

Query Match 96.5%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217; Indels 0; Gaps 0;
Matches 463; Conservative 13; Mismatches 9;
Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRLRSASNLKDKGISAIVWIPPAWKASQNDVGGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Qy 61 YDLGELFQKQRTIKYGTNRNLOAAVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLGELFQKQRTIKYGTNRNLOAAVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQSVSGEYTTIEATKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
Db 121 EVNPNRNQSVSGEYTTIEATKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
Qy 181 RGCKGWDWEVDYENGNDYLMYADIDMDHPEVVMNLRNNGVWYTNLTGLDGFRIIDAVKH 240
Db 181 RGCKGWDWEVDYENGNDYLMYADIDMDHPEVVMNLRNNGVWYTNLTGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRASATGKNMFAVAEFKNDLGAENLYLNKNTNNHSHVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRASATGKNMFAVAEFKNDLGAENLYLNKNTNNHSHVDFVPLHYNLYNA 300
Qy 301 SKSGGNDMEQIENGTVVQRPHPHVAFTVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
Db 301 SKSGGNDMEQIENGTVVQRPHPHVAFTVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
Qy 361 QGYPSVFYGYGYPHPTGVPAMSKIDPILAEARKYAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYGYGYPHPTGVPAMSKIDPILAEARKYAYGRQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKNMFMVGRNKAGQVWTDITGNRAGTGTITINADGWGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGKNMFMVGRNKAGQVWTDITGNRAGTGTITINADGWGNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 10

US-09-354-191A-7
; Sequence 7, Application US/09354191A
; Patent No. 6297038
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6297038o No. 6297038disk of No. 6297038th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,191A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/600,656
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-354-191A-7

Query Match 96.5%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISA VMI PPAWKASQNDVGYGA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISA VMI PPAWKASQNDVGYGA 60

QY 61 YLDYDLGEFNGKGTIRTKYGTNRNQLQAANVAKSNGIQYGVGVMMHKGADATENVRAV 120
DB 61 YLDYDLGEFNGKGTIRTKYGTNRNQLQAANVAKSNGIQYGVGVMMHKGADATENVRAV 120

QY 121 EVNPNRNRQEVSGEYTIETAWTKFDPGGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
DB 121 EVNPNRNRQEVSGEYTIETAWTKFDPGGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180

QY 181 RGDGKGDWEVDTEGNGYDLYMADIDMDHPEVNVNELRWGVYNTLTGLDGFRI DAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNELRWGVYNTLTGLDGFRI DAVKH 240

QY 241 IKYSFTRDWINHVRSA TKGKMFVAFWKNDLGAIENYLNKTNWHSVFDVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSA TKGKMFVAFWKNDLGAIENYLNKTNWHSVFDVPLHYNLYNA 300

QY 301 SKSGGNYDMRQIFNGTVVQRHPMAVTFVDNHDSDPEEALSFVEEWFKPLAYALTITRE 360
DB 301 SKSGGNYDMRQIFNGTVVQRHPMAVTFVDNHDSDPEEALSFVEEWFKPLAYALTITRE 360

QY 361 QGYPSVFYGDYGYGIPTHGVPAMSKIDPILAEARQKYAYGRQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGYGIPTHGVPAMSKIDPILAEARQKYAYGRQNDYLDHNNIIGWTREGNTA 420

QY 421 HPNSGLATIMSDGAGGKMFVGRNKAQGVWSDITGNRAGTGTITNADGWNFSVNGSGVS 480
DB 421 HPNSGLATIMSDGAGGKMFVGRNKAQGVWSDITGNRAGTGTITNADGWNFSVNGSGVS 480

QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 11
US-09-291-023A-13
; Sequence 13, Application US/09291023A
; Patent No. 6309871

GENERAL INFORMATION:
APPLICANT: Outtrup, Helle
APPLICANT: Borchert, Torben
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Vibeke
APPLICANT: Hoeck, Lisbeth
TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic Acid
TITLE OF INVENTION: Encoding Same
FILE REFERENCE: 5821.010-US
CURRENT APPLICATION NUMBER: US/09/291,023A
CURRENT FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: DK 1999 00438
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patent In version 3.0
SEQ ID NO 13
LENGTH: 485
TYPE: PRT
ORGANISM: Bacillus
US-09-291-023A-13

Query Match 96.5%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISA VMI PPAWKASQNDVGYGA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISA VMI PPAWKASQNDVGYGA 60

QY 61 YLDYDLGEFNGKGTIRTKYGTNRNQLQAANVAKSNGIQYGVGVMMHKGADATENVRAV 120
DB 61 YLDYDLGEFNGKGTIRTKYGTNRNQLQAANVAKSNGIQYGVGVMMHKGADATENVRAV 120

QY 121 EVNPNRNRQEVSGEYTIETAWTKFDPGGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
DB 121 EVNPNRNRQEVSGEYTIETAWTKFDPGGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180

QY 181 RGDGKGDWEVDTEGNGYDLYMADIDMDHPEVNVNELRWGVYNTLTGLDGFRI DAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNELRWGVYNTLTGLDGFRI DAVKH 240

QY 241 IKYSFTRDWINHVRSA TKGKMFVAFWKNDLGAIENYLNKTNWHSVFDVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSA TKGKMFVAFWKNDLGAIENYLNKTNWHSVFDVPLHYNLYNA 300

QY 301 SKSGGNYDMRQIFNGTVVQRHPMAVTFVDNHDSDPEEALSFVEEWFKPLAYALTITRE 360
DB 301 SKSGGNYDMRQIFNGTVVQRHPMAVTFVDNHDSDPEEALSFVEEWFKPLAYALTITRE 360

QY 361 QGYPSVFYGDYGYGIPTHGVPAMSKIDPILAEARQKYAYGRQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGYGIPTHGVPAMSKIDPILAEARQKYAYGRQNDYLDHNNIIGWTREGNTA 420

QY 421 HPNSGLATIMSDGAGGKMFVGRNKAQGVWSDITGNRAGTGTITNADGWNFSVNGSGVS 480
DB 421 HPNSGLATIMSDGAGGKMFVGRNKAQGVWSDITGNRAGTGTITNADGWNFSVNGSGVS 480

QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 12
US-09-290-734-6
; Sequence 6, Application US/09290734
; Patent No. 6361989
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Biegaard-Frantzen Henrik
APPLICANT: Outtrup, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard

; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
; US-09-290-734-6

Query Match 96.5%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLSDASNLKDGISAVWTPPAWKGSQNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLSDASNLKDGISAVWTPPAWKGSQNDVGGA 60
Qy 61 YDLYLGEFNGKQIRTKYGTGRNLOQAANALKNGIOVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYLGEFNGKQIRTKYGTGRNLOQAANALKNGIOVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTTIEAWTKFDPGKGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTIEAWTKFDPGKGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
Qy 181 RGDCGKGDWEVDTEGNYDYLMYADIDMDHPEVNVNELRNWGVWYTNLTGLDGFRIIDAVKH 240
Db 181 RGDCGKGDWEVDTEGNYDYLMYADIDMDHPEVNVNELRNWGVWYTNLTGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNDLGAENYLNKTNHNSVDFVPLHVNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNDLGAENYLNKTNHNSVDFVPLHVNLYNA 300
Qy 301 SKSGNNDMRQIFNGTVVQRHPHMAVTFVDNHDSPPEEALSFVEEFKPLAYALTLTRE 360
Db 301 SKSGNNDMRQIFNGTVVQRHPHMAVTFVDNHDSPPEEALSFVEEFKPLAYALTLTRE 360
Qy 361 QGYPSVFGYDYGIPTHGVPAWMSKIDPILAEARQYAGRONDYLDHNNIIIGWTREGNTA 420
Db 361 QGYPSVFGYDYGIPTHGVPAWMSKIDPILAEARQYAGRONDYLDHNNIIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 13

US-09-381-687-5
; Sequence 5, Application US/09381687
; Patent No. 6486113
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yuji
; APPLICANT: IKAWA, Kaori
; APPLICANT: ITO, Susumu
; APPLICANT: IGARASHI, Kazuaki
; APPLICANT: HAGIHARA, Hiroshi
; APPLICANT: HAYASHI, Yasuhiro
; APPLICANT: ARAKI, Hiroyuki
; APPLICANT: OKAZAKI, Katsuya
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
; FILE REFERENCE: 2173-0115P
; CURRENT APPLICATION NUMBER: US/09/381,687
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp. #707
; US-09-381-687-5

Query Match 96.5%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLSDASNLKDGISAVWTPPAWKGSQNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLSDASNLKDGISAVWTPPAWKGSQNDVGGA 60
Qy 61 YDLYLGEFNGKQIRTKYGTGRNLOQAANALKNGIOVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYLGEFNGKQIRTKYGTGRNLOQAANALKNGIOVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTTIEAWTKFDPGKGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTIEAWTKFDPGKGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
Qy 181 RGDCGKGDWEVDTEGNYDYLMYADIDMDHPEVNVNELRNWGVWYTNLTGLDGFRIIDAVKH 240
Db 181 RGDCGKGDWEVDTEGNYDYLMYADIDMDHPEVNVNELRNWGVWYTNLTGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNDLGAENYLNKTNHNSVDFVPLHVNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNDLGAENYLNKTNHNSVDFVPLHVNLYNA 300
Qy 301 SKSGNNDMRQIFNGTVVQRHPHMAVTFVDNHDSPPEEALSFVEEFKPLAYALTLTRE 360
Db 301 SKSGNNDMRQIFNGTVVQRHPHMAVTFVDNHDSPPEEALSFVEEFKPLAYALTLTRE 360
Qy 361 QGYPSVFGYDYGIPTHGVPAWMSKIDPILAEARQYAGRONDYLDHNNIIIGWTREGNTA 420
Db 361 QGYPSVFGYDYGIPTHGVPAWMSKIDPILAEARQYAGRONDYLDHNNIIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 14

US-09-545-586-6
; Sequence 6, Application US/09545586
; Patent No. 6528298
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgaard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6528298el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/545,586
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
; US-09-545-586-6

Query Match 96.5%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRSDASNLKDKGISAVWIPPAAWKASQNDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGITAVWIPPAAWKASQNDVGYGA 60

QY 61 YDLYDLGEFNGKGTIRTKYGTNRNQLAAVNAALNSNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLYDLGEFNGKGTIRTKYGTNRNQLAAVNAALNSNGIQVYGDVVMNHKGGADATEMVRV 120

QY 121 EVNPNNRNQSVGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
DB 121 EVNPNNRNQSVGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180

QY 181 RGDGKGDWEVDTEGNGYDLYMADIDMDHPVNVNLRNMGVYNTLGLDGFRIIDAVKH 240
DB 181 RGDGKGDWEVDTEGNGYDLYMADIDMDHPVNVNLRNMGVYNTLGLDGFRIIDAVKH 240

QY 241 IKYSFTRDWINHVRSATGKNMFVAFWKNDLGAIENYLNKTNWNHNSVFDVPLHYNLYNA 300
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DB 301 SKSGGNYDMRQIFNGTVVQRHPMHAVTFVDNHDSPPEALESFVEEWFKPLAYALTLTRE 360

QY 361 QGYPSVFGDYGYGIPTHGVPAKSKIDPILKARQKAYAGQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFGDYGYGIPTHGVPAKSKIDPILKARQKAYAGQNDYLDHNNIIGWTREGNTA 420

QY 421 HPNSGLATIMSDGAGGKMMFVGRNKGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGKMMFVGRNKGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480

QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 15
US-09-540-715A-13
; Sequence 13, Application US/09540715A
; Patent No. 6623948
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/540, 715A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/291,023
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-09-540-715A-13

Query Match 96.5%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRSDASNLKDKGISAVWIPPAAWKASQNDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGITAVWIPPAAWKASQNDVGYGA 60

QY 61 YDLYDLGEFNGKGTIRTKYGTNRNQLAAVNAALNSNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLYDLGEFNGKGTIRTKYGTNRNQLAAVNAALNSNGIQVYGDVVMNHKGGADATEMVRV 120

QY 121 EVNPNNRNQSVGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
DB 121 EVNPNNRNQSVGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180

QY 181 RGDGKGDWEVDTEGNGYDLYMADIDMDHPVNVNLRNMGVYNTLGLDGFRIIDAVKH 240
DB 181 RGDGKGDWEVDTEGNGYDLYMADIDMDHPVNVNLRNMGVYNTLGLDGFRIIDAVKH 240

QY 241 IKYSFTRDWINHVRSATGKNMFVAFWKNDLGAIENYLNKTNWNHNSVFDVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSATGKNMFVAFWKNDLGAIENYLNKTNWNHNSVFDVPLHYNLYNA 300

QY 301 SKSGGNYDMRQIFNGTVVQRHPMHAVTFVDNHDSPPEALESFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRQIFNGTVVQRHPMHAVTFVDNHDSPPEALESFVEEWFKPLAYALTLTRE 360

QY 361 QGYPSVFGDYGYGIPTHGVPAKSKIDPILKARQKAYAGQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFGDYGYGIPTHGVPAKSKIDPILKARQKAYAGQNDYLDHNNIIGWTREGNTA 420

QY 421 HPNSGLATIMSDGAGGKMMFVGRNKGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGKMMFVGRNKGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480

QY 481 IWVWK 485
DB 481 IWVWK 485

Search completed: October 7, 2004, 00:47:13
Job time : 16.0278 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:19:14 ; Search time 53.4478 Seconds
(without alignments)
2920.093 Million cell updates/sec

Title: US-09-925-576C-12

Perfect score: 2708

Sequence: 1 HHNGTGTMMQYFEWYLPND.....ADGWNFSVNGSGSVIWNK 485

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Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2708	100.0	485	9	US-09-854-346-12
2	2708	100.0	485	9	US-09-918-543-12
3	2708	100.0	485	10	US-09-925-576C-12
4	2708	100.0	485	12	US-10-327-837-24
5	2708	100.0	485	12	US-10-327-837-26
6	2708	100.0	485	14	US-10-209-812-5
7	2708	100.0	485	16	US-10-477-725-12
8	2613	96.5	485	9	US-09-769-864-6
9	2613	96.5	485	9	US-09-854-346-13
10	2613	96.5	485	10	US-09-902-188A-7
11	2613	96.5	485	10	US-09-925-576C-13
12	2613	96.5	485	12	US-10-665-667-6
13	2613	96.5	485	12	US-10-025-648-7
14	2613	96.5	485	12	US-10-327-837-6
15	2613	96.5	485	16	US-10-477-725-13

16	2596	95.9	516	16	US-10-343-212-2	Sequence 2, Appli
17	2437	90.0	485	9	US-09-769-864-2	Sequence 2, Appli
18	2437	90.0	485	9	US-09-769-864-8	Sequence 8, Appli
19	2437	90.0	485	9	US-09-854-346-4	Sequence 4, Appli
20	2437	90.0	485	9	US-09-902-188A-2	Sequence 2, Appli
21	2437	90.0	485	9	US-09-918-543-4	Sequence 4, Appli
22	2437	90.0	485	9	US-09-795-211-2	Sequence 2, Appli
23	2437	90.0	485	10	US-09-925-576C-4	Sequence 4, Appli
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25	2437	90.0	485	12	US-10-665-667-8	Sequence 8, Appli
26	2437	90.0	485	12	US-10-025-648-2	Sequence 2, Appli
27	2437	90.0	485	12	US-10-327-837-2	Sequence 2, Appli
28	2437	90.0	485	12	US-10-327-837-8	Sequence 8, Appli
29	2437	90.0	485	16	US-10-477-725-4	Sequence 4, Appli
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31	2429	89.7	485	9	US-09-769-864-7	Sequence 7, Appli
32	2429	89.7	485	9	US-09-854-346-2	Sequence 2, Appli
33	2429	89.7	485	9	US-09-902-188A-1	Sequence 1, Appli
34	2429	89.7	485	9	US-09-918-543-2	Sequence 2, Appli
35	2429	89.7	485	9	US-09-795-211-1	Sequence 1, Appli
36	2429	89.7	485	10	US-09-925-576C-2	Sequence 2, Appli
37	2429	89.7	485	12	US-10-665-667-1	Sequence 1, Appli
38	2429	89.7	485	12	US-10-665-667-7	Sequence 7, Appli
39	2429	89.7	485	12	US-10-025-648-1	Sequence 1, Appli
40	2429	89.7	485	12	US-10-327-837-1	Sequence 1, Appli
41	2429	89.7	485	12	US-10-327-837-7	Sequence 7, Appli
42	2429	89.7	485	14	US-10-184-771-12	Sequence 12, Appli
43	2429	89.7	485	16	US-10-477-725-2	Sequence 2, Appli
44	2409	89.0	516	9	US-09-986-676A-2	Sequence 2, Appli
45	2409	89.0	516	9	US-09-971-611-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-854-346-12
; Sequence 12, Application US/09854346
; Patent No. US20020068352A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020068352Alozymes A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Jorgensen, Christel Thea
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
; FILE REFERENCE: 6140.200-US
; CURRENT APPLICATION NUMBER: US/09/854,346
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-854-346-12

Query Match		100.0%;	Score 2708;	DB 9;	Length 485;
Best Local Similarity		100.0%;	Pred. No. 1e-242;		
Matches 485;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	HHNGTGTMMQYFEWYLPNDGHNHNR	LSRSDASNLKDGISAVMIPPAWK	GASQNDVGYGA	60
Qy	61	YDLYDLGEFQKQRTIRTKYGTNRQ	LQAANVNAKLSNGIQYGVVVMNH	KGGADATEMVR	120
Db	61	YDLYDLGEFQKQRTIRTKYGTNRQ	LQAANVNAKLSNGIQYGVVVMNH	KGGADATEMVR	120
Qy	121	EVNPNRNRQVSGEYTIETAWTKFDF	PGRGNTNHNFKRWTHFGVDQSK	LNNRIYKF	180
Db	121	EVNPNRNRQVSGEYTIETAWTKFDF	PGRGNTNHNFKRWTHFGVDQSK	LNNRIYKF	180
Qy	181	RGDGKGHDEVDYENGNYDYLMYAD	IDMDHPEVNVNELRNWGVYNTLT	LGLDGFDAVKH	240

Db 181 RGDGKGDWEVDYDTEGNYDYLMDADIMDHDPVNVNELRWGVTNTLGLDGFRIIDAVKH 240
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Db 241 IKYSFTRDWINHVRSAATGKMFVAEFAWKNDLGAIEYLNKTNWNHVSFVDFPLHYNLYNA 300
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Db 301 SKSGGNDYMDROIENGTVVQRHPHMAVTFVDNHDSDPEEALSFVEEWFKPLAYALTITRE 360
Qy 361 QGYPSPFYGDYIGIPTHGVPAKMSKIDPILFARQKYAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSPFYGDYIGIPTHGVPAKMSKIDPILFARQKYAYGRQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGNKMFVGRNKAQGVWTDITGNRAGTVTTINADGNGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGRNKAQGVWTDITGNRAGTVTTINADGNGNFSVNGGSVS 480
Qy 481 IWYWK 485
Db 481 IWYWK 485

RESULT 2
US-09-918-543-12
; Sequence 12, Application US/09918543
; Patent No. US2002015574A1
; GENERAL INFORMATION:
; APPLICANT: No. US2002015574A1ozymes A/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kjaerulff, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fuglsang, Claus Crone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062 200-US
; CURRENT APPLICATION NUMBER: US/09/918,543
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-918-543-12

Query Match 100.0%; Score 2708; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Qy 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQVSGEYITIAWTKFDPPGRGNTHSNFKRWYHFDGVDWDQSRKLNNRIYKF 180
Db 121 EVNPNRNQVSGEYITIAWTKFDPPGRGNTHSNFKRWYHFDGVDWDQSRKLNNRIYKF 180
Qy 181 RGDGKGDWEVDTEGNYDYLMDADIMDHDPVNVNELRWGVTNTLGLDGFRIIDAVKH 240
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Qy 241 IKYSFTRDWINHVRSAATGKMFVAEFAWKNDLGAIEYLNKTNWNHVSFVDFPLHYNLYNA 300
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Db 301 SKSGGNDYMDROIENGTVVQRHPHMAVTFVDNHDSDPEEALSFVEEWFKPLAYALTITRE 360
Qy 361 QGYPSPFYGDYIGIPTHGVPAKMSKIDPILFARQKYAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 RGDGKGDWEVDTEGNYDYLMDADIMDHDPVNVNELRWGVTNTLGLDGFRIIDAVKH 240
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Qy 481 IWYWK 485
Db 481 IWYWK 485

RESULT 3
US-09-925-576C-12
; Sequence 12, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004 204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-925-576C-12

Query Match 100.0%; Score 2708; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Qy 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQVSGEYITIAWTKFDPPGRGNTHSNFKRWYHFDGVDWDQSRKLNNRIYKF 180
Db 121 EVNPNRNQVSGEYITIAWTKFDPPGRGNTHSNFKRWYHFDGVDWDQSRKLNNRIYKF 180
Qy 181 RGDGKGDWEVDTEGNYDYLMDADIMDHDPVNVNELRWGVTNTLGLDGFRIIDAVKH 240
Db 181 RGDGKGDWEVDTEGNYDYLMDADIMDHDPVNVNELRWGVTNTLGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKMFVAEFAWKNDLGAIEYLNKTNWNHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKMFVAEFAWKNDLGAIEYLNKTNWNHVSFVDFPLHYNLYNA 300
Qy 301 SKSGGNDYMDROIENGTVVQRHPHMAVTFVDNHDSDPEEALSFVEEWFKPLAYALTITRE 360
Db 301 SKSGGNDYMDROIENGTVVQRHPHMAVTFVDNHDSDPEEALSFVEEWFKPLAYALTITRE 360
Qy 361 QGYPSPFYGDYIGIPTHGVPAKMSKIDPILFARQKYAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSPFYGDYIGIPTHGVPAKMSKIDPILFARQKYAYGRQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGNKMFVGRNKAQGVWTDITGNRAGTVTTINADGNGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGRNKAQGVWTDITGNRAGTVTTINADGNGNFSVNGGSVS 480
Qy 481 IWYWK 485
Db 481 IWYWK 485

RESULT 4

US-10-327-837-24
; Sequence 24, Application US/10327837
; Publication No. US20030211958A1

GENERAL INFORMATION:

; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hock, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-24

Query Match 100.0%; Score 2708; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HHNGTGTMMQYFEWYLPNDGNHNRLRSASNLKDKGISAVWIPPAWKASQNDVG	60
Db	1	HHNGTGTMMQYFEWYLPNDGNHNRLRSASNLKDKGISAVWIPPAWKASQNDVG	60
Qy	61	YDLVDFEFGKGTIRTKYGTNRNQLQAAVNAKLSNGIQVYGDVVMNHKGGADATEM	120
Db	61	YDLVDFEFGKGTIRTKYGTNRNQLQAAVNAKLSNGIQVYGDVVMNHKGGADATEM	120
Qy	121	EVNPNRNQEVSGEYTTTEAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF	180
Db	121	EVNPNRNQEVSGEYTTTEAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF	180
Qy	181	RGDKGMDWEVDTEGNYDYLMAADIDMDHPEVNVNLRNMGVWYTTNTLGLDGFRI	240
Db	181	RGDKGMDWEVDTEGNYDYLMAADIDMDHPEVNVNLRNMGVWYTTNTLGLDGFRI	240
Qy	241	IKYSFTRDWINHVSATGKNMFAVAEFKNDLGAENYLNKTNWNSHVSFVPLHYNLYNA	300
Db	241	IKYSFTRDWINHVSATGKNMFAVAEFKNDLGAENYLNKTNWNSHVSFVPLHYNLYNA	300
Qy	301	SKSGNVDMRQIFNGTVVQRHPMAVTFVDNHDSPQBEALESFVEEWFKPLAYALTRE	360
Db	301	SKSGNVDMRQIFNGTVVQRHPMAVTFVDNHDSPQBEALESFVEEWFKPLAYALTRE	360
Qy	361	QGYPSVFGDYGIPTHTGVPAKSKIDPILAEAROKYAGRONDYLDHNNIIGWTR	420
Db	361	QGYPSVFGDYGIPTHTGVPAKSKIDPILAEAROKYAGRONDYLDHNNIIGWTR	420
Qy	421	HPNSGLATIMSDGAGGNKMFVGRNKGAGQVWTDITGNRAGVTITNADGWGNFS	480
Db	421	HPNSGLATIMSDGAGGNKMFVGRNKGAGQVWTDITGNRAGVTITNADGWGNFS	480
Qy	481	IWNK 485	
Db	481	IWNK 485	

RESULT 5

US-10-327-837-26
; Sequence 26, Application US/10327837
; Publication No. US20030211958A1

GENERAL INFORMATION:

; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hock, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-26

Query Match 100.0%; Score 2708; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HHNGTGTMMQYFEWYLPNDGNHNRLRSASNLKDKGISAVWIPPAWKASQNDVG	60
Db	1	HHNGTGTMMQYFEWYLPNDGNHNRLRSASNLKDKGISAVWIPPAWKASQNDVG	60
Qy	61	YDLVDFEFGKGTIRTKYGTNRNQLQAAVNAKLSNGIQVYGDVVMNHKGGADATEM	120
Db	61	YDLVDFEFGKGTIRTKYGTNRNQLQAAVNAKLSNGIQVYGDVVMNHKGGADATEM	120
Qy	121	EVNPNRNQEVSGEYTTTEAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF	180
Db	121	EVNPNRNQEVSGEYTTTEAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF	180
Qy	181	RGDKGMDWEVDTEGNYDYLMAADIDMDHPEVNVNLRNMGVWYTTNTLGLDGFRI	240
Db	181	RGDKGMDWEVDTEGNYDYLMAADIDMDHPEVNVNLRNMGVWYTTNTLGLDGFRI	240
Qy	241	IKYSFTRDWINHVSATGKNMFAVAEFKNDLGAENYLNKTNWNSHVSFVPLHYNLYNA	300
Db	241	IKYSFTRDWINHVSATGKNMFAVAEFKNDLGAENYLNKTNWNSHVSFVPLHYNLYNA	300
Qy	301	SKSGNVDMRQIFNGTVVQRHPMAVTFVDNHDSPQBEALESFVEEWFKPLAYALTRE	360
Db	301	SKSGNVDMRQIFNGTVVQRHPMAVTFVDNHDSPQBEALESFVEEWFKPLAYALTRE	360
Qy	361	QGYPSVFGDYGIPTHTGVPAKSKIDPILAEAROKYAGRONDYLDHNNIIGWTR	420
Db	361	QGYPSVFGDYGIPTHTGVPAKSKIDPILAEAROKYAGRONDYLDHNNIIGWTR	420
Qy	421	HPNSGLATIMSDGAGGNKMFVGRNKGAGQVWTDITGNRAGVTITNADGWGNFS	480
Db	421	HPNSGLATIMSDGAGGNKMFVGRNKGAGQVWTDITGNRAGVTITNADGWGNFS	480
Qy	481	IWNK 485	
Db	481	IWNK 485	

RESULT 6

US-10-209-812-5
; Sequence 5, Application US/10209812
; Publication No. US20030087785A1

GENERAL INFORMATION:

; APPLICANT: Olsen, Arne Agerlin
; APPLICANT: Osten, Claus von der
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Ernst, Steffen
; APPLICANT: Roggen, Erwin Ludo


```
; TITLE OF INVENTION: A Modified Polypeptide
; FILE REFERENCE: 5666.200-US
; CURRENT APPLICATION NUMBER: US/10/209,812
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/417,359
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: PA 1998 01301
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PA 1999 01418
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/105,624
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/157,426
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
; US-10-209-812-5

Query Match      100.0%; Score 2708; DB 14; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKGASQNDVGYGA 60
Db      1  HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKGASQNDVGYGA 60
Qy      61  YDLYLGEFNGKGTIRTKYGTNRQLQAAVNALKSNGIQVYGDVVMNHKGGADATEMVRV 120
Db      61  YDLYLGEFNGKGTIRTKYGTNRQLQAAVNALKSNGIQVYGDVVMNHKGGADATEMVRV 120
Qy      121  EVNPNRNQEVSGEYTTIAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Db      121  EVNPNRNQEVSGEYTTIAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Qy      181  RGDKGWDWEVDTEGNGYDLYMADIDMDHPVVNLRNNGVWYNTLGLDGRIDAVKH 240
Db      181  RGDKGWDWEVDTEGNGYDLYMADIDMDHPVVNLRNNGVWYNTLGLDGRIDAVKH 240
Qy      241  IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAIENTYLNKTNWNHVSFVDFVPLHYNLYNA 300
Db      241  IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAIENTYLNKTNWNHVSFVDFVPLHYNLYNA 300
Qy      301  SKSGGNDMRQIFNGTVVQRHPMHAFTFVDNHDSDPEEALSFVEEWFKPLAYALTIRE 360
Db      301  SKSGGNDMRQIFNGTVVQRHPMHAFTFVDNHDSDPEEALSFVEEWFKPLAYALTIRE 360
Qy      361  QGYPSVFYGYGIPTHGVPAMKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Db      361  QGYPSVFYGYGIPTHGVPAMKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Qy      421  HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Db      421  HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Qy      481  IWVWK 485
Db      481  IWVWK 485

RESULT 7
; US-10-477-725-12
; Sequence 12, Application US/10477725
; Publication No. US20040096952A1
; GENERAL INFORMATION:
; APPLICANT: NOVOZYMES A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Thisted, Thomas
; APPLICANT: von der Osten, Claus
```

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; TITLE OF INVENTION: Alpha-amylase variant with altered properties
; FILE REFERENCE: 10182.204-US
; CURRENT APPLICATION NUMBER: US/10/477,725
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
; US-10-477-725-12

Query Match      100.0%; Score 2708; DB 16; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKGASQNDVGYGA 60
Db      1  HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKGASQNDVGYGA 60
Qy      61  YDLYLGEFNGKGTIRTKYGTNRQLQAAVNALKSNGIQVYGDVVMNHKGGADATEMVRV 120
Db      61  YDLYLGEFNGKGTIRTKYGTNRQLQAAVNALKSNGIQVYGDVVMNHKGGADATEMVRV 120
Qy      121  EVNPNRNQEVSGEYTTIAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Db      121  EVNPNRNQEVSGEYTTIAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Qy      181  RGDKGWDWEVDTEGNGYDLYMADIDMDHPVVNLRNNGVWYNTLGLDGRIDAVKH 240
Db      181  RGDKGWDWEVDTEGNGYDLYMADIDMDHPVVNLRNNGVWYNTLGLDGRIDAVKH 240
Qy      241  IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAIENTYLNKTNWNHVSFVDFVPLHYNLYNA 300
Db      241  IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAIENTYLNKTNWNHVSFVDFVPLHYNLYNA 300
Qy      301  SKSGGNDMRQIFNGTVVQRHPMHAFTFVDNHDSDPEEALSFVEEWFKPLAYALTIRE 360
Db      301  SKSGGNDMRQIFNGTVVQRHPMHAFTFVDNHDSDPEEALSFVEEWFKPLAYALTIRE 360
Qy      361  QGYPSVFYGYGIPTHGVPAMKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Db      361  QGYPSVFYGYGIPTHGVPAMKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Qy      421  HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Db      421  HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Qy      481  IWVWK 485
Db      481  IWVWK 485

RESULT 8
; US-09-769-864-6
; Sequence 6, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 6
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